(12) INTERNATIONAL APPLICATION PUBLISHED UNDER THE PATENT COOPERATION TREATY (PCT)

(19) World Intellectual Property Organization
International Bureau

(43) International Publication Date
6 May 2004 (06.05.2004)

PCT

(10) International Publication Number
WO 2004/038655 A2

(51) International Patent Classification[7]: G06N 3/00

(21) International Application Number:
PCT/IB2003/005134

(22) International Filing Date: 28 October 2003 (28.10.2003)

(25) Filing Language: English

(26) Publication Language: English

(30) Priority Data:
60/421,569 28 October 2002 (28.10.2002) US

(71) Applicants *(for all designated States except US)*: **COMMISSARIAT A L'ENERGIE ATOMIQUE** [FR/FR]; 31-33, rue de la Fédération, F-75015 Paris (FR). **CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (C.N.R.S.)** [FR/FR]; 3, rue Michel Ange, F-75794 Paris (FR).

(72) Inventors; and

(75) Inventors/Applicants *(for US only)*: **ANDRE, François** [FR/FR]; 20, rue du Petit Pont, F-78180 Montigny-Le-Bretonneux (FR). **DELAFORGE, Marcel** [FR/FR]; 26, rue Henri Rochefort, F-91000 Evry (FR). **LOISEAU, Nicolas** [FR/FR]; Résidence Les Oliviers, 5, avenue des Marots, F-31770 Colomiers (FR).

(74) Agents: **MARTIN, Jean-Jacques** et al.; Cabinet Regimbeau, 20, rue de Chazelles, F-75847 Paris Cedex 17 (FR).

(81) Designated States *(national)*: AE, AG, AL, AM, AT, AU, AZ, BA, BB, BG, BR, BY, BZ, CA, CH, CN, CO, CR, CU, CZ, DE, DK, DM, DZ, EC, EE, EG, ES, FI, GB, GD, GE, GH, GM, HR, HU, ID, IL, IN, IS, JP, KE, KG, KP, KR, KZ, LC, LK, LR, LS, LT, LU, LV, MA, MD, MG, MK, MN, MW, MX, MZ, NI, NO, NZ, OM, PG, PH, PL, PT, RO, RU, SC, SD, SE, SG, SK, SL, SY, TJ, TM, TN, TR, TT, TZ, UA, UG, US, UZ, VC, VN, YU, ZA, ZM, ZW.

(84) Designated States *(regional)*: ARIPO patent (GH, GM, KE, LS, MW, MZ, SD, SL, SZ, TZ, UG, ZM, ZW), Eurasian patent (AM, AZ, BY, KG, KZ, MD, RU, TJ, TM), European patent (AT, BE, BG, CH, CY, CZ, DE, DK, EE, ES, FI, FR, GB, GR, HU, IE, IT, LU, MC, NL, PT, RO, SE, SI, SK, TR), OAPI patent (BF, BJ, CF, CG, CI, CM, GA, GN, GQ, GW, ML, MR, NE, SN, TD, TG).

Declaration under Rule 4.17:
— *of inventorship (Rule 4.17(iv)) for US only*

Published:
— *without international search report and to be republished upon receipt of that report*

For two-letter codes and other abbreviations, refer to the "Guidance Notes on Codes and Abbreviations" appearing at the beginning of each regular issue of the PCT Gazette.

(54) Title: A METHOD FOR PERFORMING RESTRAINED DYNAMICS DOCKING OF ONE OR MULTIPLE SUBSTRATES ON MULTI-SPECIFIC ENZYMES

(57) Abstract: The present invention relates to a method for performing restrained dynamics docking of one or several substrates having allosteric or synergistic effect on enzymes presenting multipspecific and flexible active site. It also concerns a method for determining the 3D-substrates, which is the case for multispecific enzymes such as cytochrome P450, and specifically to cytochrome P450 3A4 and P450 3A7.

WO 2004/038655 A2

A method for performing restrained dynamics docking of one or multiple substrates on multi-specific enzymes

The present invention relates to a method for performing restrained dynamics docking of one or several substrates having allosteric or synergistic effect on enzymes presenting multispecific and flexible active site. It also concerns a method for determining the 3D-structure of active sites that are flexible and can adapt to different substrates, which is the case for multispecific enzymes such as cytochrome P450.

As of today, various computer graphics systems allow to generate molecular models of large molecules such as proteins from the PDB structural data obtained using X-ray crystallography and NMR. We can cite for example MODELLER, COMPOSER, MATCHMAKER (Tripos), or 3D graphical environments for molecular modeling such as SYBYL (Tripos) or INSIGHT II (Accelrys).

Substrates as well as inhibitors or agonists often act by binding to particular regions of an enzyme or receptor referred as the active site. In industry, the purpose of using these 3D models is to assess the main features of the molecules which are involved in the binding to the active site. New molecules that fit the active site can be designed.

Biological interactions are not possible without flexibility and motion. One of the principal tools in the theoretical study of motion in biological molecules is the method of molecular dynamics simulations (MD). This computational method calculates the time dependent behavior of a molecular system (Karplus and McCammon, 2002). MD simulations have provided detailed information on the fluctuations and conformational changes of proteins and nucleic acids. These methods are now routinely used to investigate the structure, dynamics and thermodynamics of biological molecules and their complexes. They are also used in the determination of structures from x-ray crystallography and from NMR experiments. The molecular dynamics simulations can be used to recreate the successive events in the binding process of a molecule, and thermodynamic parameters implicated in such process can therefore be derived, which is of great interest in the design of active molecules.

Nevertheless, the methods proposed in the art are based on a relatively low level of calculations of few parameters. It relies only on the molecule energy constrained with a fixed geometry. It relies only on the interaction energy between the molecule and the active site frozen in a fixed geometry.

Consequently, there is a need for a model replicating *in silico* the natural process of molecular interactions.

The method according to the invention provides both minimizations and molecular dynamics calculations. More specifically, it provides a new approach which is more appropriate to flexible structures, hereafter referred as "restrained dynamics docking" or "soft-restrained restrained dynamics docking". This technique employs constrained dynamics simulations, where the only constraints are active site-substrate distances.

For example, to explain and predict drug metabolism in organisms, in which the cytochrome P450 (CYP) superfamily of haem-thiolate enzymes plays a central role, it is of large interest to dispose of a molecular picture of the binding sites responsible for the biotransformation. Efficiency of the prediction is then directly related to the molecular precision of the model, which resolution must be obtained at the atomic level to exploit the model for further docking studies.

In mammalian, hepatic cytochrome P450s constitute the major enzymes involved in the metabolism of exogenic compounds. Among them, isozymes of the CYP3 family (such as CYP3A1 and 3A2 in rat, and CYP3A4, CYP3A5, CYP3A7, CYP 3A43 in human) are known to metabolize the majority of drugs in clinical use. These are multi-specific enzymes, able to metabolize a large variety of structurally diverse chemicals or substrates including steroids, linear or cyclized peptides (Delaforge et al. 1997, Delaforge et al. 2001, Aninat et al. 2001), generally fairly lipophilic, within a broad range of molecular sizes from testosterone (Mw 288) to cyclosporin A (Mw 1203).

The inventory of known substrates for CYP 3A contains a large variety of different molecules having apparently no common structural factors. Actually it can be estimated that more than five hundred utilized drugs can be recognized and metabolized by CYP 3A (Guengerich 1995, Wrighton et al. 2000, Lewis 2001). Closer inspection of the precise transformations catalyzed by CYP 3A indicates that there is an important regio- and stereo-selectivity for each substrate. The active site

can accommodate relatively rigid substrates such as aflatoxin derivatives or steroids, that are oxidized almost exclusively at a precise position. Thus CYP 3A4 catalyzes the testosterone oxidation exclusively at the 6β position, whereas CYP 3A7 oxidizes dehydroepiandrosterone (DHEA) or its 3 sulfate conjugate exclusively on the 16α position (see Figures 4A and 4B). In addition to such small substrates, CYP 3A metabolize also large molecules such as cyclosporin A (MW 1202), macrolide antibiotics (MW around 600) or ergot derivatives (MW from 500 to 700).

The recognized substrates can have endogenous origin such as steroids or can be drugs or compounds found in food. For example, grapefruit juice contains bergamottin derivatives having specific CYP 3A inhibitory activities (Schmiedlin-Ren et al. 1997). Linear peptides (Delaforge et al. 2001, Hosea et al. 2000) or cyclized peptides (Delaforge et al. 1997) containing from 2 aminoacids (called diketopiperazine, Delaforge et al. 2001, Aninat et al. 2001) to 11 amino-acids (*e.g.* cyclosporin) are also recognized.

Following this wide range substrate recognition, a tentative subclassification was established leading to a multi-site hypothesis (Hosea et al. 2000, Ekins et al. 2003) consisting of at least 2 or 3 binding zones in the active site. This hypothesis has been established on the facts that CYP 3A shows often atypical hyperbolic kinetic constants and is thus unable to reach saturation. In addition, the presence in the active site of a second substrate having a different molecular nature lead to either no modification or increased metabolism of both substrates. Such allosteric effects have been clearly described in the case of simultaneous metabolism of steroids such as testosterone and α-natphtoflavone.

Consequently, any molecular model describing correctly the multiple substrate specificity (that takes into account large variations in molecular size and chemical structures), and substrate cooperativity effects within the active site (when two or more drugs interact), is of considerable scientific and industrial interest. Such a molecular model must be able to rationalize the binding of the diverse known substrates, and the orientations of the molecules in the binding site that account for their known positions of metabolism (such as N-demethylations, benzylic hydroxylations etc.).

CYP3A4 is considered as the main hepatic form and is found in a wide variety of human organs such as intestine, brain or skin. CYP 3A5 is also present in liver and is the major 3A form present in the kidney. The 3A5 isoform is subject to genetic polymorphism. CYP 3A7 is the major 3A isoform present in the foetus whereas CYP3A43 is mainly located in adult prostate or testis. These isoforms share amino acid identities higher than 70%. (Westlind-Johnsson et al. 2003, Gellner et al. 2001, Koch et al. 2002). It is currently accepted that CYP3A4 is the most active isoform for classical P450 3A substrates whereas recent data (Williams et al. 2002) demonstrate equal or slightly reduced activity for CYP3A5 and a significantly lower metabolism capability for CYP3A7 as compared to CYP3A4. Additionally, differences have been observed in term of oxidative regioselectivity of the CYP3A7 compared to other isoforms. As an example, CYP3A7 metabolizes intensively DHEA and especially its sulfate conjugate derivative whereas CYP3A4 is a poor metabolizer. The oxidation by CYP3A7 occurs mostly in the 16α position of DHEA. In contrast, CYP3A7 metabolizes testosterone in both 6β and 16α position whereas CYP3A4 or 3A5 metabolize it almost exclusively in the 6β position (Inoue et al. 2000).

At the contrary of the P450 3A subfamily, other P450 isoforms have more rigid active site, as suggested by the narrow range of recognized substrates or inhibitors. These P450 isoforms recognize generally a small number of substrates or inhibitors having in common the same shape (i.e. P450 1A isoforms), or the same charge (i.e. CYP 2B, 2C or 2D isoforms), or the same chemical nature such as steroids (i.e. CYP19 or CYP21 isoforms) or lipids (i.e. CYP 4 family).

As no high-resolution 3D structure of CYP3A is today publicly available, due to continuing difficulties in promoting crystallization of intrinsic membrane proteins or due to an unusual conformational flexibility that would explain how CYP3A can accommodate various substrates, it is necessary to rebuild a 3D model structure, integrating the known biochemical data of CYP3A and the structural data of other members of the CYP superfamily. X-ray crystallographic determinations of several bacterial P450 enzymes in the 1990s (see Table 1 for a summary of structural data) have stimulated numerous attempts in modeling microsomal P450S such as human CYP3A4. The chapter 6 of the book "Guide to Cytochromes P450: structure and function" written by David F.V. Lewis reviews the current status of structural and

modeling investigations of the P450 family (Lewis 2001). This review was however written just before the release of the first mammalian P450 structure (2C5), still today the only one mammalian template available.

Table 1

CYP isoform crystallized	PDB code (resol.)	Organism	Function	No of residues	Reference
P450 cam (complexed by CO+camphor)	3cpp (1.9 Å)	*Pseudomonas Putida*	Camphor Monooxygenase	414	(Poulos et al. 1985) (Raag and Poulos 1989)
P450 terp	1cpt (2.3 Å)	*Pseudomonas* sp.	Alpha-terpineol hydroxylation	412	(Hasemann et al. 1994)
P450 BM3	2hpd (2 Å)	*Bacillus megaterium*	Fatty acid monooxygenase	471	(Ravichandran et al. 1993)
P450 eryF (6-deoxyerythro -nolide B bound)	1oxa (2.1 Å)	*Saccharopolyspora erythraea*	Erythromycin biosynthesis 6S-hydroxylation of 6-deoxyerythronolide B	403	(Cupp-Vickery and Poulos 1995)
P450 nor	1rom (2 Å)	Fusarium oxysporum (denitrifying fungus)	Nitric Oxide Reductase	403	(Park et al. 1997)
P450 2C5	1dt6 (3 Å)	(membrane-type Mammalian) Rabbit	Progesterone 21-Hydroxylase	473 (487)	(Williams et al. 2000)
P450 CYP119 4-Phenylimidazole Bound	1f4t (1.93 Å)	*Sulfobolus Solfactaricus* Thermophilic bact.	unknown	368	(Yano et al. 2000)
P450 CYP51 4-Phenylimidazole Bound	1e9x (2.1 Å)	*Mycobacterium Tuberculosis*	14 α-sterol demethylase	455 (451)	(Podust et al. 2001)

Table 1: the eight X-ray crystal structures of P450s available in 2002: six bacterial, one fungal (P450 nor), one mammalian (CYP2C5). The $P450_{cam}$, $P450_{terp}$, $P450_{eryF}$, $P450_{nor}$ belong to class I P450s enzymes, whereas $P450_{BM3}$ belongs to class II enzymes, like microsomal enzymes CYP2C5 and 3A. $P450_{BM3}$ structure is therefore *a priori* more relevant to rebuilding a structural model of CYP3A, but since the CYP2C5 X-Ray structure has been released, it became obvious that the structural homology between the other bacterial enzymes and microsomal enzymes was better than expected from the poor homology of primary structure (< 25% identity). Then, the relevance of using class I and class II structures together for rebuilding models of class II P450s was no more questionable. In the two examples described in the present invention, the structural model of human CYP3A4 was rebuilt using the six

first structures listed above, with no preference in the structural alignment, and the structural model of human CYP3A7 was rebuilt using four structures among those listed above with again no preference in the structural alignment, *i.e.* $P450_{BM3}$, P450 EryF, P450 2C5 and CYP51, one of the last published structural sets. CYP119 was not incorporated into the modeling process.

All the proposed models of CYP3A4 obtained by homology modeling are thus so far based on bacterial crystal structure templates: the first was proposed by Ferenczy and Morris and used the X-ray structure of bacterial $P450_{cam}$ as unique template structure (Ferenczy and Morris 1989). Another model was built later by David F.V. Lewis, using also a unique template structure, the $P450_{BM3}$ structure, which was supposed to be more relevant as a template since this P450 was the only one class II enzyme with known three-dimensional structure (Lewis et al. 1996). A third model, based on a multiple structure template, was built by Szklarz and Halpert, using the four first X-ray crystal structures available $P450_{cam}$, $P450_{terp}$, $P450_{eryF}$, and $P450_{BM3}$. This four-bacterial template approach strategy is closer to our rebuilding strategy, but was still missing some relevance in the absence of a mammalian template. In our hands, the incorporation of the mammalian 2C5 crystal structure into rebuilding steps of models of cytochrome P450 3A proved to be decisive. Inclusion of 2C5 crystal structure had indeed a profound effect on the structural alignment with the five non-mammalian structures, resulting in a different topology of the active site and a marked divergence between the model and each individual template. The advantage of our multiple-template approach resides essentially in the availability of a final template that can be used to rebuild various mammalian cytochromes P450. Up to now there is no available crystal structure or structural model of human CYP3A5, CYP 3A7, CYP3A43 or other mammalian CYP3A.

More recently, two new bacterial P450 crystal structures emerged in the literature (Table 1): CYP51 (PDB code 1e9x), from *Mycobacterium tuberculosis*, that catalyzes the oxidative removal of 14α-methyl group from sterol precursors in sterol biosynthesis in yeast and fungi (ergosterol), plants (phytosterol) and mammals (cholesterol), for its potential in the design of antifungal agents (Podust et al. 2001). And CYP119 (PDB code 1f4t), from the thermophilic archaeon *Sulfolobus solfataricus*, the first P450 identified in *Archaea*, for its interest in

understanding the enhanced thermal stability of the structure, especially in the region of the active site (Yano et al. 2000). Those two structures have been shown to exhibit the typical bacterial P450 fold, with some exceptions in the topology. They have not been included as structural templates in the modeling steps of the CYP3A4 model described in example 1. The names of newly discovered P450s follow the now accepted nomenclature of David R. Nelson (Nelson 1999).

The protein databank (Brookhaven Protein Databank, http://www.rcsb.org/pdb/) currently indicates that there are 76 separate crystal structures available for the eight crystallized P450s, plus 7 crystal structures on hold (Sept 1st, 2002), the majority of which containing either bound substrates or inhibitors. Table 1 provides the relevant information about the structural templates used for human CYP3A model rebuilding. The idea behind homology modeling is that proteins belonging to the same functional class and showing a strong sequence identity, adopt a similar fold (review in (Hilbert et al. 1993)). Known analogous structures are then used to generate a template or parent structure for the unknown protein to be modeled. The reliability of the various methods employed depend mostly on the number of experimental 3D structures that can be aligned. Knowing that for pairs of distantly related proteins (with residue identity of about 20%) the regions having the same fold will represent less than half of each molecule, the regions where the folds differ will predominate, and the divergence of sequence must be compensated by a higher number of homologous proteins to align (Chothia and Lesk 1986). Below 50% of sequence identity, the deviation in structurally not conserved regions becomes significant, and loop regions are difficult to predict. It is generally accepted that below 20% of sequence identity, the prediction turns out to be hazardous, and fold assignment methods are best replaced by *ab initio* methods, that ideally attempt to predict the native structure only from the primary sequence of the protein to be modeled. But produced models so far had the correct fold for only a few small protein domains (Sanchez et al. 2000).

The strategy of model rebuilding in the P450 family is strongly driven by the low degree of homology between bacterial and mammal cytochrome P450s (Table 2).

Table 2

PDB code	Swiss-Prot entry name	CP37_ HUMAN	CP34_ HUMAN	CP51_ MYCTU	CPXW_ SULSO	CPC5_ RABIT	CPXA_ PSEPU	CPXL_ PSESP	CPXB_ BACME	CPXJ_ SACER	NOR_ FUSOX
n.s.	CP37_HUMAN										
n.s.	CP34_HUMAN	88.4 % 501 aa									
1E9X	CP51_MYCTU (CYP51)	27.7 % 372 aa	26.9 % 405 aa								
1F4T	CPXW_SULSO (CYP119)	24.5 % 330 aa	25.4 % 410 aa	25.7 % 385 aa							
1DT6	CPC5_RABIT (CYP2C5)	27.9 % 481 aa	28.4 % 497 aa	23.4 % 427 aa	23.5 % 344 aa						
3CPP	CPXA_PSEPU (P450 cam)	23.3 % 335 aa	21.3 % 399 aa	21.9 % 407 aa	26.6 % 387 aa	24.2 % 480 aa					
1CPT	CPXL_PSESP (P450 terp)	24.8 % 452 aa	24.4 % 356 aa	27.8 % 446 aa	29.3 % 409 aa	24.4 % 451 aa	27.4 % 398 aa				
2HPD-A	CPXB_BACME (P450 BM3)	31.8 % 409 aa	29.9 % 445 aa	27.1 % 443 aa	24.5 % 396 aa	22.7 % 480 aa	23.1 % 485 aa	24.0 % 363 aa			
1OXA	CPXJ_SACER (P450 eryF)	25.5 % 415 aa	26.0 % 334 aa	27.7 % 423 aa	30.8 % 396 aa	24.4 % 443 aa	24.0 % 391 aa	28.6 % 420 aa	22.6 % 389 aa		
1ROM	NOR_FUSOX (P450 nor)	23.7 % 354 aa	22.9 % 415 aa	23.1 % 442 aa	27.7 % 379 aa	21.4 % 351 aa	29.0 % 379 aa	31.5 % 409 aa	23.0 % 265 aa	32.7 % 395 aa	

Table 2: Sequence identities between the various crystallized cytochrome P450s and human CYP3A4 and CYP3A7 using BLOSUM 62 matrix (source LALIGN, http://www.infobiogen.fr/services/analyseq/cgi-bin/lfastap_in.pl, algorithm of Huang and Miller LALIGN that finds the best local alignments between two sequences, version 2.1u03 April 2000, published in *Adv. Appl. Math.* 1991, **12** : 373-381). The P450 BM3 structure, Swissprot code name CPXB_BACME, corresponds to the structure of a fusion protein of P450 and a reductase domain, so that it displays twice the number of residues.

Our global scheme, which steps are described hereafter, is founded on a combination of methods developed in the literature for different purposes in protein structure determination studies. The principle of the primary steps, until the generation of a correct alignment of P450 primary sequences, is described in Jean et al. 1997. The last steps are summarized in Loiseau 2002.

Therefore, in a first object, the invention relates to a method for designing a 3-dimentional (3-D) model of a protein, the 3-D representation of at least three family members has already been experimentally obtained, [said 3-D representation presenting similarities], comprising the steps of:

a. identification of common structural blocks (CSBs) among said members of said family,

b. alignment of the amino-acids primary sequence of said family members according to said structural similarities, represented by said CSBs, in order to obtain a first alignment,

c. alignment of said protein as compared on said first alignment, in order to obtain a second alignment, wherein:

i. alignment of said protein is performed in order to optimize the amino-acids alignment between said protein and said first alignment,
when one or more consensus amino-acid exists in said aligned CSBs in said first alignment, and in the amino-acid sequence of said protein, said consensus amino-acids are anchors of said second alignment,

ii. no insertion or deletion of amino-acids can be performed in the aligned CSBs, wherein insertion or deletions are possible in out-of-block regions, if better to align the primary amino-acids sequences,

d. definition of the 3-D structure of CSBs of said protein, according to the 3-D structure of the CSBs of said family members,

e. definition of the global constraints (distance and angular constraints) derived from the comparisons of the structural templates in CSBs, and definition of the local constraints (distance and angular constraints) for the atoms of residues that are not structurally determined after step d. (that are not in the CSBs),

f. selection of rotamers,

g. determination of a family of 3-D model structures of said protein, taking into account said 3-D structure of CSBs obtained in step **d.**, said global and local constraints defined in step **e.**, and said rotamers defined in step **f.**,

h. optimization of said family of 3-D models obtained in step **g.**, by

i discarding structures that present topological defects, and

ii recalculating 3-D structures by taking electrostatic forces into account,

and performing the method again from step **e.** downward, with modifications in the alignment between the primary sequence of said protein and said first alignment, when the obtained model structures do not satisfactorily account for known mutations having biological effects.

In the present invention, the term "backbone atoms" refers to the C, N, Cα, and O atoms of a protein that are common to all amino acid building blocks or involved in the peptide linkage. When the protein structure is described as a trajectory in internal coordinates such as α, τ angles, or is a low-resolution crystallographic structure, backbone atoms stand only for Cα atoms of each residue.

In the present invention, the term "similarities" is used in the search for structural fragments conserved between the template proteins, that is fragments that have similar local trajectories in the backbone internal coordinate space. Two protein fragments have "similar" local trajectories when they are matched according to two adjustable parameters, the mesh and the margin (Jean et al. 1997).

In the present invention, the term "common structural blocks (CSB)" define the protein fragments of equal length that are found similar between all the template proteins in the internal coordinate representation.

In the present invention, the term "first alignment" refers to the alignment imposed by the CSBs, that is the structural alignment between template proteins defined by

CSBs sequences. This alignment is totally independent on the primary sequence of the template proteins.

In the present invention, the term "out-of-block regions" designates all other protein fragments located out of and between the CSBs, *i.e.* that are not structurally conserved in the internal coordinate space. There is no information of sequence alignment for these regions (see in Figure 1 regions that are not colored), since they are not relevant for structural conservation. Out-of-block regions are passively reconstructed with the rest of the structure during the calculation steps.

In the present invention, the term "global constraints" refers to geometric constraints that are assigned to atoms of residues from CSBs, and that can be derived by computing all distance or angle information available within CSBs or between CSB.

In the present invention, the term "local constraints" refers to loose structural constraints that are assigned to residues of out-of-block regions, in order to restrict their backbone conformation to allowed regions of the Ramachandran diagram.

In the present invention, the term "rotamers" defines the low energy side-chain conformations of residues. The use of a library of rotamers allows determining or modeling a structure with the most likely side-chain conformations, saving time and producing a structure that is more likely to be correct.

For identification of CSBs between all selected 3D structures:

CSBs define the common local folds found similar in the template proteins, and are used as building blocks to set up the fold of the model (results in Loiseau 2002). The non conserved regions, that can be parts of secondary structures or non-structured regions as loops, will be rebuilt with no initial structural information.

For multiple alignment of crystalline P450s, on the basis of CSBs determination:

Once the structurally conserved elements are identified, a first structural alignment between the template proteins is derived. The following step involves the localization of these elements in the target sequence. Sequence pairwise comparisons between selected crystal structures and CYP3A (Table 2) show low sequence identity, so that online tools of multiple alignment such as CLUSTALW or PHD (Heidelberg) fail to produce an clear-cut alignment. Instead, local alignment tools, such as that described in Jean et al. 1997, were used to match the CSB profile to the target sequence, where a matrix is slid along the sequence and a

score of similarity (based on a standard matrix such as BLOSUM62) is calculated for each position. Online tools of multiple alignment such as CLUSTALW 1.8 can be further used for assessment of accuracy.

The target sequence of human cytochrome P450 3A is thus aligned against the multiple alignment obtained from the CSBs. This produces the key sequence alignment which allows the generation of the template structure used for the rebuilding of the various CYP3A models. Following steps involve:

1) Generation of distance and dihedral angles constraints.
2) Selection of rotamers for side chains in CSBs.
3) Calculation of a set of structures using DYANA software. Loops are rebuilt between CSBs.
4) Structure optimization under XPLOR software (Brünger 1992).

In a preferred embodiment, said 3-D representation of family members has been obtained by crystallography or NMR.

The alignment of said common structural blocks in steps **b.** and **c.** can be performed by use of the GOK software as described in Jean et al., 1997.

In addition, step **d.** is preferably performed according to the following rules:

i. at a given position, when residues are identical between all the template structures and the target sequence, the 3D coordinates of the reference residues are purely assigned to the target residue,
ii. When residues differ, only the coordinates of the backbone atoms are assigned (Cα), and sometimes Cβ or Cγ when they exist.

The definition of rebuilding global constraints in step **e.** is performed by using all available geometrical information intra- and inter-CSB (distances and angles), issued from the comparisons of the structural templates, each geometric constraint being defined as an interval. On another hand, the definition of local constraints for out-of-blocks residues is performed by analysis of the allowed regions in Ramachandran diagram.

Furthermore, distances and angles defining global constraints are preferably selected in step **e.** by the following rules:

i. all distances for which the lower boundary is less than 8 Å,
ii. all the distances involving at least one side-chain atom, to preserve the spatial arrangement between CSBs

iii. all the distances involving atoms of any active group such as an heme group, to fix as much as possible the neighborhood of said active group, such as an iron atom.

The distance of 8 Å is chosen in order to reduce drastically the total number of constraints to take into account in the computation, and to allow to excessively constrain the model.

Angular constraints are preferably selected in step **e.** by the following rule:

i. dihedral angles ϕ and ψ of all residues located in CSBs are defined as constraints, given by the average values of corresponding ϕ, ψ angles in said family members +/- the calculated standard deviation.

To practice the method of the invention, rotamers in step **f.** can be selected from the couples according to the tables of Dunbrack and Karplus and step **g.** can be performed with the DYANA software, as described in Güntert et al, 1997.

In addition, the optimization in step **h.** comprises the use of the X-Plor software, as described in A. T. Brünger, X-PLOR, version 3.1.

The method according to the invention is particularly applicable to a cytochrome P450 subfamily 3A comprising mammal and human cytochromes P450 3A]

In a preferred embodiment, said mammal cytochrome P450 3A is selected from the group comprising CYP3A6 (SEQ ID N°14), CYP3A12 (SEQ ID N°16), CYP3A29 (SEQ ID N°17) and CYP3A13 (SEQ ID N°18).

In another preferred embodiment, said human cytochrome P450 subfamily 3A is selected from the group comprising CYP3A4 (SEQ ID N°11), CYP3A7 (SEQ ID N°15), CYP3A5 (SEQ ID N°12) and CYP3A43 (SEQ ID N°13).

The method is applicable as well to human cytochrome of the subfamily P450 3A4, wherein said family members that are used for performing said first alignment for designing a 3-D model of CYP3A4 are chosen from Nor (SEQ ID N° 1), Ery F (SEQ ID N° 2), terp (SEQ ID N° 3), Cam (SEQ ID N° 4), BM3 (SEQ ID N° 5) and 2C5 (SEQ ID N° 6).

The method is applicable as well to human cytochrome of the subfamily 3A7, wherein family members that are used for performing said first alignment for designing a 3-D model of CYP3A7 are chosen from Ery F (SEQ ID N° 2), BM3 (SEQ ID N° 5), CYP51 (SEQ ID N° 8) and 2C5 (SEQ ID N° 6).

The method is applicable as well to other mammalian cytochrome P450 3A isoforms.

In a second object, the invention is directed to 3-D structure model of a protein, obtained by the method as described above.

In a preferred embodiment, the protein is a cytochrome P450 subfamily 3A comprising mammal and human cytochromes P450 3A

In another preferred embodiment, the protein is selected from the group comprising CYP3A6 (SEQ ID N°14), CYP3A12 (SEQ ID N°16), CYP3A29 (SEQ ID N°17) and CYP3A13 (SEQ ID N°18).

In still another preferred embodiment, the protein is a human cytochrome P450 subfamily 3A selected from the group comprising CYP3A4 (SEQ ID N°11), CYP3A7 (SEQ ID N°15), CYP3A5 (SEQ ID N°12) and CYP3A43 (SEQ ID N°13).

In still another preferred embodiment, the protein is a human cytochrome P450 3A4 or 3A7.

Regarding the rebuilt P450 3A4 model, the main residues involved in the recognition of the substrate are **C97; R104; F101; F107; F247; F303 and C376.**

More specifically, C97 and C376 are found in positions compatible with the formation of a disufide bridge allowing limited or enhanced flexibility of corresponding protein domains, while R104 is involved in the capture of the substrate that is close to the entrance site, and allows to accompany it to the active site. F303 is involved in the recognition of the substrate in the active site. F107; F247 and F303 are involved in the recognition at the modulation site responsible for positive regulation. Role of F303 in the active site has already been suggested by studies of Domanski et al. 1998 in the SRS 4 region (mutants I300, F303, A304, and T308).

Features of this model comprise the 3-D atomic coordinates of **Table 3.**

Table 3

In a preferred embodiment, the residues C97; R104; F101; F107; F247; F303 and C376 are involved in the CYP 3A4 for the recognition and uptake of the substrate at the entry site, and its binding into the active site having the 3-D atomic coordinates of Table 3.

Regarding the P450 3A7 model, features comprise the 3-D atomic coordinates of **Table 4.**

Table 4

In a preferred embodiment the residues Q79; F102; R105; R106; F108; F248; F304 and E374 are involved in the CYP 3A7 for the recognition and uptake of the substrate at the entry site, and its binding into the active having the 3-D atomic coordinates of Table 4.

In a third object, the invention contemplates a method for designing a protein, biological functions of which are altered, comprising:

a) obtaining a 3-D model of said protein by the method as depicted above,

b) analyzing said model of step a., and determining the amino-acids that are putatively involved in the biological functions of said protein,

c) changing said amino-acids by mutating the corresponding nucleotides on the nucleic acid sequence coding for said protein, in order to obtain a mutated protein having altered properties.

In the present invention, the term "altered properties" means that the generated protein is altered in its enzymatic properties, such as the substrate recognition, the movements associated to the entrance or the exit of the substrate, the multiple binding at the active site, the allosteric behaviour, the electron transfer, the coupling to the P450 reductase.

In another object, the invention relates to a computer-assisted method for performing restrained dynamics docking of a substrate on an enzyme, a 3-D structure of which is available, comprising the steps:

j. determining a force field, and independently simulating the presence of said enzyme in said force field,

k. minimizing the potential energy (Ep) linked to said force field of said 3-D structure, wherein the spatial position of some atoms of said enzyme is fixed, and wherein the other atoms are mobile, by allowing mobility of the mobile atoms, by

i. simulating an increase in temperature (in order to give kinetic energy),

ii. and minimizing the potential energy by re-specifying the temperature as 0 Kelvin (K)

l. optionally repeating step k in order to obtain other Ep minima, wherein said Ep minima are such that the structure of the protein remains folded,

m. minimizing Ep in said force field of said 3-D structure, wherein all the atoms of the protein are mobile, by

i. simulating an increase in temperature (in order to give kinetic energy), and

ii. minimizing the potential energy by re-specifying the temperature as 0 Kelvin (K)

n. simulating, at 0 K the presence of said substrate next to said enzyme,

o. optionally generating a molecular dynamics simulation on said substrate and enzyme (simulating an increase in temperature, in order to allow mobility of the atoms)

p. generating some constraints to said substrate, in order to impose that it has interaction with said enzyme,

q. generating a molecular dynamics simulation on said substrate and enzyme, with said constraints imposed in step **p.**,

r. optionally, generating a molecular dynamics simulation on said substrate and enzyme without said constraints of step **p.**

In the present invention, the term "restrained dynamics docking" means a procedure by which the docking of the substrate is simulated using molecular dynamics (MD) simulations under constraints that are specified by the user.

In the present invention, the term "soft-restrained dynamics docking" refers to a restrained dynamics docking in which the substrate-protein distance constraints are loose, with force field parameters associated to the constraints as low as 1 or 2 Kcal/mol.

In the present invention, the term "constraints" when applied to substrate docking refers to a distance imposed between atoms of the protein, generally from the active site (such as atoms of the heme group), and atoms of the substrate. These distance restraints are defined as intervals, where the distance range is large enough to allow the free movement of the substrate within the active site.

In a preferred embodiment of this method for performing restrained dynamics docking, said fixed atoms in step **k.** are the backbone atoms N-Cα-CO in the first minimization step and only Cα in subsequent minimization steps.

In another preferred embodiment of this method, kinetic energy is simulated by temperature increase to about 100 K for about 5-20 ns.

The force field in step **j.** comprises forces linked to:

a. the distance between atoms,

b. the angles of valence,

c. the dihedral angles,

d. the deformation with regard to planar geometry,

e. the electrostatic field,

f. the Van der Waals forces,

g. hydrogen bonds.

The constraints in step **p.** are attraction constraints to force said substrate in the active site, and wherein said constraints are not prejudiced to the exact spatial conformation of the substrate in the active site. These constraints are final distance constraints between some atoms of said substrate and some atoms of amino-acids present in said active site.

In the present invention, the term "final distance constraints", when applied to substrate docking, means distances imposed between atoms from the heme group (such as the iron atom), and atoms of the substrate. These distance contraints are defined as intervals, and are related to the final position of the substrate in the vicinity of the heme group before metabolization.

Preferably, step **o.** is performed with a simulated temperature of between about 15 and 50 K, step **q.** is performed with a simulated temperature of between about 15 and 50 K, and step **r.** is performed with a simulated temperature of between about 200 and 350 K.

This method is particularly suited for multispecific protein such as a cytochrome 36 P450 subfamily 3A comprising mammal and human cytochromes.

The cytochrome can be cytochrome P450 3A4 or any of all other P450 from the 3A subfamily, and said structure can be the structure obtained by the method of the invention described above, in particular the model structures which atomic coordinates are listed in Tables 3 and 4 for CYP3A4 and CYP3A7.

The substrate can be a small organic compound which size can range for example from MW 288 (testosterone) to MW 1203 (cyclosporine A).

In a preferred embodiment said substrate is testosterone.

In another object, the invention is aimed at a computer-assisted method for performing restrained dynamics docking of at least two substrates on an enzyme, a 3-D structure of which is available, consisting of performing the steps **j, k, l, m, n, o, p, q and r** depicted above with a first substrate and repeating said steps with a second substrate when the first substrate reaches an unconstrained state after molecular dynamics simulations.

The first and second substrates can be the same molecule or different molecules.

The first and second substrates can display either allosteric or synergistic effect.

This method can be practiced with substrates that are inhibitors (competitive, uncompetitive, non competitive) or display an inhibitor-base mechanism. It can also be practiced with an agonist and any molecule interfering with the biological function of the protein.

In preferred embodiments:

- the first and second substrates are the same molecule.
- the first and second substrates are different molecules.
- the first and second substrates display an allosteric effect.
- the first and second substrates display a synergistic effect.
- at least one of the substrates is an inhibitor or display an inhibitor-based mechanism.
- at least one of the substrates is an agonist.

In another embodiment, this method also embraces a successive repeat of the steps **j, k, l, m, n, o, p, q and r** depicted above with a 3rd, 4th or 5th substrate, some of them being the same or different molecules.

In this method for performing restrained dynamics docking, said fixed atoms in step **k.** are the backbone atoms N-Cα-CO in the first minimization step and only Cα in subsequent minimization steps.

In addition, kinetic energy is simulated by temperature increase to about 100 K for about 5-20 ns.

The force field in step **j.** comprises preferably forces linked to

a. the distance between atoms,
b. the angles of valence,
c. the dihedral angles,
d. the deformation with regard to planar geometry,
e. the electrostatic field,
f. the Van der Waals forces,
g. hydrogen bonds.

The constraints in step **p.** are preferable attraction constraints to force said substrate in the active site, and wherein said constraints are not prejudiced to the exact spatial conformation of the substrate in the active site. These constraints are final distance

constraints between some atoms of said substrate and some atoms of amino-acids present in said active site.

Preferably, step **o.** is performed with a simulated temperature of between about 15 and 50 K, step **q.** is performed with a simulated temperature of between about 15 and 50 K, and step **r.** is performed with a simulated temperature of between about 200 and 350 K.

This method is particularly suited for multispecific protein such as a cytochrome P450. The cytochrome can be cytochrome P450 3A4, or any of all other P450 of the 3A subfamily and said structure can be the structure obtained by the method of the invention described above, in particular the model structures which atomic coordinates are listed in Tables 3 and 4 for CYP3A4 and CYP3A7.

In a preferred embodiment:

- said cytochrome is cytochrome P450 3A4, and said structure is the structure obtained by the above-described method, in particular the above-described model structure,
- said first and second substrates are small organic compounds which size can range from MW 288 (testosterone) to MW 1203 (cyclosporine A),
- said substrate is testosterone.

The invention is also directed to the use of the method for designing a 3-D model of a protein and to the computer-assisted method for performing restrained dynamics docking as mentioned above for screening, designing or identifying natural, unnatural substrates or substrate analogs, as well as inhibitors, activators or modulators of said enzyme.

Another object of the invention is the use of these methods for determining the effect of a first substrate on a second substrate, which can also be applied to pharmaceutical products.

The invention contemplates the use of these methods for determining the effect of a first bound testosterone molecule on the access of a second testosterone molecule as well as for determining the mutual effect of a testosterone molecule with alpha-naphtoflavone (αNF) molecule.

The invention is also directed to :

* The use of the above described computer-assisted methods for determining the oxidative modification of the substrate according to the proximity to the heme of a part of the substrate to give rise to metabolite.
  The oxidized or reduced molecule derived from a given substrate modified after positioning at the right distance to the heme is called metabolite.
* The use of the above described computer-assisted methods, for performing dynamic docking of the said metabolite, either in the absence or in the presence of the second substrate in the calculation.
* The use of the above described computer-assisted methods for dynamic docking to compare the energy of the bound metabolite relatively to the energy of its parent substrate bound, in order to determine if the exit of the given metabolite from the enzyme is favored or not.
* The use of the above described computer-assisted methods for dynamic docking to study the different exit pathways that are accessible to the metabolite, either in the absence or in the presence of the second substrate in the calculation.

The distance and angular constraints derived from CSBs common to the crystallized cytochromes P450 used as structural templates, are applied to conserved atoms of CSBs of the target protein. The DYANA software (Güntert et al. 1997) allows to rebuild directly the whole structure of the target protein on the basis of its primary sequence, by taking into account these geometric constraints. Out-of-blocks residues are rebuilt *ab initio* by selecting the most favorable solutions in terms of minimal global potential energy. As examples, actual tables 3 and 4 display the atomic coordinates of structural models obtained by applying DYANA calculation to target protein sequences CYP3A4 and CYP3A7 respectively.

TABLE 3 :Providing the coordinates of the CYP3A4 model

```
HEADER    CYP3A4
TITLE     MODEL OF HUMAN CYTOCHROME P450 CYP3A4
AUTHOR    N. LOISEAU,F.ANDRE,C.MINOLETTI,M.DELAFORGE
SEQRES   1   452  SER TYR HIS LYS GLY PHE CYS MET PHE ASP MET GLU CYS
SEQRES   2   452  HIS LYS LYS TYR GLY LYS VAL TRP GLY PHE TYR ASP GLY
SEQRES   3   452  GLN GLN PRO VAL LEU ALA ILE THR ASP PRO ASP MET ILE
SEQRES   4   452  LYS THR VAL LEU VAL LYS GLU CYS TYR SER VAL PHE THR
SEQRES   5   452  ASN ARG ARG PRO PHE GLY PRO VAL GLY PHE MET LYS SER
SEQRES   6   452  ALA ILE SER ILE ALA GLU ASP GLU GLU TRP LYS ARG LEU
SEQRES   7   452  ARG SER LEU LEU SER PRO THR PHE THR SER GLY LYS LEU
SEQRES   8   452  LYS GLU MET VAL PRO ILE ILE ALA GLN TYR GLY ASP VAL
SEQRES   9   452  LEU VAL ARG ASN LEU ARG ARG GLU ALA GLU THR GLY LYS
SEQRES  10   452  PRO VAL THR LEU LYS ASP VAL PHE GLY ALA TYR SER MET
SEQRES  11   452  ASP VAL ILE THR SER THR SER PHE GLY VAL ASN ILE ASP
SEQRES  12   452  SER LEU ASN ASN PRO GLN ASP PRO PHE VAL GLU ASN THR
SEQRES  13   452  LYS LYS LEU LEU ARG PHE ASP PHE LEU ASP PRO PHE PHE
SEQRES  14   452  LEU SER ILE THR VAL PHE PRO PHE LEU ILE PRO ILE LEU
SEQRES  15   452  GLU VAL LEU ASN ILE CYS VAL PHE PRO ARG GLU VAL THR
SEQRES  16   452  ASN PHE LEU ARG LYS SER VAL LYS ARG MET LYS GLU SER
SEQRES  17   452  ARG LEU GLU ASP THR GLN LYS HIS ARG VAL ASP PHE LEU
SEQRES  18   452  GLN LEU MET ILE ASP SER GLN ASN SER LYS GLU THR GLU
SEQRES  19   452  SER HIS LYS ALA LEU SER ASP LEU GLU LEU VAL ALA GLN
SEQRES  20   452  SER ILE ILE PHE ILE PHE ALA GLY TYR GLU THR THR SER
SEQRES  21   452  SER VAL LEU SER PHE ILE MET TYR GLU LEU ALA THR HIS
SEQRES  22   452  PRO ASP VAL GLN GLN LYS LEU GLN GLU GLU ILE ASP ALA
SEQRES  23   452  VAL LEU PRO ASN LYS ALA PRO PRO THR TYR ASP THR VAL
SEQRES  24   452  LEU GLN MET GLU TYR LEU ASP MET VAL VAL ASN GLU THR
SEQRES  25   452  LEU ARG LEU PHE PRO ILE ALA MET ARG LEU GLU ARG VAL
SEQRES  26   452  CYS LYS LYS ASP VAL GLU ILE ASN GLY MET PHE ILE PRO
SEQRES  27   452  LYS GLY TRP VAL VAL MET ILE PRO SER TYR ALA LEU HIS
SEQRES  28   452  ARG ASP PRO LYS TYR TRP THR GLU PRO GLU LYS PHE LEU
SEQRES  29   452  PRO GLU ARG PHE SER LYS LYS ASN LYS ASP ASN ILE ASP
SEQRES  30   452  PRO TYR ILE TYR THR PRO PHE GLY SER GLY PRO ARG ASN
SEQRES  31   452  CYS ILE GLY MET ARG PHE ALA LEU MET ASN MET LYS LEU
SEQRES  32   452  ALA LEU ILE ARG VAL LEU GLN ASN PHE SER PHE LYS PRO
SEQRES  33   452  CYS LYS GLU THR GLN ILE PRO LEU LYS LEU SER LEU GLY
SEQRES  34   452  GLY LEU LEU GLN PRO GLU LYS PRO VAL VAL LEU LYS VAL
SEQRES  35   452  GLU SER ARG ASP GLY THR VAL SER GLY ALA
HET     HEM    600
HETNAM  HEM    HEME
HETSYN  HEM    3,7,12,17-TETRAMETHYL-8,13-DIVINYL-2,18-PORPHINEDIPROPIONIC ACID
FORMUL  HEM    C34 H34 N4 O4 FE1
ATOM      1  N   SER   51       9.999  -1.760  -4.543  1.00  0.00          3A4
ATOM      2  CA  SER   51      10.718  -0.477  -4.293  1.00  0.00          3A4
ATOM      3  CB  SER   51       9.949   0.731  -4.939  1.00  0.00          3A4
ATOM      4  OG  SER   51       8.601   0.876  -4.493  1.00  0.00          3A4
ATOM      5  C   SER   51      10.962  -0.281  -2.815  1.00  0.00          3A4
ATOM      6  O   SER   51      10.277  -0.855  -1.969  1.00  0.00          3A4
ATOM      7  N   TYR   52      11.974   0.569  -2.482  1.00  0.00          3A4
ATOM      8  CA  TYR   52      12.433   0.860  -1.131  1.00  0.00          3A4
ATOM      9  CB  TYR   52      13.983   0.783  -0.979  1.00  0.00          3A4
ATOM     10  CG  TYR   52      14.459  -0.572  -1.430  1.00  0.00          3A4
ATOM     11  CD1 TYR   52      14.143  -1.732  -0.699  1.00  0.00          3A4
ATOM     12  CD2 TYR   52      15.210  -0.701  -2.611  1.00  0.00          3A4
ATOM     13  CE1 TYR   52      14.574  -2.994  -1.138  1.00  0.00          3A4
ATOM     14  CE2 TYR   52      15.651  -1.954  -3.052  1.00  0.00          3A4
ATOM     15  CZ  TYR   52      15.334  -3.105  -2.314  1.00  0.00          3A4
ATOM     16  OH  TYR   52      15.784  -4.370  -2.751  1.00  0.00          3A4
ATOM     17  C   TYR   52      11.971   2.246  -0.755  1.00  0.00          3A4
ATOM     18  O   TYR   52      12.178   3.208  -1.494  1.00  0.00          3A4
ATOM     19  N   HIS   53      11.321   2.350   0.429  1.00  0.00          3A4
ATOM     20  CA  HIS   53      10.747   3.568   0.953  1.00  0.00          3A4
ATOM     21  ND1 HIS   53       7.857   1.850   1.039  1.00  0.00          3A4
ATOM     22  CG  HIS   53       8.485   2.636   0.097  1.00  0.00          3A4
ATOM     23  CB  HIS   53       9.322   3.861   0.386  1.00  0.00          3A4
ATOM     24  NE2 HIS   53       7.438   0.923  -0.936  1.00  0.00          3A4
ATOM     25  CD2 HIS   53       8.216   2.053  -1.104  1.00  0.00          3A4
ATOM     26  CE1 HIS   53       7.247   0.842   0.368  1.00  0.00          3A4
ATOM     27  C   HIS   53      10.751   3.386   2.448  1.00  0.00          3A4
ATOM     28  O   HIS   53       9.715   3.183   3.080  1.00  0.00          3A4
ATOM     29  N   LYS   54      11.973   3.461   3.043  1.00  0.00          3A4
```

ATOM	30	CA	LYS	54	12.265	3.262	4.451	1.00	0.00	3A4
ATOM	31	CB	LYS	54	13.401	2.217	4.659	1.00	0.00	3A4
ATOM	32	CG	LYS	54	13.053	0.819	4.120	1.00	0.00	3A4
ATOM	33	CD	LYS	54	14.220	-0.183	4.148	1.00	0.00	3A4
ATOM	34	CE	LYS	54	14.793	-0.500	5.540	1.00	0.00	3A4
ATOM	35	NZ	LYS	54	13.763	-1.087	6.431	1.00	0.00	3A4
ATOM	36	C	LYS	54	12.660	4.603	5.025	1.00	0.00	3A4
ATOM	37	O	LYS	54	13.829	4.851	5.317	1.00	0.00	3A4
ATOM	38	N	GLY	55	11.656	5.510	5.181	1.00	0.00	3A4
ATOM	39	CA	GLY	55	11.819	6.901	5.560	1.00	0.00	3A4
ATOM	40	C	GLY	55	11.464	7.113	7.003	1.00	0.00	3A4
ATOM	41	O	GLY	55	10.305	7.002	7.400	1.00	0.00	3A4
ATOM	42	N	PHE	56	12.502	7.439	7.817	1.00	0.00	3A4
ATOM	43	CA	PHE	56	12.451	7.714	9.250	1.00	0.00	3A4
ATOM	44	CB	PHE	56	13.646	7.051	10.010	1.00	0.00	3A4
ATOM	45	CG	PHE	56	13.966	5.681	9.448	1.00	0.00	3A4
ATOM	46	CD1	PHE	56	15.250	5.415	8.926	1.00	0.00	3A4
ATOM	47	CD2	PHE	56	12.987	4.669	9.370	1.00	0.00	3A4
ATOM	48	CE1	PHE	56	15.543	4.185	8.320	1.00	0.00	3A4
ATOM	49	CE2	PHE	56	13.271	3.445	8.747	1.00	0.00	3A4
ATOM	50	CZ	PHE	56	14.550	3.205	8.224	1.00	0.00	3A4
ATOM	51	C	PHE	56	12.446	9.211	9.542	1.00	0.00	3A4
ATOM	52	O	PHE	56	11.957	9.670	10.570	1.00	0.00	3A4
ATOM	53	N	CYS	57	12.971	10.054	8.624	1.00	0.00	3A4
ATOM	54	CA	CYS	57	13.048	11.500	8.782	1.00	0.00	3A4
ATOM	55	CB	CYS	57	13.902	12.161	7.665	1.00	0.00	3A4
ATOM	56	SG	CYS	57	15.312	11.121	7.176	1.00	0.00	3A4
ATOM	57	C	CYS	57	11.705	12.171	8.760	1.00	0.00	3A4
ATOM	58	O	CYS	57	11.446	13.160	9.434	1.00	0.00	3A4
ATOM	59	N	MET	58	10.778	11.585	7.975	1.00	0.00	3A4
ATOM	60	CA	MET	58	9.402	12.000	7.870	1.00	0.00	3A4
ATOM	61	CB	MET	58	8.715	11.289	6.694	1.00	0.00	3A4
ATOM	62	CG	MET	58	9.360	11.641	5.343	1.00	0.00	3A4
ATOM	63	SD	MET	58	8.469	11.004	3.887	1.00	0.00	3A4
ATOM	64	CE	MET	58	8.922	9.256	4.080	1.00	0.00	3A4
ATOM	65	C	MET	58	8.612	11.706	9.122	1.00	0.00	3A4
ATOM	66	O	MET	58	7.740	12.480	9.487	1.00	0.00	3A4
ATOM	67	N	PHE	59	8.963	10.612	9.844	1.00	0.00	3A4
ATOM	68	CA	PHE	59	8.394	10.230	11.122	1.00	0.00	3A4
ATOM	69	CB	PHE	59	8.732	8.752	11.449	1.00	0.00	3A4
ATOM	70	CG	PHE	59	7.865	8.152	12.538	1.00	0.00	3A4
ATOM	71	CD1	PHE	59	6.477	8.002	12.350	1.00	0.00	3A4
ATOM	72	CD2	PHE	59	8.430	7.747	13.764	1.00	0.00	3A4
ATOM	73	CE1	PHE	59	5.671	7.462	13.364	1.00	0.00	3A4
ATOM	74	CE2	PHE	59	7.627	7.208	14.780	1.00	0.00	3A4
ATOM	75	CZ	PHE	59	6.247	7.065	14.579	1.00	0.00	3A4
ATOM	76	C	PHE	59	8.881	11.119	12.255	1.00	0.00	3A4
ATOM	77	O	PHE	59	8.110	11.479	13.139	1.00	0.00	3A4
ATOM	78	N	ASP	60	10.162	11.568	12.226	1.00	0.00	3A4
ATOM	79	CA	ASP	60	10.690	12.515	13.200	1.00	0.00	3A4
ATOM	80	CB	ASP	60	12.225	12.651	13.131	1.00	0.00	3A4
ATOM	81	CG	ASP	60	12.906	11.313	13.450	1.00	0.00	3A4
ATOM	82	OD1	ASP	60	12.613	10.736	14.532	1.00	0.00	3A4
ATOM	83	OD2	ASP	60	13.743	10.859	12.624	1.00	0.00	3A4
ATOM	84	C	ASP	60	10.102	13.900	13.031	1.00	0.00	3A4
ATOM	85	O	ASP	60	9.841	14.603	14.000	1.00	0.00	3A4
ATOM	86	N	MET	61	9.809	14.318	11.780	1.00	0.00	3A4
ATOM	87	CA	MET	61	9.130	15.564	11.481	1.00	0.00	3A4
ATOM	88	CB	MET	61	9.224	15.881	9.987	1.00	0.00	3A4
ATOM	89	CG	MET	61	10.590	16.349	9.497	1.00	0.00	3A4
ATOM	90	SD	MET	61	10.659	16.502	7.686	1.00	0.00	3A4
ATOM	91	CE	MET	61	12.223	17.411	7.689	1.00	0.00	3A4
ATOM	92	C	MET	61	7.653	15.548	11.870	1.00	0.00	3A4
ATOM	93	O	MET	61	7.073	16.551	12.274	1.00	0.00	3A4
ATOM	94	N	GLU	62	7.012	14.358	11.819	1.00	0.00	3A4
ATOM	95	CA	GLU	62	5.653	14.159	12.272	1.00	0.00	3A4
ATOM	96	CB	GLU	62	5.077	12.770	11.933	1.00	0.00	3A4
ATOM	97	CG	GLU	62	4.640	12.657	10.462	1.00	0.00	3A4
ATOM	98	CD	GLU	62	4.351	11.190	10.120	1.00	0.00	3A4
ATOM	99	OE1	GLU	62	3.429	10.603	10.748	1.00	0.00	3A4
ATOM	100	OE2	GLU	62	5.048	10.637	9.227	1.00	0.00	3A4
ATOM	101	C	GLU	62	5.522	14.338	13.751	1.00	0.00	3A4

ATOM	102	O	GLU	62	4.508	14.819	14.225	1.00	0.00	3A4
ATOM	103	N	CYS	63	6.605	14.104	14.522	1.00	0.00	3A4
ATOM	104	CA	CYS	63	6.664	14.441	15.921	1.00	0.00	3A4
ATOM	105	CB	CYS	63	7.902	13.805	16.588	1.00	0.00	3A4
ATOM	106	SG	CYS	63	7.977	11.995	16.382	1.00	0.00	3A4
ATOM	107	C	CYS	63	6.526	15.952	16.211	1.00	0.00	3A4
ATOM	108	O	CYS	63	6.277	16.322	17.335	1.00	0.00	3A4
ATOM	109	N	HIS	64	6.436	16.853	15.182	1.00	0.00	3A4
ATOM	110	CA	HIS	64	5.487	17.970	15.236	1.00	0.00	3A4
ATOM	111	ND1	HIS	64	4.140	20.440	16.744	1.00	0.00	3A4
ATOM	112	CG	HIS	64	5.232	20.460	15.904	1.00	0.00	3A4
ATOM	113	CB	HIS	64	6.151	19.284	15.666	1.00	0.00	3A4
ATOM	114	NE2	HIS	64	4.280	22.506	15.939	1.00	0.00	3A4
ATOM	115	CD2	HIS	64	5.301	21.731	15.420	1.00	0.00	3A4
ATOM	116	CE1	HIS	64	3.608	21.687	16.726	1.00	0.00	3A4
ATOM	117	C	HIS	64	4.780	18.138	13.901	1.00	0.00	3A4
ATOM	118	O	HIS	64	3.812	17.438	13.610	1.00	0.00	3A4
ATOM	119	N	LYS	65	5.240	19.107	13.073	1.00	0.00	3A4
ATOM	120	CA	LYS	65	4.699	19.426	11.766	1.00	0.00	3A4
ATOM	121	CB	LYS	65	3.264	20.052	11.761	1.00	0.00	3A4
ATOM	122	CG	LYS	65	2.994	21.171	12.783	1.00	0.00	3A4
ATOM	123	CD	LYS	65	1.557	21.704	12.722	1.00	0.00	3A4
ATOM	124	CE	LYS	65	1.220	22.723	13.820	1.00	0.00	3A4
ATOM	125	NZ	LYS	65	2.052	23.944	13.700	1.00	0.00	3A4
ATOM	126	C	LYS	65	5.705	20.365	11.146	1.00	0.00	3A4
ATOM	127	O	LYS	65	5.958	20.315	9.944	1.00	0.00	3A4
ATOM	128	N	LYS	66	6.332	21.227	12.000	1.00	0.00	3A4
ATOM	129	CA	LYS	66	7.517	22.020	11.730	1.00	0.00	3A4
ATOM	130	CB	LYS	66	7.373	23.548	12.037	1.00	0.00	3A4
ATOM	131	CG	LYS	66	6.519	24.352	11.039	1.00	0.00	3A4
ATOM	132	CD	LYS	66	5.001	24.175	11.175	1.00	0.00	3A4
ATOM	133	CE	LYS	66	4.191	25.119	10.278	1.00	0.00	3A4
ATOM	134	NZ	LYS	66	2.736	24.881	10.442	1.00	0.00	3A4
ATOM	135	C	LYS	66	8.551	21.370	12.620	1.00	0.00	3A4
ATOM	136	O	LYS	66	9.100	20.332	12.253	1.00	0.00	3A4
ATOM	137	N	TYR	67	8.772	21.934	13.838	1.00	0.00	3A4
ATOM	138	CA	TYR	67	9.441	21.263	14.936	1.00	0.00	3A4
ATOM	139	CB	TYR	67	11.005	21.348	14.926	1.00	0.00	3A4
ATOM	140	CG	TYR	67	11.555	20.265	14.028	1.00	0.00	3A4
ATOM	141	CD1	TYR	67	11.325	18.909	14.336	1.00	0.00	3A4
ATOM	142	CD2	TYR	67	12.250	20.569	12.847	1.00	0.00	3A4
ATOM	143	CE1	TYR	67	11.798	17.884	13.506	1.00	0.00	3A4
ATOM	144	CE2	TYR	67	12.720	19.550	12.006	1.00	0.00	3A4
ATOM	145	CZ	TYR	67	12.507	18.207	12.342	1.00	0.00	3A4
ATOM	146	OH	TYR	67	13.010	17.184	11.509	1.00	0.00	3A4
ATOM	147	C	TYR	67	8.880	21.880	16.194	1.00	0.00	3A4
ATOM	148	O	TYR	67	8.905	23.092	16.404	1.00	0.00	3A4
ATOM	149	N	GLY	68	8.343	20.969	17.043	1.00	0.00	3A4
ATOM	150	CA	GLY	68	7.620	21.161	18.278	1.00	0.00	3A4
ATOM	151	C	GLY	68	8.251	20.139	19.164	1.00	0.00	3A4
ATOM	152	O	GLY	68	8.314	18.954	18.839	1.00	0.00	3A4
ATOM	153	N	LYS	69	8.864	20.642	20.260	1.00	0.00	3A4
ATOM	154	CA	LYS	69	10.301	20.592	20.404	1.00	0.00	3A4
ATOM	155	CB	LYS	69	10.795	21.997	20.802	1.00	0.00	3A4
ATOM	156	CG	LYS	69	10.332	23.112	19.844	1.00	0.00	3A4
ATOM	157	CD	LYS	69	10.770	24.527	20.225	1.00	0.00	3A4
ATOM	158	CE	LYS	69	9.876	25.161	21.300	1.00	0.00	3A4
ATOM	159	NZ	LYS	69	10.236	26.582	21.514	1.00	0.00	3A4
ATOM	160	C	LYS	69	10.811	19.541	21.360	1.00	0.00	3A4
ATOM	161	O	LYS	69	11.914	19.033	21.177	1.00	0.00	3A4
ATOM	162	N	VAL	70	10.033	19.200	22.410	1.00	0.00	3A4
ATOM	163	CA	VAL	70	10.427	18.227	23.408	1.00	0.00	3A4
ATOM	164	CB	VAL	70	10.984	18.837	24.696	1.00	0.00	3A4
ATOM	165	CG1	VAL	70	12.504	18.835	24.571	1.00	0.00	3A4
ATOM	166	CG2	VAL	70	10.344	20.206	25.037	1.00	0.00	3A4
ATOM	167	C	VAL	70	9.212	17.394	23.695	1.00	0.00	3A4
ATOM	168	O	VAL	70	8.176	17.901	24.111	1.00	0.00	3A4
ATOM	169	N	TRP	71	9.337	16.067	23.484	1.00	0.00	3A4
ATOM	170	CA	TRP	71	8.255	15.133	23.636	1.00	0.00	3A4
ATOM	171	CB	TRP	71	7.614	14.787	22.260	1.00	0.00	3A4
ATOM	172	CG	TRP	71	6.390	13.874	22.229	1.00	0.00	3A4
ATOM	173	CD2	TRP	71	5.135	14.145	22.880	1.00	0.00	3A4

ATOM	174	CD1	TRP	71	6.251	12.660	21.615	1.00	0.00	3A4
ATOM	175	NE1	TRP	71	4.996	12.146	21.846	1.00	0.00	3A4
ATOM	176	CE2	TRP	71	4.292	13.040	22.624	1.00	0.00	3A4
ATOM	177	CE3	TRP	71	4.695	15.227	23.643	1.00	0.00	3A4
ATOM	178	CZ2	TRP	71	2.995	12.995	23.131	1.00	0.00	3A4
ATOM	179	CZ3	TRP	71	3.388	15.180	24.153	1.00	0.00	3A4
ATOM	180	CH2	TRP	71	2.551	14.080	23.902	1.00	0.00	3A4
ATOM	181	C	TRP	71	8.828	13.911	24.261	1.00	0.00	3A4
ATOM	182	O	TRP	71	9.989	13.584	24.059	1.00	0.00	3A4
ATOM	183	N	GLY	72	7.987	13.188	25.027	1.00	0.00	3A4
ATOM	184	CA	GLY	72	8.345	11.936	25.647	1.00	0.00	3A4
ATOM	185	C	GLY	72	7.812	10.809	24.804	1.00	0.00	3A4
ATOM	186	O	GLY	72	6.679	10.850	24.336	1.00	0.00	3A4
ATOM	187	N	PHE	73	8.645	9.773	24.586	1.00	0.00	3A4
ATOM	188	CA	PHE	73	8.334	8.591	23.820	1.00	0.00	3A4
ATOM	189	CB	PHE	73	9.278	8.443	22.586	1.00	0.00	3A4
ATOM	190	CG	PHE	73	8.893	7.320	21.647	1.00	0.00	3A4
ATOM	191	CD1	PHE	73	9.691	6.162	21.549	1.00	0.00	3A4
ATOM	192	CD2	PHE	73	7.717	7.398	20.877	1.00	0.00	3A4
ATOM	193	CE1	PHE	73	9.320	5.105	20.707	1.00	0.00	3A4
ATOM	194	CE2	PHE	73	7.344	6.343	20.030	1.00	0.00	3A4
ATOM	195	CZ	PHE	73	8.146	5.196	19.947	1.00	0.00	3A4
ATOM	196	C	PHE	73	8.515	7.451	24.788	1.00	0.00	3A4
ATOM	197	O	PHE	73	9.257	7.543	25.757	1.00	0.00	3A4
ATOM	198	N	TYR	74	7.826	6.328	24.540	1.00	0.00	3A4
ATOM	199	CA	TYR	74	7.884	5.174	25.397	1.00	0.00	3A4
ATOM	200	CB	TYR	74	6.631	5.032	26.304	1.00	0.00	3A4
ATOM	201	CG	TYR	74	5.298	5.291	25.625	1.00	0.00	3A4
ATOM	202	CD1	TYR	74	4.515	4.223	25.146	1.00	0.00	3A4
ATOM	203	CD2	TYR	74	4.797	6.603	25.491	1.00	0.00	3A4
ATOM	204	CE1	TYR	74	3.279	4.456	24.524	1.00	0.00	3A4
ATOM	205	CE2	TYR	74	3.564	6.844	24.870	1.00	0.00	3A4
ATOM	206	CZ	TYR	74	2.804	5.769	24.384	1.00	0.00	3A4
ATOM	207	OH	TYR	74	1.560	6.006	23.757	1.00	0.00	3A4
ATOM	208	C	TYR	74	8.100	4.007	24.486	1.00	0.00	3A4
ATOM	209	O	TYR	74	7.256	3.682	23.658	1.00	0.00	3A4
ATOM	210	N	ASP	75	9.272	3.357	24.603	1.00	0.00	3A4
ATOM	211	CA	ASP	75	9.664	2.238	23.778	1.00	0.00	3A4
ATOM	212	CB	ASP	75	11.110	2.479	23.220	1.00	0.00	3A4
ATOM	213	CG	ASP	75	11.483	1.556	22.044	1.00	0.00	3A4
ATOM	214	OD1	ASP	75	10.755	1.577	21.015	1.00	0.00	3A4
ATOM	215	OD2	ASP	75	12.500	0.822	22.166	1.00	0.00	3A4
ATOM	216	C	ASP	75	9.580	1.007	24.657	1.00	0.00	3A4
ATOM	217	O	ASP	75	9.275	1.091	25.845	1.00	0.00	3A4
ATOM	218	N	GLY	76	9.925	-0.191	24.123	1.00	0.00	3A4
ATOM	219	CA	GLY	76	10.101	-1.403	24.908	1.00	0.00	3A4
ATOM	220	C	GLY	76	11.420	-1.335	25.643	1.00	0.00	3A4
ATOM	221	O	GLY	76	12.463	-1.562	25.039	1.00	0.00	3A4
ATOM	222	N	GLN	77	11.349	-0.928	26.946	1.00	0.00	3A4
ATOM	223	CA	GLN	77	12.393	-0.521	27.882	1.00	0.00	3A4
ATOM	224	CB	GLN	77	13.760	-1.300	27.835	1.00	0.00	3A4
ATOM	225	CG	GLN	77	14.891	-0.783	26.903	1.00	0.00	3A4
ATOM	226	CD	GLN	77	15.977	-1.843	26.760	1.00	0.00	3A4
ATOM	227	OE1	GLN	77	16.121	-2.718	27.611	1.00	0.00	3A4
ATOM	228	NE2	GLN	77	16.759	-1.765	25.648	1.00	0.00	3A4
ATOM	229	C	GLN	77	12.593	0.983	27.782	1.00	0.00	3A4
ATOM	230	O	GLN	77	12.935	1.504	26.719	1.00	0.00	3A4
ATOM	231	N	GLN	78	12.365	1.707	28.918	1.00	0.00	3A4
ATOM	232	CA	GLN	78	12.698	3.105	29.188	1.00	0.00	3A4
ATOM	233	CB	GLN	78	14.220	3.411	28.944	1.00	0.00	3A4
ATOM	234	CG	GLN	78	14.774	4.789	29.381	1.00	0.00	3A4
ATOM	235	CD	GLN	78	14.622	5.043	30.889	1.00	0.00	3A4
ATOM	236	OE1	GLN	78	14.409	4.138	31.694	1.00	0.00	3A4
ATOM	237	NE2	GLN	78	14.757	6.336	31.296	1.00	0.00	3A4
ATOM	238	C	GLN	78	11.820	4.135	28.453	1.00	0.00	3A4
ATOM	239	O	GLN	78	11.794	4.125	27.222	1.00	0.00	3A4
ATOM	240	N	PRO	79	11.120	5.089	29.129	1.00	0.00	3A4
ATOM	241	CA	PRO	79	10.604	6.330	28.550	1.00	0.00	3A4
ATOM	242	CD	PRO	79	10.730	4.946	30.533	1.00	0.00	3A4
ATOM	243	CB	PRO	79	9.535	6.798	29.557	1.00	0.00	3A4
ATOM	244	CG	PRO	79	10.001	6.244	30.911	1.00	0.00	3A4
ATOM	245	C	PRO	79	11.734	7.327	28.383	1.00	0.00	3A4

ATOM	246	O	PRO	79	12.582	7.447	29.260	1.00	0.00	3A4
ATOM	247	N	VAL	80	11.782	8.012	27.228	1.00	0.00	3A4
ATOM	248	CA	VAL	80	12.870	8.876	26.835	1.00	0.00	3A4
ATOM	249	CB	VAL	80	13.698	8.283	25.679	1.00	0.00	3A4
ATOM	250	CG1	VAL	80	14.441	7.026	26.173	1.00	0.00	3A4
ATOM	251	CG2	VAL	80	12.828	7.928	24.440	1.00	0.00	3A4
ATOM	252	C	VAL	80	12.250	10.173	26.392	1.00	0.00	3A4
ATOM	253	O	VAL	80	11.117	10.204	25.939	1.00	0.00	3A4
ATOM	254	N	LEU	81	13.003	11.285	26.466	1.00	0.00	3A4
ATOM	255	CA	LEU	81	12.603	12.575	25.948	1.00	0.00	3A4
ATOM	256	CB	LEU	81	12.958	13.700	26.945	1.00	0.00	3A4
ATOM	257	CG	LEU	81	12.302	15.079	26.699	1.00	0.00	3A4
ATOM	258	CD1	LEU	81	10.822	15.078	27.116	1.00	0.00	3A4
ATOM	259	CD2	LEU	81	13.057	16.197	27.437	1.00	0.00	3A4
ATOM	260	C	LEU	81	13.352	12.751	24.647	1.00	0.00	3A4
ATOM	261	O	LEU	81	14.529	12.427	24.569	1.00	0.00	3A4
ATOM	262	N	ALA	82	12.695	13.249	23.585	1.00	0.00	3A4
ATOM	263	CA	ALA	82	13.260	13.415	22.267	1.00	0.00	3A4
ATOM	264	CB	ALA	82	12.433	12.689	21.183	1.00	0.00	3A4
ATOM	265	C	ALA	82	13.288	14.890	21.990	1.00	0.00	3A4
ATOM	266	O	ALA	82	12.251	15.546	22.002	1.00	0.00	3A4
ATOM	267	N	ILE	83	14.498	15.436	21.733	1.00	0.00	3A4
ATOM	268	CA	ILE	83	14.742	16.837	21.486	1.00	0.00	3A4
ATOM	269	CB	ILE	83	16.032	17.330	22.124	1.00	0.00	3A4
ATOM	270	CG2	ILE	83	15.944	18.846	22.217	1.00	0.00	3A4
ATOM	271	CG1	ILE	83	16.359	16.727	23.506	1.00	0.00	3A4
ATOM	272	CD	ILE	83	15.380	17.044	24.634	1.00	0.00	3A4
ATOM	273	C	ILE	83	14.831	17.000	19.986	1.00	0.00	3A4
ATOM	274	O	ILE	83	15.706	16.418	19.358	1.00	0.00	3A4
ATOM	275	N	THR	84	13.915	17.773	19.367	1.00	0.00	3A4
ATOM	276	CA	THR	84	13.796	17.851	17.920	1.00	0.00	3A4
ATOM	277	CB	THR	84	12.384	17.503	17.457	1.00	0.00	3A4
ATOM	278	OG1	THR	84	11.371	18.330	18.025	1.00	0.00	3A4
ATOM	279	CG2	THR	84	12.085	16.027	17.808	1.00	0.00	3A4
ATOM	280	C	THR	84	14.259	19.175	17.344	1.00	0.00	3A4
ATOM	281	O	THR	84	14.500	19.282	16.144	1.00	0.00	3A4
ATOM	282	N	ASP	85	14.371	20.231	18.176	1.00	0.00	3A4
ATOM	283	CA	ASP	85	14.595	21.594	17.732	1.00	0.00	3A4
ATOM	284	CB	ASP	85	13.703	22.550	18.577	1.00	0.00	3A4
ATOM	285	CG	ASP	85	13.371	23.873	17.872	1.00	0.00	3A4
ATOM	286	OD1	ASP	85	12.666	23.828	16.828	1.00	0.00	3A4
ATOM	287	OD2	ASP	85	13.808	24.942	18.373	1.00	0.00	3A4
ATOM	288	C	ASP	85	16.050	21.928	17.888	1.00	0.00	3A4
ATOM	289	O	ASP	85	16.660	21.452	18.843	1.00	0.00	3A4
ATOM	290	N	PRO	86	16.683	22.732	17.024	1.00	0.00	3A4
ATOM	291	CA	PRO	86	18.101	23.035	17.076	1.00	0.00	3A4
ATOM	292	CD	PRO	86	16.102	23.257	15.807	1.00	0.00	3A4
ATOM	293	CB	PRO	86	18.421	23.751	15.747	1.00	0.00	3A4
ATOM	294	CG	PRO	86	17.079	24.309	15.294	1.00	0.00	3A4
ATOM	295	C	PRO	86	18.425	23.863	18.284	1.00	0.00	3A4
ATOM	296	O	PRO	86	19.466	23.647	18.892	1.00	0.00	3A4
ATOM	297	N	ASP	87	17.511	24.756	18.711	1.00	0.00	3A4
ATOM	298	CA	ASP	87	17.636	25.559	19.902	1.00	0.00	3A4
ATOM	299	CB	ASP	87	16.417	26.494	20.029	1.00	0.00	3A4
ATOM	300	CG	ASP	87	16.305	27.442	18.820	1.00	0.00	3A4
ATOM	301	OD1	ASP	87	17.357	27.851	18.258	1.00	0.00	3A4
ATOM	302	OD2	ASP	87	15.148	27.764	18.439	1.00	0.00	3A4
ATOM	303	C	ASP	87	17.724	24.745	21.171	1.00	0.00	3A4
ATOM	304	O	ASP	87	18.546	25.018	22.032	1.00	0.00	3A4
ATOM	305	N	MET	88	16.902	23.678	21.253	1.00	0.00	3A4
ATOM	306	CA	MET	88	16.847	22.776	22.375	1.00	0.00	3A4
ATOM	307	CB	MET	88	15.536	22.000	22.396	1.00	0.00	3A4
ATOM	308	CG	MET	88	14.362	22.948	22.644	1.00	0.00	3A4
ATOM	309	SD	MET	88	12.947	22.177	23.469	1.00	0.00	3A4
ATOM	310	CE	MET	88	13.722	21.914	25.087	1.00	0.00	3A4
ATOM	311	C	MET	88	18.007	21.812	22.436	1.00	0.00	3A4
ATOM	312	O	MET	88	18.524	21.506	23.506	1.00	0.00	3A4
ATOM	313	N	ILE	89	18.500	21.349	21.264	1.00	0.00	3A4
ATOM	314	CA	ILE	89	19.637	20.450	21.170	1.00	0.00	3A4
ATOM	315	CB	ILE	89	19.679	19.800	19.793	1.00	0.00	3A4
ATOM	316	CG2	ILE	89	21.088	19.217	19.442	1.00	0.00	3A4
ATOM	317	CG1	ILE	89	18.596	18.681	19.910	1.00	0.00	3A4

ATOM	318	CD	ILE	89	18.390	17.678	18.773	1.00	0.00	3A4
ATOM	319	C	ILE	89	20.916	21.161	21.538	1.00	0.00	3A4
ATOM	320	O	ILE	89	21.722	20.655	22.310	1.00	0.00	3A4
ATOM	321	N	LYS	90	21.096	22.421	21.089	1.00	0.00	3A4
ATOM	322	CA	LYS	90	22.214	23.250	21.481	1.00	0.00	3A4
ATOM	323	CB	LYS	90	22.225	24.577	20.719	1.00	0.00	3A4
ATOM	324	CG	LYS	90	23.531	25.387	20.790	1.00	0.00	3A4
ATOM	325	CD	LYS	90	23.546	26.569	19.811	1.00	0.00	3A4
ATOM	326	CE	LYS	90	24.875	27.339	19.774	1.00	0.00	3A4
ATOM	327	NZ	LYS	90	25.167	27.975	21.082	1.00	0.00	3A4
ATOM	328	C	LYS	90	22.221	23.564	22.961	1.00	0.00	3A4
ATOM	329	O	LYS	90	23.248	23.567	23.612	1.00	0.00	3A4
ATOM	330	N	THR	91	21.031	23.752	23.561	1.00	0.00	3A4
ATOM	331	CA	THR	91	20.855	23.981	24.981	1.00	0.00	3A4
ATOM	332	CB	THR	91	19.434	24.380	25.293	1.00	0.00	3A4
ATOM	333	OG1	THR	91	19.170	25.637	24.681	1.00	0.00	3A4
ATOM	334	CG2	THR	91	19.109	24.554	26.810	1.00	0.00	3A4
ATOM	335	C	THR	91	21.198	22.782	25.817	1.00	0.00	3A4
ATOM	336	O	THR	91	21.850	22.889	26.851	1.00	0.00	3A4
ATOM	337	N	VAL	92	20.849	21.578	25.307	1.00	0.00	3A4
ATOM	338	CA	VAL	92	21.125	20.315	25.945	1.00	0.00	3A4
ATOM	339	CB	VAL	92	20.299	19.178	25.353	1.00	0.00	3A4
ATOM	340	CG1	VAL	92	21.025	18.247	24.370	1.00	0.00	3A4
ATOM	341	CG2	VAL	92	19.643	18.370	26.498	1.00	0.00	3A4
ATOM	342	C	VAL	92	22.600	20.047	26.089	1.00	0.00	3A4
ATOM	343	O	VAL	92	22.991	19.412	27.041	1.00	0.00	3A4
ATOM	344	N	LEU	93	23.483	20.706	25.311	1.00	0.00	3A4
ATOM	345	CA	LEU	93	24.914	20.851	25.543	1.00	0.00	3A4
ATOM	346	CB	LEU	93	25.432	21.742	24.407	1.00	0.00	3A4
ATOM	347	CG	LEU	93	26.456	21.108	23.525	1.00	0.00	3A4
ATOM	348	CD1	LEU	93	25.796	19.892	22.820	1.00	0.00	3A4
ATOM	349	CD2	LEU	93	26.955	22.238	22.601	1.00	0.00	3A4
ATOM	350	C	LEU	93	25.419	21.473	26.847	1.00	0.00	3A4
ATOM	351	O	LEU	93	24.654	21.997	27.655	1.00	0.00	3A4
ATOM	352	N	VAL	94	26.774	21.385	27.035	1.00	0.00	3A4
ATOM	353	CA	VAL	94	27.599	21.729	28.196	1.00	0.00	3A4
ATOM	354	CB	VAL	94	27.328	23.082	28.879	1.00	0.00	3A4
ATOM	355	CG1	VAL	94	28.368	23.358	30.001	1.00	0.00	3A4
ATOM	356	CG2	VAL	94	27.427	24.201	27.813	1.00	0.00	3A4
ATOM	357	C	VAL	94	27.515	20.540	29.137	1.00	0.00	3A4
ATOM	358	O	VAL	94	26.875	20.578	30.188	1.00	0.00	3A4
ATOM	359	N	LYS	95	28.141	19.421	28.690	1.00	0.00	3A4
ATOM	360	CA	LYS	95	28.019	18.101	29.261	1.00	0.00	3A4
ATOM	361	CB	LYS	95	27.404	17.078	28.259	1.00	0.00	3A4
ATOM	362	CG	LYS	95	27.757	17.284	26.778	1.00	0.00	3A4
ATOM	363	CD	LYS	95	27.133	16.199	25.898	1.00	0.00	3A4
ATOM	364	CE	LYS	95	27.017	16.559	24.413	1.00	0.00	3A4
ATOM	365	NZ	LYS	95	28.338	16.819	23.809	1.00	0.00	3A4
ATOM	366	C	LYS	95	29.379	17.675	29.736	1.00	0.00	3A4
ATOM	367	O	LYS	95	30.123	16.990	29.040	1.00	0.00	3A4
ATOM	368	N	GLU	96	29.703	18.085	30.988	1.00	0.00	3A4
ATOM	369	CA	GLU	96	30.926	17.783	31.698	1.00	0.00	3A4
ATOM	370	CB	GLU	96	31.795	19.051	31.950	1.00	0.00	3A4
ATOM	371	CG	GLU	96	31.039	20.290	32.486	1.00	0.00	3A4
ATOM	372	CD	GLU	96	32.012	21.467	32.599	1.00	0.00	3A4
ATOM	373	OE1	GLU	96	31.790	22.493	31.901	1.00	0.00	3A4
ATOM	374	OE2	GLU	96	32.990	21.357	33.388	1.00	0.00	3A4
ATOM	375	C	GLU	96	30.517	17.078	32.969	1.00	0.00	3A4
ATOM	376	O	GLU	96	30.732	17.576	34.073	1.00	0.00	3A4
ATOM	377	N	CYS	97	29.924	15.869	32.763	1.00	0.00	3A4
ATOM	378	CA	CYS	97	29.436	14.865	33.693	1.00	0.00	3A4
ATOM	379	CB	CYS	97	29.558	15.141	35.235	1.00	0.00	3A4
ATOM	380	SG	CYS	97	29.186	13.706	36.313	1.00	0.00	3A4
ATOM	381	C	CYS	97	28.000	14.633	33.277	1.00	0.00	3A4
ATOM	382	O	CYS	97	27.076	15.253	33.800	1.00	0.00	3A4
ATOM	383	N	TYR	98	27.817	13.703	32.305	1.00	0.00	3A4
ATOM	384	CA	TYR	98	26.556	13.216	31.782	1.00	0.00	3A4
ATOM	385	CB	TYR	98	26.197	13.814	30.380	1.00	0.00	3A4
ATOM	386	CG	TYR	98	25.205	14.939	30.543	1.00	0.00	3A4
ATOM	387	CD1	TYR	98	25.573	16.198	31.050	1.00	0.00	3A4
ATOM	388	CD2	TYR	98	23.862	14.731	30.197	1.00	0.00	3A4
ATOM	389	CE1	TYR	98	24.626	17.224	31.198	1.00	0.00	3A4

ATOM	390	CE2	TYR	98	22.901	15.740	30.351	1.00	0.00	3A4
ATOM	391	CZ	TYR	98	23.286	16.993	30.849	1.00	0.00	3A4
ATOM	392	OH	TYR	98	22.323	18.015	30.999	1.00	0.00	3A4
ATOM	393	C	TYR	98	26.800	11.735	31.683	1.00	0.00	3A4
ATOM	394	O	TYR	98	27.629	11.292	30.891	1.00	0.00	3A4
ATOM	395	N	SER	99	26.097	10.928	32.531	1.00	0.00	3A4
ATOM	396	CA	SER	99	26.414	9.536	32.838	1.00	0.00	3A4
ATOM	397	CB	SER	99	25.870	9.141	34.247	1.00	0.00	3A4
ATOM	398	OG	SER	99	26.515	7.992	34.791	1.00	0.00	3A4
ATOM	399	C	SER	99	25.931	8.568	31.771	1.00	0.00	3A4
ATOM	400	O	SER	99	24.885	8.764	31.156	1.00	0.00	3A4
ATOM	401	N	VAL	100	26.759	7.507	31.524	1.00	0.00	3A4
ATOM	402	CA	VAL	100	26.647	6.426	30.542	1.00	0.00	3A4
ATOM	403	CB	VAL	100	25.344	5.612	30.576	1.00	0.00	3A4
ATOM	404	CG1	VAL	100	25.483	4.356	29.677	1.00	0.00	3A4
ATOM	405	CG2	VAL	100	25.062	5.167	32.031	1.00	0.00	3A4
ATOM	406	C	VAL	100	26.977	6.962	29.152	1.00	0.00	3A4
ATOM	407	O	VAL	100	28.088	6.758	28.673	1.00	0.00	3A4
ATOM	408	N	PHE	101	26.002	7.682	28.517	1.00	0.00	3A4
ATOM	409	CA	PHE	101	26.131	8.581	27.372	1.00	0.00	3A4
ATOM	410	CB	PHE	101	27.487	9.383	27.359	1.00	0.00	3A4
ATOM	411	CG	PHE	101	27.503	10.546	26.402	1.00	0.00	3A4
ATOM	412	CD1	PHE	101	26.587	11.609	26.522	1.00	0.00	3A4
ATOM	413	CD2	PHE	101	28.432	10.563	25.350	1.00	0.00	3A4
ATOM	414	CE1	PHE	101	26.580	12.640	25.573	1.00	0.00	3A4
ATOM	415	CE2	PHE	101	28.435	11.597	24.418	1.00	0.00	3A4
ATOM	416	CZ	PHE	101	27.492	12.629	24.516	1.00	0.00	3A4
ATOM	417	C	PHE	101	25.860	7.863	26.049	1.00	0.00	3A4
ATOM	418	O	PHE	101	25.613	8.506	25.030	1.00	0.00	3A4
ATOM	419	N	THR	102	25.881	6.507	26.048	1.00	0.00	3A4
ATOM	420	CA	THR	102	25.468	5.674	24.939	1.00	0.00	3A4
ATOM	421	CB	THR	102	26.561	5.456	23.875	1.00	0.00	3A4
ATOM	422	OG1	THR	102	26.134	4.618	22.803	1.00	0.00	3A4
ATOM	423	CG2	THR	102	27.920	4.971	24.441	1.00	0.00	3A4
ATOM	424	C	THR	102	24.949	4.448	25.660	1.00	0.00	3A4
ATOM	425	O	THR	102	25.680	3.511	25.976	1.00	0.00	3A4
ATOM	426	N	ASN	103	23.629	4.491	25.991	1.00	0.00	3A4
ATOM	427	CA	ASN	103	22.973	3.634	26.965	1.00	0.00	3A4
ATOM	428	CB	ASN	103	22.145	4.482	28.000	1.00	0.00	3A4
ATOM	429	CG	ASN	103	21.193	5.519	27.373	1.00	0.00	3A4
ATOM	430	OD1	ASN	103	21.530	6.702	27.345	1.00	0.00	3A4
ATOM	431	ND2	ASN	103	19.993	5.093	26.893	1.00	0.00	3A4
ATOM	432	C	ASN	103	22.171	2.529	26.295	1.00	0.00	3A4
ATOM	433	O	ASN	103	22.526	2.061	25.214	1.00	0.00	3A4
ATOM	434	N	ARG	104	21.099	2.084	27.018	1.00	0.00	3A4
ATOM	435	CA	ARG	104	20.255	0.904	26.922	1.00	0.00	3A4
ATOM	436	CB	ARG	104	20.057	0.305	25.521	1.00	0.00	3A4
ATOM	437	CG	ARG	104	19.266	1.224	24.571	1.00	0.00	3A4
ATOM	438	CD	ARG	104	19.318	0.794	23.096	1.00	0.00	3A4
ATOM	439	NE	ARG	104	20.722	1.001	22.589	1.00	0.00	3A4
ATOM	440	CZ	ARG	104	21.086	0.812	21.280	1.00	0.00	3A4
ATOM	441	NH1	ARG	104	22.383	1.027	20.912	1.00	0.00	3A4
ATOM	442	NH2	ARG	104	20.184	0.403	20.340	1.00	0.00	3A4
ATOM	443	C	ARG	104	20.801	-0.116	27.892	1.00	0.00	3A4
ATOM	444	O	ARG	104	21.996	-0.173	28.177	1.00	0.00	3A4
ATOM	445	N	ARG	105	19.899	-0.953	28.439	1.00	0.00	3A4
ATOM	446	CA	ARG	105	20.180	-1.924	29.470	1.00	0.00	3A4
ATOM	447	CB	ARG	105	18.917	-2.306	30.269	1.00	0.00	3A4
ATOM	448	CG	ARG	105	18.288	-1.109	31.012	1.00	0.00	3A4
ATOM	449	CD	ARG	105	17.273	-0.267	30.201	1.00	0.00	3A4
ATOM	450	NE	ARG	105	16.999	1.019	30.940	1.00	0.00	3A4
ATOM	451	CZ	ARG	105	17.736	2.168	30.769	1.00	0.00	3A4
ATOM	452	NH1	ARG	105	17.471	3.253	31.550	1.00	0.00	3A4
ATOM	453	NH2	ARG	105	18.734	2.262	29.841	1.00	0.00	3A4
ATOM	454	C	ARG	105	20.851	-3.183	28.984	1.00	0.00	3A4
ATOM	455	O	ARG	105	21.862	-3.545	29.576	1.00	0.00	3A4
ATOM	456	N	PRO	106	20.439	-3.879	27.908	1.00	0.00	3A4
ATOM	457	CA	PRO	106	21.118	-5.066	27.409	1.00	0.00	3A4
ATOM	458	CD	PRO	106	19.166	-3.707	27.212	1.00	0.00	3A4
ATOM	459	CB	PRO	106	20.292	-5.535	26.208	1.00	0.00	3A4
ATOM	460	CG	PRO	106	19.354	-4.383	25.861	1.00	0.00	3A4
ATOM	461	C	PRO	106	22.531	-4.785	26.960	1.00	0.00	3A4

ATOM	462	O	PRO	106	23.412	-5.580	27.239	1.00	0.00	3A4
ATOM	463	N	PHE	107	22.789	-3.612	26.347	1.00	0.00	3A4
ATOM	464	CA	PHE	107	24.092	-3.149	25.939	1.00	0.00	3A4
ATOM	465	CB	PHE	107	23.996	-1.854	25.067	1.00	0.00	3A4
ATOM	466	CG	PHE	107	23.377	-2.185	23.730	1.00	0.00	3A4
ATOM	467	CD1	PHE	107	24.194	-2.404	22.604	1.00	0.00	3A4
ATOM	468	CD2	PHE	107	21.982	-2.301	23.578	1.00	0.00	3A4
ATOM	469	CE1	PHE	107	23.633	-2.730	21.360	1.00	0.00	3A4
ATOM	470	CE2	PHE	107	21.415	-2.640	22.342	1.00	0.00	3A4
ATOM	471	CZ	PHE	107	22.243	-2.850	21.231	1.00	0.00	3A4
ATOM	472	C	PHE	107	24.996	-2.874	27.117	1.00	0.00	3A4
ATOM	473	O	PHE	107	26.183	-3.178	27.071	1.00	0.00	3A4
ATOM	474	N	GLY	108	24.445	-2.352	28.235	1.00	0.00	3A4
ATOM	475	CA	GLY	108	25.169	-2.115	29.465	1.00	0.00	3A4
ATOM	476	C	GLY	108	25.703	-3.372	30.122	1.00	0.00	3A4
ATOM	477	O	GLY	108	26.825	-3.365	30.623	1.00	0.00	3A4
ATOM	478	N	PRO	109	24.957	-4.476	30.112	1.00	0.00	3A4
ATOM	479	CA	PRO	109	25.476	-5.825	30.348	1.00	0.00	3A4
ATOM	480	CD	PRO	109	24.065	-4.305	31.286	1.00	0.00	3A4
ATOM	481	CB	PRO	109	24.191	-6.637	30.615	1.00	0.00	3A4
ATOM	482	CG	PRO	109	23.330	-5.658	31.433	1.00	0.00	3A4
ATOM	483	C	PRO	109	26.330	-6.541	29.318	1.00	0.00	3A4
ATOM	484	O	PRO	109	27.456	-6.908	29.658	1.00	0.00	3A4
ATOM	485	N	VAL	110	25.774	-6.864	28.119	1.00	0.00	3A4
ATOM	486	CA	VAL	110	26.331	-7.778	27.133	1.00	0.00	3A4
ATOM	487	CB	VAL	110	25.389	-8.936	26.768	1.00	0.00	3A4
ATOM	488	CG1	VAL	110	25.412	-9.943	27.938	1.00	0.00	3A4
ATOM	489	CG2	VAL	110	23.943	-8.492	26.450	1.00	0.00	3A4
ATOM	490	C	VAL	110	26.744	-6.971	25.923	1.00	0.00	3A4
ATOM	491	O	VAL	110	25.981	-6.165	25.392	1.00	0.00	3A4
ATOM	492	N	GLY	111	28.021	-7.174	25.497	1.00	0.00	3A4
ATOM	493	CA	GLY	111	28.732	-6.403	24.496	1.00	0.00	3A4
ATOM	494	C	GLY	111	29.773	-5.622	25.245	1.00	0.00	3A4
ATOM	495	O	GLY	111	29.468	-4.588	25.839	1.00	0.00	3A4
ATOM	496	N	PHE	112	31.035	-6.136	25.266	1.00	0.00	3A4
ATOM	497	CA	PHE	112	32.105	-5.711	26.158	1.00	0.00	3A4
ATOM	498	CB	PHE	112	32.907	-6.929	26.720	1.00	0.00	3A4
ATOM	499	CG	PHE	112	31.979	-7.800	27.529	1.00	0.00	3A4
ATOM	500	CD1	PHE	112	31.631	-9.095	27.096	1.00	0.00	3A4
ATOM	501	CD2	PHE	112	31.424	-7.318	28.732	1.00	0.00	3A4
ATOM	502	CE1	PHE	112	30.746	-9.883	27.847	1.00	0.00	3A4
ATOM	503	CE2	PHE	112	30.537	-8.104	29.480	1.00	0.00	3A4
ATOM	504	CZ	PHE	112	30.195	-9.387	29.035	1.00	0.00	3A4
ATOM	505	C	PHE	112	33.050	-4.749	25.472	1.00	0.00	3A4
ATOM	506	O	PHE	112	34.190	-5.078	25.148	1.00	0.00	3A4
ATOM	507	N	MET	113	32.562	-3.489	25.295	1.00	0.00	3A4
ATOM	508	CA	MET	113	33.296	-2.314	24.869	1.00	0.00	3A4
ATOM	509	CB	MET	113	32.602	-1.505	23.728	1.00	0.00	3A4
ATOM	510	CG	MET	113	32.554	-2.210	22.356	1.00	0.00	3A4
ATOM	511	SD	MET	113	31.429	-3.639	22.184	1.00	0.00	3A4
ATOM	512	CE	MET	113	29.851	-2.787	22.471	1.00	0.00	3A4
ATOM	513	C	MET	113	33.386	-1.481	26.125	1.00	0.00	3A4
ATOM	514	O	MET	113	32.371	-1.027	26.652	1.00	0.00	3A4
ATOM	515	N	LYS	114	34.630	-1.321	26.660	1.00	0.00	3A4
ATOM	516	CA	LYS	114	34.932	-0.910	28.025	1.00	0.00	3A4
ATOM	517	CB	LYS	114	36.207	-1.643	28.544	1.00	0.00	3A4
ATOM	518	CG	LYS	114	36.129	-3.170	28.392	1.00	0.00	3A4
ATOM	519	CD	LYS	114	37.411	-3.890	28.832	1.00	0.00	3A4
ATOM	520	CE	LYS	114	37.355	-5.417	28.667	1.00	0.00	3A4
ATOM	521	NZ	LYS	114	37.190	-5.806	27.244	1.00	0.00	3A4
ATOM	522	C	LYS	114	35.074	0.600	28.136	1.00	0.00	3A4
ATOM	523	O	LYS	114	34.485	1.339	27.348	1.00	0.00	3A4
ATOM	524	N	SER	115	35.857	1.092	29.141	1.00	0.00	3A4
ATOM	525	CA	SER	115	35.955	2.486	29.566	1.00	0.00	3A4
ATOM	526	CB	SER	115	36.419	2.597	31.048	1.00	0.00	3A4
ATOM	527	OG	SER	115	35.505	1.921	31.901	1.00	0.00	3A4
ATOM	528	C	SER	115	36.891	3.307	28.696	1.00	0.00	3A4
ATOM	529	O	SER	115	38.106	3.302	28.890	1.00	0.00	3A4
ATOM	530	N	ALA	116	36.300	4.041	27.709	1.00	0.00	3A4
ATOM	531	CA	ALA	116	36.990	4.902	26.770	1.00	0.00	3A4
ATOM	532	CB	ALA	116	36.806	4.440	25.323	1.00	0.00	3A4
ATOM	533	C	ALA	116	36.445	6.277	26.942	1.00	0.00	3A4

ATOM	534	O	ALA	116	35.934	6.634	27.995	1.00	0.00	3A4
ATOM	535	N	ILE	117	36.498	7.116	25.886	1.00	0.00	3A4
ATOM	536	CA	ILE	117	36.054	8.497	25.985	1.00	0.00	3A4
ATOM	537	CB	ILE	117	36.818	9.363	24.999	1.00	0.00	3A4
ATOM	538	CG2	ILE	117	36.637	8.922	23.524	1.00	0.00	3A4
ATOM	539	CG1	ILE	117	36.647	10.857	25.212	1.00	0.00	3A4
ATOM	540	CD	ILE	117	37.122	11.262	26.574	1.00	0.00	3A4
ATOM	541	C	ILE	117	34.556	8.659	25.822	1.00	0.00	3A4
ATOM	542	O	ILE	117	33.924	9.474	26.492	1.00	0.00	3A4
ATOM	543	N	SER	118	33.923	7.843	24.946	1.00	0.00	3A4
ATOM	544	CA	SER	118	32.533	8.033	24.588	1.00	0.00	3A4
ATOM	545	CB	SER	118	32.205	7.525	23.146	1.00	0.00	3A4
ATOM	546	OG	SER	118	32.499	6.147	22.946	1.00	0.00	3A4
ATOM	547	C	SER	118	31.585	7.455	25.606	1.00	0.00	3A4
ATOM	548	O	SER	118	30.395	7.686	25.524	1.00	0.00	3A4
ATOM	549	N	ILE	119	32.084	6.735	26.630	1.00	0.00	3A4
ATOM	550	CA	ILE	119	31.251	6.157	27.657	1.00	0.00	3A4
ATOM	551	CB	ILE	119	31.480	4.637	27.705	1.00	0.00	3A4
ATOM	552	CG2	ILE	119	32.895	4.296	28.225	1.00	0.00	3A4
ATOM	553	CG1	ILE	119	30.373	3.794	28.400	1.00	0.00	3A4
ATOM	554	CD	ILE	119	29.071	3.681	27.605	1.00	0.00	3A4
ATOM	555	C	ILE	119	31.475	6.827	29.005	1.00	0.00	3A4
ATOM	556	O	ILE	119	30.894	6.426	30.013	1.00	0.00	3A4
ATOM	557	N	ALA	120	32.350	7.862	29.050	1.00	0.00	3A4
ATOM	558	CA	ALA	120	32.876	8.420	30.276	1.00	0.00	3A4
ATOM	559	CB	ALA	120	34.429	8.417	30.275	1.00	0.00	3A4
ATOM	560	C	ALA	120	32.403	9.821	30.537	1.00	0.00	3A4
ATOM	561	O	ALA	120	32.153	10.624	29.642	1.00	0.00	3A4
ATOM	562	N	GLU	121	32.338	10.132	31.847	1.00	0.00	3A4
ATOM	563	CA	GLU	121	31.987	11.402	32.421	1.00	0.00	3A4
ATOM	564	CB	GLU	121	31.189	11.213	33.742	1.00	0.00	3A4
ATOM	565	CG	GLU	121	29.884	10.420	33.613	1.00	0.00	3A4
ATOM	566	CD	GLU	121	30.124	8.902	33.618	1.00	0.00	3A4
ATOM	567	OE1	GLU	121	29.800	8.241	32.594	1.00	0.00	3A4
ATOM	568	OE2	GLU	121	30.631	8.385	34.649	1.00	0.00	3A4
ATOM	569	C	GLU	121	33.282	12.104	32.738	1.00	0.00	3A4
ATOM	570	O	GLU	121	34.307	11.460	32.947	1.00	0.00	3A4
ATOM	571	N	ASP	122	33.267	13.450	32.868	1.00	0.00	3A4
ATOM	572	CA	ASP	122	34.366	14.255	33.384	1.00	0.00	3A4
ATOM	573	CB	ASP	122	33.940	15.762	33.320	1.00	0.00	3A4
ATOM	574	CG	ASP	122	35.057	16.786	33.606	1.00	0.00	3A4
ATOM	575	OD1	ASP	122	34.911	17.556	34.593	1.00	0.00	3A4
ATOM	576	OD2	ASP	122	36.057	16.817	32.842	1.00	0.00	3A4
ATOM	577	C	ASP	122	34.615	13.879	34.870	1.00	0.00	3A4
ATOM	578	O	ASP	122	33.636	13.610	35.566	1.00	0.00	3A4
ATOM	579	N	GLU	123	35.863	13.792	35.421	1.00	0.00	3A4
ATOM	580	CA	GLU	123	37.162	14.248	34.972	1.00	0.00	3A4
ATOM	581	CB	GLU	123	37.993	14.687	36.197	1.00	0.00	3A4
ATOM	582	CG	GLU	123	37.348	15.854	36.968	1.00	0.00	3A4
ATOM	583	CD	GLU	123	38.253	16.265	38.134	1.00	0.00	3A4
ATOM	584	OE1	GLU	123	38.764	17.417	38.116	1.00	0.00	3A4
ATOM	585	OE2	GLU	123	38.443	15.431	39.060	1.00	0.00	3A4
ATOM	586	C	GLU	123	37.950	13.205	34.211	1.00	0.00	3A4
ATOM	587	O	GLU	123	39.000	13.494	33.638	1.00	0.00	3A4
ATOM	588	N	GLU	124	37.449	11.951	34.149	1.00	0.00	3A4
ATOM	589	CA	GLU	124	38.063	10.827	33.460	1.00	0.00	3A4
ATOM	590	CB	GLU	124	37.284	9.523	33.756	1.00	0.00	3A4
ATOM	591	CG	GLU	124	37.186	9.213	35.261	1.00	0.00	3A4
ATOM	592	CD	GLU	124	36.410	7.908	35.465	1.00	0.00	3A4
ATOM	593	OE1	GLU	124	37.010	6.933	35.993	1.00	0.00	3A4
ATOM	594	OE2	GLU	124	35.204	7.870	35.096	1.00	0.00	3A4
ATOM	595	C	GLU	124	38.109	11.000	31.965	1.00	0.00	3A4
ATOM	596	O	GLU	124	39.087	10.727	31.279	1.00	0.00	3A4
ATOM	597	N	TRP	125	37.027	11.579	31.425	1.00	0.00	3A4
ATOM	598	CA	TRP	125	36.896	11.901	30.029	1.00	0.00	3A4
ATOM	599	CB	TRP	125	35.456	12.317	29.760	1.00	0.00	3A4
ATOM	600	CG	TRP	125	35.096	13.136	28.553	1.00	0.00	3A4
ATOM	601	CD2	TRP	125	34.736	14.501	28.811	1.00	0.00	3A4
ATOM	602	CD1	TRP	125	34.423	12.765	27.428	1.00	0.00	3A4
ATOM	603	NE1	TRP	125	33.701	13.815	26.942	1.00	0.00	3A4
ATOM	604	CE2	TRP	125	33.805	14.860	27.829	1.00	0.00	3A4
ATOM	605	CE3	TRP	125	35.040	15.361	29.870	1.00	0.00	3A4

```
ATOM    606  CZ2 TRP   125      33.124  16.059  27.921  1.00  0.00          3A4
ATOM    607  CZ3 TRP   125      34.396  16.599  29.921  1.00  0.00          3A4
ATOM    608  CH2 TRP   125      33.421  16.924  28.984  1.00  0.00          3A4
ATOM    609  C   TRP   125      37.893  12.940  29.585  1.00  0.00          3A4
ATOM    610  O   TRP   125      38.564  12.734  28.590  1.00  0.00          3A4
ATOM    611  N   LYS   126      38.066  14.068  30.315  1.00  0.00          3A4
ATOM    612  CA  LYS   126      38.948  15.161  29.915  1.00  0.00          3A4
ATOM    613  CB  LYS   126      38.776  16.362  30.855  1.00  0.00          3A4
ATOM    614  CG  LYS   126      39.424  17.682  30.406  1.00  0.00          3A4
ATOM    615  CD  LYS   126      39.026  18.858  31.300  1.00  0.00          3A4
ATOM    616  CE  LYS   126      39.634  20.191  30.845  1.00  0.00          3A4
ATOM    617  NZ  LYS   126      39.206  21.296  31.735  1.00  0.00          3A4
ATOM    618  C   LYS   126      40.413  14.775  29.867  1.00  0.00          3A4
ATOM    619  O   LYS   126      41.152  15.173  28.977  1.00  0.00          3A4
ATOM    620  N   ARG   127      40.830  13.884  30.785  1.00  0.00          3A4
ATOM    621  CA  ARG   127      42.152  13.315  30.821  1.00  0.00          3A4
ATOM    622  CB  ARG   127      42.369  12.556  32.148  1.00  0.00          3A4
ATOM    623  CG  ARG   127      42.319  13.460  33.385  1.00  0.00          3A4
ATOM    624  CD  ARG   127      42.230  12.652  34.686  1.00  0.00          3A4
ATOM    625  NE  ARG   127      42.079  13.613  35.835  1.00  0.00          3A4
ATOM    626  CZ  ARG   127      41.521  13.267  37.040  1.00  0.00          3A4
ATOM    627  NH1 ARG   127      41.438  14.206  38.026  1.00  0.00          3A4
ATOM    628  NH2 ARG   127      41.040  12.009  37.276  1.00  0.00          3A4
ATOM    629  C   ARG   127      42.448  12.378  29.678  1.00  0.00          3A4
ATOM    630  O   ARG   127      43.503  12.464  29.060  1.00  0.00          3A4
ATOM    631  N   LEU   128      41.487  11.489  29.329  1.00  0.00          3A4
ATOM    632  CA  LEU   128      41.614  10.553  28.227  1.00  0.00          3A4
ATOM    633  CB  LEU   128      40.552   9.436  28.305  1.00  0.00          3A4
ATOM    634  CG  LEU   128      40.710   8.475  29.510  1.00  0.00          3A4
ATOM    635  CD1 LEU   128      39.492   7.536  29.620  1.00  0.00          3A4
ATOM    636  CD2 LEU   128      42.026   7.670  29.503  1.00  0.00          3A4
ATOM    637  C   LEU   128      41.513  11.260  26.900  1.00  0.00          3A4
ATOM    638  O   LEU   128      42.307  10.998  26.016  1.00  0.00          3A4
ATOM    639  N   ARG   129      40.613  12.256  26.764  1.00  0.00          3A4
ATOM    640  CA  ARG   129      40.455  13.056  25.570  1.00  0.00          3A4
ATOM    641  CB  ARG   129      39.248  13.995  25.706  1.00  0.00          3A4
ATOM    642  CG  ARG   129      38.865  14.698  24.411  1.00  0.00          3A4
ATOM    643  CD  ARG   129      37.443  15.285  24.477  1.00  0.00          3A4
ATOM    644  NE  ARG   129      36.965  15.632  23.089  1.00  0.00          3A4
ATOM    645  CZ  ARG   129      37.094  16.870  22.512  1.00  0.00          3A4
ATOM    646  NH1 ARG   129      36.589  17.069  21.260  1.00  0.00          3A4
ATOM    647  NH2 ARG   129      37.709  17.907  23.155  1.00  0.00          3A4
ATOM    648  C   ARG   129      41.673  13.896  25.247  1.00  0.00          3A4
ATOM    649  O   ARG   129      42.125  13.963  24.109  1.00  0.00          3A4
ATOM    650  N   SER   130      42.292  14.491  26.294  1.00  0.00          3A4
ATOM    651  CA  SER   130      43.486  15.299  26.191  1.00  0.00          3A4
ATOM    652  CB  SER   130      43.870  16.030  27.515  1.00  0.00          3A4
ATOM    653  OG  SER   130      42.925  17.049  27.812  1.00  0.00          3A4
ATOM    654  C   SER   130      44.691  14.547  25.703  1.00  0.00          3A4
ATOM    655  O   SER   130      45.506  15.121  25.002  1.00  0.00          3A4
ATOM    656  N   LEU   131      44.822  13.241  26.004  1.00  0.00          3A4
ATOM    657  CA  LEU   131      45.894  12.396  25.508  1.00  0.00          3A4
ATOM    658  CB  LEU   131      45.835  11.013  26.195  1.00  0.00          3A4
ATOM    659  CG  LEU   131      46.473  11.008  27.591  1.00  0.00          3A4
ATOM    660  CD1 LEU   131      45.836   9.924  28.474  1.00  0.00          3A4
ATOM    661  CD2 LEU   131      48.005  10.845  27.482  1.00  0.00          3A4
ATOM    662  C   LEU   131      45.875  12.189  24.006  1.00  0.00          3A4
ATOM    663  O   LEU   131      46.913  12.177  23.361  1.00  0.00          3A4
ATOM    664  N   LEU   132      44.675  12.059  23.421  1.00  0.00          3A4
ATOM    665  CA  LEU   132      44.436  11.692  22.040  1.00  0.00          3A4
ATOM    666  CB  LEU   132      43.113  10.883  21.884  1.00  0.00          3A4
ATOM    667  CG  LEU   132      42.628  10.220  23.187  1.00  0.00          3A4
ATOM    668  CD1 LEU   132      41.170   9.739  23.225  1.00  0.00          3A4
ATOM    669  CD2 LEU   132      43.579   9.147  23.759  1.00  0.00          3A4
ATOM    670  C   LEU   132      44.339  12.896  21.142  1.00  0.00          3A4
ATOM    671  O   LEU   132      44.709  12.862  19.975  1.00  0.00          3A4
ATOM    672  N   SER   133      43.808  14.009  21.685  1.00  0.00          3A4
ATOM    673  CA  SER   133      43.570  15.239  20.967  1.00  0.00          3A4
ATOM    674  CB  SER   133      42.882  16.277  21.854  1.00  0.00          3A4
ATOM    675  OG  SER   133      43.525  16.664  23.058  1.00  0.00          3A4
ATOM    676  C   SER   133      44.766  15.878  20.280  1.00  0.00          3A4
ATOM    677  O   SER   133      44.586  16.429  19.192  1.00  0.00          3A4
```

ATOM	678	N	PRO	134	46.017	15.798	20.777	1.00	0.00	3A4
ATOM	679	CA	PRO	134	47.159	16.327	20.076	1.00	0.00	3A4
ATOM	680	CD	PRO	134	46.405	15.537	22.155	1.00	0.00	3A4
ATOM	681	CB	PRO	134	48.327	16.318	21.087	1.00	0.00	3A4
ATOM	682	CG	PRO	134	47.635	16.387	22.434	1.00	0.00	3A4
ATOM	683	C	PRO	134	47.567	15.563	18.844	1.00	0.00	3A4
ATOM	684	O	PRO	134	48.106	16.175	17.927	1.00	0.00	3A4
ATOM	685	N	THR	135	47.305	14.235	18.803	1.00	0.00	3A4
ATOM	686	CA	THR	135	47.657	13.342	17.727	1.00	0.00	3A4
ATOM	687	CB	THR	135	47.864	11.912	18.232	1.00	0.00	3A4
ATOM	688	OG1	THR	135	46.681	11.299	18.729	1.00	0.00	3A4
ATOM	689	CG2	THR	135	48.889	11.953	19.387	1.00	0.00	3A4
ATOM	690	C	THR	135	46.639	13.419	16.594	1.00	0.00	3A4
ATOM	691	O	THR	135	46.921	13.057	15.460	1.00	0.00	3A4
ATOM	692	N	PHE	136	45.420	13.916	16.895	1.00	0.00	3A4
ATOM	693	CA	PHE	136	44.322	13.979	15.962	1.00	0.00	3A4
ATOM	694	CB	PHE	136	43.007	13.434	16.581	1.00	0.00	3A4
ATOM	695	CG	PHE	136	43.069	12.028	17.109	1.00	0.00	3A4
ATOM	696	CD1	PHE	136	42.397	11.733	18.297	1.00	0.00	3A4
ATOM	697	CD2	PHE	136	43.793	10.992	16.495	1.00	0.00	3A4
ATOM	698	CE1	PHE	136	42.237	10.417	18.717	1.00	0.00	3A4
ATOM	699	CE2	PHE	136	43.668	9.665	16.926	1.00	0.00	3A4
ATOM	700	CZ	PHE	136	42.847	9.372	18.017	1.00	0.00	3A4
ATOM	701	C	PHE	136	44.074	15.402	15.465	1.00	0.00	3A4
ATOM	702	O	PHE	136	42.971	15.703	15.025	1.00	0.00	3A4
ATOM	703	N	THR	137	45.088	16.323	15.493	1.00	0.00	3A4
ATOM	704	CA	THR	137	44.944	17.764	15.224	1.00	0.00	3A4
ATOM	705	CB	THR	137	46.098	18.572	15.830	1.00	0.00	3A4
ATOM	706	OG1	THR	137	46.156	18.321	17.228	1.00	0.00	3A4
ATOM	707	CG2	THR	137	45.936	20.108	15.640	1.00	0.00	3A4
ATOM	708	C	THR	137	44.796	18.094	13.739	1.00	0.00	3A4
ATOM	709	O	THR	137	43.885	18.830	13.359	1.00	0.00	3A4
ATOM	710	N	SER	138	45.685	17.534	12.870	1.00	0.00	3A4
ATOM	711	CA	SER	138	45.656	17.677	11.419	1.00	0.00	3A4
ATOM	712	CB	SER	138	47.076	17.874	10.806	1.00	0.00	3A4
ATOM	713	OG	SER	138	47.648	19.086	11.280	1.00	0.00	3A4
ATOM	714	C	SER	138	45.012	16.431	10.860	1.00	0.00	3A4
ATOM	715	O	SER	138	43.868	16.450	10.408	1.00	0.00	3A4
ATOM	716	N	GLY	139	45.756	15.304	10.953	1.00	0.00	3A4
ATOM	717	CA	GLY	139	45.288	13.957	10.734	1.00	0.00	3A4
ATOM	718	C	GLY	139	45.698	13.207	11.960	1.00	0.00	3A4
ATOM	719	O	GLY	139	46.061	13.818	12.961	1.00	0.00	3A4
ATOM	720	N	LYS	140	45.629	11.847	11.918	1.00	0.00	3A4
ATOM	721	CA	LYS	140	45.777	10.945	13.054	1.00	0.00	3A4
ATOM	722	CB	LYS	140	44.729	9.786	13.048	1.00	0.00	3A4
ATOM	723	CG	LYS	140	43.246	10.097	13.336	1.00	0.00	3A4
ATOM	724	CD	LYS	140	42.846	11.560	13.252	1.00	0.00	3A4
ATOM	725	CE	LYS	140	41.456	11.872	13.770	1.00	0.00	3A4
ATOM	726	NZ	LYS	140	41.193	13.331	13.606	1.00	0.00	3A4
ATOM	727	C	LYS	140	47.165	10.340	13.065	1.00	0.00	3A4
ATOM	728	O	LYS	140	47.330	9.123	12.976	1.00	0.00	3A4
ATOM	729	N	LEU	141	48.195	11.212	13.185	1.00	0.00	3A4
ATOM	730	CA	LEU	141	49.585	10.835	13.207	1.00	0.00	3A4
ATOM	731	CB	LEU	141	50.096	10.321	11.825	1.00	0.00	3A4
ATOM	732	CG	LEU	141	51.411	9.530	11.812	1.00	0.00	3A4
ATOM	733	CD1	LEU	141	52.059	9.603	10.425	1.00	0.00	3A4
ATOM	734	CD2	LEU	141	51.161	8.066	12.211	1.00	0.00	3A4
ATOM	735	C	LEU	141	50.286	12.100	13.623	1.00	0.00	3A4
ATOM	736	O	LEU	141	50.455	12.362	14.813	1.00	0.00	3A4
ATOM	737	N	LYS	142	50.687	12.924	12.618	1.00	0.00	3A4
ATOM	738	CA	LYS	142	51.307	14.222	12.760	1.00	0.00	3A4
ATOM	739	CB	LYS	142	52.868	14.192	12.729	1.00	0.00	3A4
ATOM	740	CG	LYS	142	53.516	13.465	13.915	1.00	0.00	3A4
ATOM	741	CD	LYS	142	55.045	13.555	13.916	1.00	0.00	3A4
ATOM	742	CE	LYS	142	55.714	12.858	15.108	1.00	0.00	3A4
ATOM	743	NZ	LYS	142	55.454	11.401	15.086	1.00	0.00	3A4
ATOM	744	C	LYS	142	50.813	15.068	11.606	1.00	0.00	3A4
ATOM	745	O	LYS	142	50.704	16.287	11.736	1.00	0.00	3A4
ATOM	746	N	GLU	143	50.529	14.432	10.433	1.00	0.00	3A4
ATOM	747	CA	GLU	143	50.169	15.105	9.198	1.00	0.00	3A4
ATOM	748	CB	GLU	143	51.389	15.242	8.234	1.00	0.00	3A4
ATOM	749	CG	GLU	143	51.158	16.046	6.935	1.00	0.00	3A4

ATOM	750	CD	GLU	143	50.774	17.493	7.267	1.00	0.00	3A4
ATOM	751	OE1	GLU	143	51.602	18.194	7.909	1.00	0.00	3A4
ATOM	752	OE2	GLU	143	49.651	17.917	6.882	1.00	0.00	3A4
ATOM	753	C	GLU	143	49.047	14.324	8.559	1.00	0.00	3A4
ATOM	754	O	GLU	143	47.898	14.760	8.605	1.00	0.00	3A4
ATOM	755	N	MET	144	49.393	13.160	7.926	1.00	0.00	3A4
ATOM	756	CA	MET	144	48.584	12.130	7.300	1.00	0.00	3A4
ATOM	757	CB	MET	144	47.303	11.759	8.070	1.00	0.00	3A4
ATOM	758	CG	MET	144	47.567	10.932	9.334	1.00	0.00	3A4
ATOM	759	SD	MET	144	48.269	9.267	9.019	1.00	0.00	3A4
ATOM	760	CE	MET	144	47.029	8.504	7.928	1.00	0.00	3A4
ATOM	761	C	MET	144	48.192	12.409	5.879	1.00	0.00	3A4
ATOM	762	O	MET	144	47.891	11.472	5.150	1.00	0.00	3A4
ATOM	763	N	VAL	145	48.169	13.678	5.428	1.00	0.00	3A4
ATOM	764	CA	VAL	145	47.650	14.088	4.130	1.00	0.00	3A4
ATOM	765	CB	VAL	145	47.693	15.597	3.949	1.00	0.00	3A4
ATOM	766	CG1	VAL	145	46.839	16.061	2.734	1.00	0.00	3A4
ATOM	767	CG2	VAL	145	47.128	16.245	5.237	1.00	0.00	3A4
ATOM	768	C	VAL	145	48.261	13.425	2.906	1.00	0.00	3A4
ATOM	769	O	VAL	145	47.501	13.014	2.026	1.00	0.00	3A4
ATOM	770	N	PRO	146	49.595	13.235	2.821	1.00	0.00	3A4
ATOM	771	CA	PRO	146	50.226	12.490	1.741	1.00	0.00	3A4
ATOM	772	CD	PRO	146	50.623	13.942	3.599	1.00	0.00	3A4
ATOM	773	CB	PRO	146	51.743	12.625	1.988	1.00	0.00	3A4
ATOM	774	CG	PRO	146	51.872	13.954	2.721	1.00	0.00	3A4
ATOM	775	C	PRO	146	49.826	11.029	1.698	1.00	0.00	3A4
ATOM	776	O	PRO	146	49.678	10.483	0.613	1.00	0.00	3A4
ATOM	777	N	ILE	147	49.572	10.388	2.863	1.00	0.00	3A4
ATOM	778	CA	ILE	147	49.098	9.027	2.976	1.00	0.00	3A4
ATOM	779	CB	ILE	147	49.254	8.469	4.382	1.00	0.00	3A4
ATOM	780	CG2	ILE	147	48.993	6.930	4.422	1.00	0.00	3A4
ATOM	781	CG1	ILE	147	50.685	8.809	4.901	1.00	0.00	3A4
ATOM	782	CD	ILE	147	51.018	8.281	6.300	1.00	0.00	3A4
ATOM	783	C	ILE	147	47.660	8.881	2.564	1.00	0.00	3A4
ATOM	784	O	ILE	147	47.306	7.899	1.922	1.00	0.00	3A4
ATOM	785	N	ILE	148	46.789	9.866	2.875	1.00	0.00	3A4
ATOM	786	CA	ILE	148	45.386	9.833	2.503	1.00	0.00	3A4
ATOM	787	CB	ILE	148	44.570	10.932	3.172	1.00	0.00	3A4
ATOM	788	CG2	ILE	148	43.057	10.768	2.811	1.00	0.00	3A4
ATOM	789	CG1	ILE	148	44.675	10.809	4.718	1.00	0.00	3A4
ATOM	790	CD	ILE	148	44.158	12.030	5.488	1.00	0.00	3A4
ATOM	791	C	ILE	148	45.218	9.888	1.005	1.00	0.00	3A4
ATOM	792	O	ILE	148	44.486	9.106	0.407	1.00	0.00	3A4
ATOM	793	N	ALA	149	46.000	10.765	0.350	1.00	0.00	3A4
ATOM	794	CA	ALA	149	46.058	10.923	-1.086	1.00	0.00	3A4
ATOM	795	CB	ALA	149	46.983	12.097	-1.414	1.00	0.00	3A4
ATOM	796	C	ALA	149	46.539	9.682	-1.803	1.00	0.00	3A4
ATOM	797	O	ALA	149	45.965	9.246	-2.797	1.00	0.00	3A4
ATOM	798	N	GLN	150	47.578	9.019	-1.243	1.00	0.00	3A4
ATOM	799	CA	GLN	150	48.121	7.780	-1.753	1.00	0.00	3A4
ATOM	800	CB	GLN	150	49.342	7.295	-0.954	1.00	0.00	3A4
ATOM	801	CG	GLN	150	50.637	8.037	-1.297	1.00	0.00	3A4
ATOM	802	CD	GLN	150	51.737	7.586	-0.326	1.00	0.00	3A4
ATOM	803	OE1	GLN	150	52.080	6.406	-0.292	1.00	0.00	3A4
ATOM	804	NE2	GLN	150	52.300	8.525	0.483	1.00	0.00	3A4
ATOM	805	C	GLN	150	47.129	6.663	-1.774	1.00	0.00	3A4
ATOM	806	O	GLN	150	46.962	5.992	-2.789	1.00	0.00	3A4
ATOM	807	N	TYR	151	46.371	6.500	-0.658	1.00	0.00	3A4
ATOM	808	CA	TYR	151	45.418	5.431	-0.538	1.00	0.00	3A4
ATOM	809	CB	TYR	151	44.853	5.227	0.859	1.00	0.00	3A4
ATOM	810	CG	TYR	151	44.181	3.823	0.880	1.00	0.00	3A4
ATOM	811	CD1	TYR	151	43.188	3.417	1.745	1.00	0.00	3A4
ATOM	812	CD2	TYR	151	44.795	2.750	0.124	1.00	0.00	3A4
ATOM	813	CE1	TYR	151	42.443	2.274	1.345	1.00	0.00	3A4
ATOM	814	CE2	TYR	151	44.170	1.533	-0.113	1.00	0.00	3A4
ATOM	815	CZ	TYR	151	42.935	1.315	0.454	1.00	0.00	3A4
ATOM	816	OH	TYR	151	42.254	0.104	0.201	1.00	0.00	3A4
ATOM	817	C	TYR	151	44.221	5.669	-1.449	1.00	0.00	3A4
ATOM	818	O	TYR	151	43.738	4.750	-2.103	1.00	0.00	3A4
ATOM	819	N	GLY	152	43.775	6.936	-1.554	1.00	0.00	3A4
ATOM	820	CA	GLY	152	42.703	7.368	-2.423	1.00	0.00	3A4
ATOM	821	C	GLY	152	42.962	7.025	-3.877	1.00	0.00	3A4

```
ATOM    822  O   GLY   152      42.122   6.466  -4.565  1.00  0.00          3A4
ATOM    823  N   ASP   153      44.194   7.284  -4.339  1.00  0.00          3A4
ATOM    824  CA  ASP   153      44.647   6.996  -5.674  1.00  0.00          3A4
ATOM    825  CB  ASP   153      46.061   7.586  -5.844  1.00  0.00          3A4
ATOM    826  CG  ASP   153      45.993   9.119  -5.945  1.00  0.00          3A4
ATOM    827  OD1 ASP   153      45.014   9.650  -6.534  1.00  0.00          3A4
ATOM    828  OD2 ASP   153      46.922   9.784  -5.416  1.00  0.00          3A4
ATOM    829  C   ASP   153      44.703   5.521  -6.007  1.00  0.00          3A4
ATOM    830  O   ASP   153      44.288   5.096  -7.076  1.00  0.00          3A4
ATOM    831  N   VAL   154      45.154   4.686  -5.048  1.00  0.00          3A4
ATOM    832  CA  VAL   154      45.173   3.235  -5.160  1.00  0.00          3A4
ATOM    833  CB  VAL   154      45.878   2.605  -3.968  1.00  0.00          3A4
ATOM    834  CG1 VAL   154      45.770   1.054  -3.875  1.00  0.00          3A4
ATOM    835  CG2 VAL   154      47.373   2.989  -4.067  1.00  0.00          3A4
ATOM    836  C   VAL   154      43.793   2.651  -5.283  1.00  0.00          3A4
ATOM    837  O   VAL   154      43.531   1.783  -6.112  1.00  0.00          3A4
ATOM    838  N   LEU   155      42.842   3.184  -4.494  1.00  0.00          3A4
ATOM    839  CA  LEU   155      41.460   2.758  -4.505  1.00  0.00          3A4
ATOM    840  CB  LEU   155      40.697   3.480  -3.395  1.00  0.00          3A4
ATOM    841  CG  LEU   155      41.005   3.018  -1.989  1.00  0.00          3A4
ATOM    842  CD1 LEU   155      40.785   4.226  -1.096  1.00  0.00          3A4
ATOM    843  CD2 LEU   155      40.117   1.825  -1.591  1.00  0.00          3A4
ATOM    844  C   LEU   155      40.732   3.082  -5.782  1.00  0.00          3A4
ATOM    845  O   LEU   155      39.955   2.295  -6.313  1.00  0.00          3A4
ATOM    846  N   VAL   156      41.020   4.276  -6.333  1.00  0.00          3A4
ATOM    847  CA  VAL   156      40.441   4.744  -7.564  1.00  0.00          3A4
ATOM    848  CB  VAL   156      40.709   6.216  -7.769  1.00  0.00          3A4
ATOM    849  CG1 VAL   156      40.208   6.709  -9.147  1.00  0.00          3A4
ATOM    850  CG2 VAL   156      39.887   6.989  -6.709  1.00  0.00          3A4
ATOM    851  C   VAL   156      40.956   3.916  -8.726  1.00  0.00          3A4
ATOM    852  O   VAL   156      40.186   3.474  -9.566  1.00  0.00          3A4
ATOM    853  N   ARG   157      42.263   3.571  -8.714  1.00  0.00          3A4
ATOM    854  CA  ARG   157      42.881   2.692  -9.687  1.00  0.00          3A4
ATOM    855  CB  ARG   157      44.400   2.603  -9.480  1.00  0.00          3A4
ATOM    856  CG  ARG   157      45.201   1.988 -10.646  1.00  0.00          3A4
ATOM    857  CD  ARG   157      46.718   1.949 -10.406  1.00  0.00          3A4
ATOM    858  NE  ARG   157      47.008   0.982  -9.282  1.00  0.00          3A4
ATOM    859  CZ  ARG   157      47.582   1.328  -8.084  1.00  0.00          3A4
ATOM    860  NH1 ARG   157      47.753   0.362  -7.136  1.00  0.00          3A4
ATOM    861  NH2 ARG   157      47.975   2.607  -7.807  1.00  0.00          3A4
ATOM    862  C   ARG   157      42.316   1.305  -9.694  1.00  0.00          3A4
ATOM    863  O   ARG   157      42.062   0.746 -10.749  1.00  0.00          3A4
ATOM    864  N   ASN   158      42.004   0.746  -8.509  1.00  0.00          3A4
ATOM    865  CA  ASN   158      41.363  -0.540  -8.359  1.00  0.00          3A4
ATOM    866  CB  ASN   158      41.312  -0.962  -6.875  1.00  0.00          3A4
ATOM    867  CG  ASN   158      42.725  -1.184  -6.308  1.00  0.00          3A4
ATOM    868  OD1 ASN   158      43.710  -1.336  -7.029  1.00  0.00          3A4
ATOM    869  ND2 ASN   158      42.827  -1.211  -4.951  1.00  0.00          3A4
ATOM    870  C   ASN   158      39.959  -0.569  -8.928  1.00  0.00          3A4
ATOM    871  O   ASN   158      39.541  -1.568  -9.503  1.00  0.00          3A4
ATOM    872  N   LEU   159      39.205   0.547  -8.840  1.00  0.00          3A4
ATOM    873  CA  LEU   159      37.900   0.698  -9.460  1.00  0.00          3A4
ATOM    874  CB  LEU   159      37.181   1.944  -8.901  1.00  0.00          3A4
ATOM    875  CG  LEU   159      36.392   1.845  -7.590  1.00  0.00          3A4
ATOM    876  CD1 LEU   159      35.846   3.252  -7.275  1.00  0.00          3A4
ATOM    877  CD2 LEU   159      35.226   0.844  -7.672  1.00  0.00          3A4
ATOM    878  C   LEU   159      37.986   0.850 -10.979  1.00  0.00          3A4
ATOM    879  O   LEU   159      37.180   0.311 -11.731  1.00  0.00          3A4
ATOM    880  N   ARG   160      39.032   1.542 -11.475  1.00  0.00          3A4
ATOM    881  CA  ARG   160      39.316   1.707 -12.887  1.00  0.00          3A4
ATOM    882  CB  ARG   160      40.462   2.697 -13.097  1.00  0.00          3A4
ATOM    883  CG  ARG   160      40.032   4.151 -12.829  1.00  0.00          3A4
ATOM    884  CD  ARG   160      41.097   5.224 -13.106  1.00  0.00          3A4
ATOM    885  NE  ARG   160      42.243   5.069 -12.147  1.00  0.00          3A4
ATOM    886  CZ  ARG   160      43.077   6.096 -11.785  1.00  0.00          3A4
ATOM    887  NH1 ARG   160      44.114   5.859 -10.932  1.00  0.00          3A4
ATOM    888  NH2 ARG   160      42.889   7.363 -12.251  1.00  0.00          3A4
ATOM    889  C   ARG   160      39.687   0.420 -13.585  1.00  0.00          3A4
ATOM    890  O   ARG   160      39.428   0.250 -14.767  1.00  0.00          3A4
ATOM    891  N   ARG   161      40.250  -0.548 -12.834  1.00  0.00          3A4
ATOM    892  CA  ARG   161      40.597  -1.870 -13.293  1.00  0.00          3A4
ATOM    893  CB  ARG   161      41.743  -2.432 -12.420  1.00  0.00          3A4
```

ATOM	894	CG	ARG	161	43.082	-1.717	-12.670	1.00	0.00	3A4
ATOM	895	CD	ARG	161	44.093	-1.838	-11.519	1.00	0.00	3A4
ATOM	896	NE	ARG	161	44.400	-3.285	-11.257	1.00	0.00	3A4
ATOM	897	CZ	ARG	161	45.172	-3.692	-10.198	1.00	0.00	3A4
ATOM	898	NH1	ARG	161	45.396	-5.024	-10.010	1.00	0.00	3A4
ATOM	899	NH2	ARG	161	45.720	-2.792	-9.328	1.00	0.00	3A4
ATOM	900	C	ARG	161	39.432	-2.837	-13.270	1.00	0.00	3A4
ATOM	901	O	ARG	161	39.618	-4.026	-13.474	1.00	0.00	3A4
ATOM	902	N	GLU	162	38.181	-2.341	-13.060	1.00	0.00	3A4
ATOM	903	CA	GLU	162	36.943	-3.106	-13.121	1.00	0.00	3A4
ATOM	904	CB	GLU	162	35.704	-2.403	-12.447	1.00	0.00	3A4
ATOM	905	CG	GLU	162	35.006	-1.245	-13.229	1.00	0.00	3A4
ATOM	906	CD	GLU	162	33.961	-0.524	-12.375	1.00	0.00	3A4
ATOM	907	OE1	GLU	162	34.331	-0.002	-11.289	1.00	0.00	3A4
ATOM	908	OE2	GLU	162	32.779	-0.469	-12.809	1.00	0.00	3A4
ATOM	909	C	GLU	162	36.578	-3.419	-14.538	1.00	0.00	3A4
ATOM	910	O	GLU	162	36.521	-2.577	-15.435	1.00	0.00	3A4
ATOM	911	N	ALA	163	36.386	-4.746	-14.788	1.00	0.00	3A4
ATOM	912	CA	ALA	163	36.408	-5.391	-16.091	1.00	0.00	3A4
ATOM	913	CB	ALA	163	37.029	-6.809	-15.993	1.00	0.00	3A4
ATOM	914	C	ALA	163	35.037	-5.494	-16.717	1.00	0.00	3A4
ATOM	915	O	ALA	163	34.019	-5.308	-16.051	1.00	0.00	3A4
ATOM	916	N	GLU	164	35.042	-5.771	-18.059	1.00	0.00	3A4
ATOM	917	CA	GLU	164	33.935	-5.860	-19.009	1.00	0.00	3A4
ATOM	918	CB	GLU	164	32.661	-6.587	-18.459	1.00	0.00	3A4
ATOM	919	CG	GLU	164	31.701	-7.151	-19.531	1.00	0.00	3A4
ATOM	920	CD	GLU	164	30.505	-7.813	-18.839	1.00	0.00	3A4
ATOM	921	OE1	GLU	164	29.737	-7.082	-18.156	1.00	0.00	3A4
ATOM	922	OE2	GLU	164	30.342	-9.055	-18.984	1.00	0.00	3A4
ATOM	923	C	GLU	164	33.612	-4.461	-19.520	1.00	0.00	3A4
ATOM	924	O	GLU	164	32.462	-4.138	-19.797	1.00	0.00	3A4
ATOM	925	N	THR	165	34.671	-3.592	-19.572	1.00	0.00	3A4
ATOM	926	CA	THR	165	34.730	-2.131	-19.714	1.00	0.00	3A4
ATOM	927	CB	THR	165	34.039	-1.480	-20.938	1.00	0.00	3A4
ATOM	928	OG1	THR	165	32.615	-1.557	-20.965	1.00	0.00	3A4
ATOM	929	CG2	THR	165	34.604	-2.115	-22.228	1.00	0.00	3A4
ATOM	930	C	THR	165	34.372	-1.470	-18.379	1.00	0.00	3A4
ATOM	931	O	THR	165	35.235	-0.931	-17.690	1.00	0.00	3A4
ATOM	932	N	GLY	166	33.075	-1.547	-17.996	1.00	0.00	3A4
ATOM	933	CA	GLY	166	32.567	-1.129	-16.720	1.00	0.00	3A4
ATOM	934	C	GLY	166	31.084	-1.094	-16.877	1.00	0.00	3A4
ATOM	935	O	GLY	166	30.541	-0.151	-17.449	1.00	0.00	3A4
ATOM	936	N	LYS	167	30.386	-2.143	-16.363	1.00	0.00	3A4
ATOM	937	CA	LYS	167	28.935	-2.211	-16.262	1.00	0.00	3A4
ATOM	938	CB	LYS	167	28.217	-3.202	-17.239	1.00	0.00	3A4
ATOM	939	CG	LYS	167	28.165	-2.770	-18.713	1.00	0.00	3A4
ATOM	940	CD	LYS	167	29.336	-3.252	-19.574	1.00	0.00	3A4
ATOM	941	CE	LYS	167	29.134	-2.949	-21.066	1.00	0.00	3A4
ATOM	942	NZ	LYS	167	30.208	-3.554	-21.890	1.00	0.00	3A4
ATOM	943	C	LYS	167	28.582	-2.486	-14.802	1.00	0.00	3A4
ATOM	944	O	LYS	167	27.816	-1.688	-14.271	1.00	0.00	3A4
ATOM	945	N	PRO	168	29.041	-3.521	-14.057	1.00	0.00	3A4
ATOM	946	CA	PRO	168	28.796	-3.641	-12.622	1.00	0.00	3A4
ATOM	947	CD	PRO	168	29.518	-4.787	-14.626	1.00	0.00	3A4
ATOM	948	CB	PRO	168	28.695	-5.165	-12.400	1.00	0.00	3A4
ATOM	949	CG	PRO	168	29.625	-5.777	-13.459	1.00	0.00	3A4
ATOM	950	C	PRO	168	29.938	-3.027	-11.812	1.00	0.00	3A4
ATOM	951	O	PRO	168	31.100	-3.303	-12.110	1.00	0.00	3A4
ATOM	952	N	VAL	169	29.609	-2.275	-10.724	1.00	0.00	3A4
ATOM	953	CA	VAL	169	30.441	-2.280	-9.531	1.00	0.00	3A4
ATOM	954	CB	VAL	169	31.674	-1.381	-9.591	1.00	0.00	3A4
ATOM	955	CG1	VAL	169	31.356	0.130	-9.641	1.00	0.00	3A4
ATOM	956	CG2	VAL	169	32.702	-1.746	-8.502	1.00	0.00	3A4
ATOM	957	C	VAL	169	29.535	-1.926	-8.382	1.00	0.00	3A4
ATOM	958	O	VAL	169	28.623	-1.120	-8.526	1.00	0.00	3A4
ATOM	959	N	THR	170	29.805	-2.498	-7.184	1.00	0.00	3A4
ATOM	960	CA	THR	170	29.193	-2.121	-5.931	1.00	0.00	3A4
ATOM	961	CB	THR	170	28.902	-3.314	-5.038	1.00	0.00	3A4
ATOM	962	OG1	THR	170	28.066	-4.231	-5.734	1.00	0.00	3A4
ATOM	963	CG2	THR	170	28.173	-2.877	-3.736	1.00	0.00	3A4
ATOM	964	C	THR	170	30.178	-1.183	-5.305	1.00	0.00	3A4
ATOM	965	O	THR	170	31.232	-1.589	-4.831	1.00	0.00	3A4

ATOM	966	N	LEU	171	29.854	0.126	-5.296	1.00	0.00	3A4
ATOM	967	CA	LEU	171	30.705	1.177	-4.769	1.00	0.00	3A4
ATOM	968	CB	LEU	171	30.055	2.555	-5.044	1.00	0.00	3A4
ATOM	969	CG	LEU	171	30.547	3.319	-6.282	1.00	0.00	3A4
ATOM	970	CD1	LEU	171	29.654	4.563	-6.453	1.00	0.00	3A4
ATOM	971	CD2	LEU	171	32.040	3.710	-6.194	1.00	0.00	3A4
ATOM	972	C	LEU	171	30.998	1.069	-3.277	1.00	0.00	3A4
ATOM	973	O	LEU	171	32.076	1.436	-2.831	1.00	0.00	3A4
ATOM	974	N	LYS	172	30.072	0.510	-2.464	1.00	0.00	3A4
ATOM	975	CA	LYS	172	30.261	0.291	-1.041	1.00	0.00	3A4
ATOM	976	CB	LYS	172	28.920	-0.132	-0.376	1.00	0.00	3A4
ATOM	977	CG	LYS	172	28.909	-0.334	1.158	1.00	0.00	3A4
ATOM	978	CD	LYS	172	29.194	0.939	1.969	1.00	0.00	3A4
ATOM	979	CE	LYS	172	29.078	0.766	3.488	1.00	0.00	3A4
ATOM	980	NZ	LYS	172	30.110	-0.160	4.012	1.00	0.00	3A4
ATOM	981	C	LYS	172	31.330	-0.744	-0.748	1.00	0.00	3A4
ATOM	982	O	LYS	172	32.274	-0.492	-0.010	1.00	0.00	3A4
ATOM	983	N	ASP	173	31.243	-1.937	-1.374	1.00	0.00	3A4
ATOM	984	CA	ASP	173	32.134	-3.048	-1.103	1.00	0.00	3A4
ATOM	985	CB	ASP	173	31.447	-4.365	-1.539	1.00	0.00	3A4
ATOM	986	CG	ASP	173	32.095	-5.634	-0.940	1.00	0.00	3A4
ATOM	987	OD1	ASP	173	32.129	-5.750	0.315	1.00	0.00	3A4
ATOM	988	OD2	ASP	173	32.559	-6.496	-1.735	1.00	0.00	3A4
ATOM	989	C	ASP	173	33.491	-2.909	-1.760	1.00	0.00	3A4
ATOM	990	O	ASP	173	34.487	-3.361	-1.199	1.00	0.00	3A4
ATOM	991	N	VAL	174	33.571	-2.272	-2.947	1.00	0.00	3A4
ATOM	992	CA	VAL	174	34.804	-2.128	-3.702	1.00	0.00	3A4
ATOM	993	CB	VAL	174	34.550	-2.192	-5.209	1.00	0.00	3A4
ATOM	994	CG1	VAL	174	35.866	-2.225	-6.033	1.00	0.00	3A4
ATOM	995	CG2	VAL	174	33.783	-3.513	-5.482	1.00	0.00	3A4
ATOM	996	C	VAL	174	35.560	-0.866	-3.321	1.00	0.00	3A4
ATOM	997	O	VAL	174	36.767	-0.793	-3.522	1.00	0.00	3A4
ATOM	998	N	PHE	175	34.889	0.162	-2.748	1.00	0.00	3A4
ATOM	999	CA	PHE	175	35.513	1.457	-2.585	1.00	0.00	3A4
ATOM	1000	CB	PHE	175	34.996	2.458	-3.637	1.00	0.00	3A4
ATOM	1001	CG	PHE	175	35.738	3.789	-3.669	1.00	0.00	3A4
ATOM	1002	CD1	PHE	175	35.169	4.936	-3.079	1.00	0.00	3A4
ATOM	1003	CD2	PHE	175	37.019	3.896	-4.239	1.00	0.00	3A4
ATOM	1004	CE1	PHE	175	35.866	6.153	-3.047	1.00	0.00	3A4
ATOM	1005	CE2	PHE	175	37.703	5.120	-4.237	1.00	0.00	3A4
ATOM	1006	CZ	PHE	175	37.136	6.244	-3.628	1.00	0.00	3A4
ATOM	1007	C	PHE	175	35.362	1.997	-1.219	1.00	0.00	3A4
ATOM	1008	O	PHE	175	36.347	2.184	-0.509	1.00	0.00	3A4
ATOM	1009	N	GLY	176	34.105	2.318	-0.836	1.00	0.00	3A4
ATOM	1010	CA	GLY	176	33.755	3.060	0.352	1.00	0.00	3A4
ATOM	1011	C	GLY	176	34.098	2.332	1.609	1.00	0.00	3A4
ATOM	1012	O	GLY	176	34.413	2.958	2.614	1.00	0.00	3A4
ATOM	1013	N	ALA	177	34.126	0.976	1.565	1.00	0.00	3A4
ATOM	1014	CA	ALA	177	34.485	0.144	2.688	1.00	0.00	3A4
ATOM	1015	CB	ALA	177	33.968	-1.294	2.532	1.00	0.00	3A4
ATOM	1016	C	ALA	177	35.962	0.124	2.957	1.00	0.00	3A4
ATOM	1017	O	ALA	177	36.406	0.327	4.080	1.00	0.00	3A4
ATOM	1018	N	TYR	178	36.777	-0.058	1.903	1.00	0.00	3A4
ATOM	1019	CA	TYR	178	38.203	-0.242	2.016	1.00	0.00	3A4
ATOM	1020	CB	TYR	178	38.721	-0.724	0.638	1.00	0.00	3A4
ATOM	1021	CG	TYR	178	38.656	-2.235	0.593	1.00	0.00	3A4
ATOM	1022	CD1	TYR	178	37.893	-2.854	-0.416	1.00	0.00	3A4
ATOM	1023	CD2	TYR	178	39.236	-3.052	1.584	1.00	0.00	3A4
ATOM	1024	CE1	TYR	178	37.711	-4.243	-0.441	1.00	0.00	3A4
ATOM	1025	CE2	TYR	178	39.039	-4.442	1.580	1.00	0.00	3A4
ATOM	1026	CZ	TYR	178	38.282	-5.040	0.562	1.00	0.00	3A4
ATOM	1027	OH	TYR	178	38.091	-6.439	0.553	1.00	0.00	3A4
ATOM	1028	C	TYR	178	38.966	1.017	2.362	1.00	0.00	3A4
ATOM	1029	O	TYR	178	39.918	0.985	3.127	1.00	0.00	3A4
ATOM	1030	N	SER	179	38.545	2.180	1.822	1.00	0.00	3A4
ATOM	1031	CA	SER	179	39.171	3.471	2.018	1.00	0.00	3A4
ATOM	1032	CB	SER	179	38.412	4.545	1.196	1.00	0.00	3A4
ATOM	1033	OG	SER	179	39.108	5.787	1.074	1.00	0.00	3A4
ATOM	1034	C	SER	179	39.344	3.878	3.465	1.00	0.00	3A4
ATOM	1035	O	SER	179	40.445	4.039	3.966	1.00	0.00	3A4
ATOM	1036	N	MET	180	38.263	3.919	4.233	1.00	0.00	3A4
ATOM	1037	CA	MET	180	38.328	4.314	5.621	1.00	0.00	3A4

ATOM	1038	CB	MET	180	36.898	4.623	5.984	1.00	0.00	3A4
ATOM	1039	CG	MET	180	36.729	5.941	5.189	1.00	0.00	3A4
ATOM	1040	SD	MET	180	35.589	5.903	3.791	1.00	0.00	3A4
ATOM	1041	CE	MET	180	36.564	7.153	2.893	1.00	0.00	3A4
ATOM	1042	C	MET	180	38.961	3.325	6.527	1.00	0.00	3A4
ATOM	1043	O	MET	180	39.602	3.684	7.513	1.00	0.00	3A4
ATOM	1044	N	ASP	181	38.892	2.030	6.144	1.00	0.00	3A4
ATOM	1045	CA	ASP	181	39.455	1.016	6.971	1.00	0.00	3A4
ATOM	1046	CB	ASP	181	38.927	-0.386	6.705	1.00	0.00	3A4
ATOM	1047	CG	ASP	181	38.781	-1.148	5.400	1.00	0.00	3A4
ATOM	1048	OD1	ASP	181	39.773	-1.165	4.635	1.00	0.00	3A4
ATOM	1049	OD2	ASP	181	37.728	-1.810	5.195	1.00	0.00	3A4
ATOM	1050	C	ASP	181	40.963	0.976	6.884	1.00	0.00	3A4
ATOM	1051	O	ASP	181	41.663	0.876	7.886	1.00	0.00	3A4
ATOM	1052	N	VAL	182	41.515	1.163	5.671	1.00	0.00	3A4
ATOM	1053	CA	VAL	182	42.946	1.238	5.464	1.00	0.00	3A4
ATOM	1054	CB	VAL	182	43.279	1.227	4.010	1.00	0.00	3A4
ATOM	1055	CG1	VAL	182	44.767	1.508	3.706	1.00	0.00	3A4
ATOM	1056	CG2	VAL	182	42.889	-0.181	3.532	1.00	0.00	3A4
ATOM	1057	C	VAL	182	43.593	2.408	6.151	1.00	0.00	3A4
ATOM	1058	O	VAL	182	44.676	2.298	6.708	1.00	0.00	3A4
ATOM	1059	N	ILE	183	42.877	3.540	6.210	1.00	0.00	3A4
ATOM	1060	CA	ILE	183	43.341	4.740	6.855	1.00	0.00	3A4
ATOM	1061	CB	ILE	183	42.480	5.913	6.432	1.00	0.00	3A4
ATOM	1062	CG2	ILE	183	42.783	7.205	7.220	1.00	0.00	3A4
ATOM	1063	CG1	ILE	183	42.712	6.215	4.926	1.00	0.00	3A4
ATOM	1064	CD	ILE	183	44.121	6.672	4.516	1.00	0.00	3A4
ATOM	1065	C	ILE	183	43.365	4.589	8.352	1.00	0.00	3A4
ATOM	1066	O	ILE	183	44.321	4.972	9.017	1.00	0.00	3A4
ATOM	1067	N	THR	184	42.323	3.969	8.947	1.00	0.00	3A4
ATOM	1068	CA	THR	184	42.311	3.780	10.379	1.00	0.00	3A4
ATOM	1069	CB	THR	184	40.896	3.599	10.968	1.00	0.00	3A4
ATOM	1070	OG1	THR	184	40.842	3.873	12.369	1.00	0.00	3A4
ATOM	1071	CG2	THR	184	40.253	2.222	10.686	1.00	0.00	3A4
ATOM	1072	C	THR	184	43.288	2.710	10.811	1.00	0.00	3A4
ATOM	1073	O	THR	184	43.934	2.838	11.842	1.00	0.00	3A4
ATOM	1074	N	SER	185	43.544	1.697	9.955	1.00	0.00	3A4
ATOM	1075	CA	SER	185	44.571	0.701	10.179	1.00	0.00	3A4
ATOM	1076	CB	SER	185	44.486	-0.452	9.173	1.00	0.00	3A4
ATOM	1077	OG	SER	185	43.278	-1.178	9.354	1.00	0.00	3A4
ATOM	1078	C	SER	185	45.975	1.270	10.157	1.00	0.00	3A4
ATOM	1079	O	SER	185	46.793	0.962	11.011	1.00	0.00	3A4
ATOM	1080	N	THR	186	46.255	2.211	9.238	1.00	0.00	3A4
ATOM	1081	CA	THR	186	47.523	2.905	9.158	1.00	0.00	3A4
ATOM	1082	CB	THR	186	47.674	3.626	7.845	1.00	0.00	3A4
ATOM	1083	OG1	THR	186	46.613	4.495	7.478	1.00	0.00	3A4
ATOM	1084	CG2	THR	186	47.869	2.559	6.746	1.00	0.00	3A4
ATOM	1085	C	THR	186	47.770	3.895	10.256	1.00	0.00	3A4
ATOM	1086	O	THR	186	48.906	4.171	10.627	1.00	0.00	3A4
ATOM	1087	N	SER	187	46.676	4.433	10.825	1.00	0.00	3A4
ATOM	1088	CA	SER	187	46.674	5.311	11.961	1.00	0.00	3A4
ATOM	1089	CB	SER	187	45.260	5.983	12.078	1.00	0.00	3A4
ATOM	1090	OG	SER	187	45.037	6.742	13.262	1.00	0.00	3A4
ATOM	1091	C	SER	187	47.012	4.556	13.221	1.00	0.00	3A4
ATOM	1092	O	SER	187	47.753	5.052	14.047	1.00	0.00	3A4
ATOM	1093	N	PHE	188	46.490	3.324	13.352	1.00	0.00	3A4
ATOM	1094	CA	PHE	188	46.634	2.477	14.511	1.00	0.00	3A4
ATOM	1095	CB	PHE	188	45.408	1.520	14.609	1.00	0.00	3A4
ATOM	1096	CG	PHE	188	44.440	2.221	15.507	1.00	0.00	3A4
ATOM	1097	CD1	PHE	188	43.828	3.428	15.112	1.00	0.00	3A4
ATOM	1098	CD2	PHE	188	44.425	1.853	16.860	1.00	0.00	3A4
ATOM	1099	CE1	PHE	188	43.309	4.298	16.068	1.00	0.00	3A4
ATOM	1100	CE2	PHE	188	43.917	2.727	17.815	1.00	0.00	3A4
ATOM	1101	CZ	PHE	188	43.370	3.945	17.418	1.00	0.00	3A4
ATOM	1102	C	PHE	188	47.882	1.665	14.537	1.00	0.00	3A4
ATOM	1103	O	PHE	188	48.386	1.332	15.605	1.00	0.00	3A4
ATOM	1104	N	GLY	189	48.414	1.335	13.350	1.00	0.00	3A4
ATOM	1105	CA	GLY	189	49.610	0.550	13.208	1.00	0.00	3A4
ATOM	1106	C	GLY	189	49.281	-0.923	13.101	1.00	0.00	3A4
ATOM	1107	O	GLY	189	50.025	-1.788	13.555	1.00	0.00	3A4
ATOM	1108	N	VAL	190	48.147	-1.240	12.428	1.00	0.00	3A4
ATOM	1109	CA	VAL	190	47.745	-2.576	12.011	1.00	0.00	3A4

ATOM	1110	CB	VAL	190	46.239	-2.768	11.929	1.00	0.00	3A4
ATOM	1111	CG1	VAL	190	45.823	-4.253	11.759	1.00	0.00	3A4
ATOM	1112	CG2	VAL	190	45.621	-2.217	13.235	1.00	0.00	3A4
ATOM	1113	C	VAL	190	48.306	-2.843	10.635	1.00	0.00	3A4
ATOM	1114	O	VAL	190	48.419	-1.948	9.801	1.00	0.00	3A4
ATOM	1115	N	ASN	191	48.675	-4.105	10.372	1.00	0.00	3A4
ATOM	1116	CA	ASN	191	49.636	-4.477	9.377	1.00	0.00	3A4
ATOM	1117	CB	ASN	191	49.869	-5.997	9.517	1.00	0.00	3A4
ATOM	1118	CG	ASN	191	51.211	-6.502	8.934	1.00	0.00	3A4
ATOM	1119	OD1	ASN	191	52.277	-6.160	9.445	1.00	0.00	3A4
ATOM	1120	ND2	ASN	191	51.156	-7.322	7.848	1.00	0.00	3A4
ATOM	1121	C	ASN	191	49.394	-4.146	7.970	1.00	0.00	3A4
ATOM	1122	O	ASN	191	48.268	-4.363	7.523	1.00	0.00	3A4
ATOM	1123	N	ILE	192	50.505	-3.532	7.398	1.00	0.00	3A4
ATOM	1124	CA	ILE	192	50.796	-3.011	6.064	1.00	0.00	3A4
ATOM	1125	CB	ILE	192	49.572	-3.045	5.191	1.00	0.00	3A4
ATOM	1126	CG2	ILE	192	48.539	-2.012	5.843	1.00	0.00	3A4
ATOM	1127	CG1	ILE	192	49.850	-3.205	3.643	1.00	0.00	3A4
ATOM	1128	CD	ILE	192	50.855	-4.296	3.249	1.00	0.00	3A4
ATOM	1129	C	ILE	192	51.332	-1.562	6.101	1.00	0.00	3A4
ATOM	1130	O	ILE	192	51.714	-1.049	7.152	1.00	0.00	3A4
ATOM	1131	N	ASP	193	51.273	-0.876	4.912	1.00	0.00	3A4
ATOM	1132	CA	ASP	193	51.280	0.551	4.649	1.00	0.00	3A4
ATOM	1133	CB	ASP	193	52.500	0.950	3.755	1.00	0.00	3A4
ATOM	1134	CG	ASP	193	52.747	2.473	3.713	1.00	0.00	3A4
ATOM	1135	OD1	ASP	193	52.690	3.055	2.596	1.00	0.00	3A4
ATOM	1136	OD2	ASP	193	52.993	3.065	4.798	1.00	0.00	3A4
ATOM	1137	C	ASP	193	49.942	0.941	3.982	1.00	0.00	3A4
ATOM	1138	O	ASP	193	49.555	2.107	4.042	1.00	0.00	3A4
ATOM	1139	N	SER	194	49.199	-0.025	3.351	1.00	0.00	3A4
ATOM	1140	CA	SER	194	47.801	0.108	2.935	1.00	0.00	3A4
ATOM	1141	CB	SER	194	47.674	0.859	1.564	1.00	0.00	3A4
ATOM	1142	OG	SER	194	48.568	0.364	0.570	1.00	0.00	3A4
ATOM	1143	C	SER	194	47.072	-1.263	2.877	1.00	0.00	3A4
ATOM	1144	O	SER	194	47.201	-1.949	1.864	1.00	0.00	3A4
ATOM	1145	N	LEU	195	46.300	-1.682	3.968	1.00	0.00	3A4
ATOM	1146	CA	LEU	195	45.506	-2.928	4.205	1.00	0.00	3A4
ATOM	1147	CB	LEU	195	44.616	-3.155	2.908	1.00	0.00	3A4
ATOM	1148	CG	LEU	195	43.358	-4.046	2.893	1.00	0.00	3A4
ATOM	1149	CD1	LEU	195	42.566	-3.731	1.614	1.00	0.00	3A4
ATOM	1150	CD2	LEU	195	43.591	-5.569	2.963	1.00	0.00	3A4
ATOM	1151	C	LEU	195	46.313	-4.231	4.384	1.00	0.00	3A4
ATOM	1152	O	LEU	195	46.823	-4.525	3.303	1.00	0.00	3A4
ATOM	1153	N	ASN	196	46.462	-5.133	5.522	1.00	0.00	3A4
ATOM	1154	CA	ASN	196	46.660	-6.447	5.007	1.00	0.00	3A4
ATOM	1155	CB	ASN	196	48.141	-6.561	4.645	1.00	0.00	3A4
ATOM	1156	CG	ASN	196	48.532	-7.677	3.641	1.00	0.00	3A4
ATOM	1157	OD1	ASN	196	49.287	-8.581	3.992	1.00	0.00	3A4
ATOM	1158	ND2	ASN	196	48.039	-7.601	2.374	1.00	0.00	3A4
ATOM	1159	C	ASN	196	46.000	-7.578	5.603	1.00	0.00	3A4
ATOM	1160	O	ASN	196	44.826	-7.879	5.338	1.00	0.00	3A4
ATOM	1161	N	ASN	197	46.757	-8.297	6.407	1.00	0.00	3A4
ATOM	1162	CA	ASN	197	46.317	-9.599	6.859	1.00	0.00	3A4
ATOM	1163	CB	ASN	197	47.456	-10.511	7.443	1.00	0.00	3A4
ATOM	1164	CG	ASN	197	48.572	-10.689	6.405	1.00	0.00	3A4
ATOM	1165	OD1	ASN	197	48.334	-11.249	5.336	1.00	0.00	3A4
ATOM	1166	ND2	ASN	197	49.810	-10.219	6.717	1.00	0.00	3A4
ATOM	1167	C	ASN	197	45.160	-9.556	7.804	1.00	0.00	3A4
ATOM	1168	O	ASN	197	44.307	-10.439	7.761	1.00	0.00	3A4
ATOM	1169	N	PRO	198	45.075	-8.496	8.595	1.00	0.00	3A4
ATOM	1170	CA	PRO	198	44.013	-8.420	9.555	1.00	0.00	3A4
ATOM	1171	CD	PRO	198	46.277	-7.818	9.154	1.00	0.00	3A4
ATOM	1172	CB	PRO	198	44.652	-7.631	10.641	1.00	0.00	3A4
ATOM	1173	CG	PRO	198	46.123	-7.908	10.628	1.00	0.00	3A4
ATOM	1174	C	PRO	198	42.754	-7.786	9.085	1.00	0.00	3A4
ATOM	1175	O	PRO	198	41.799	-7.743	9.865	1.00	0.00	3A4
ATOM	1176	N	GLN	199	42.701	-7.279	7.830	1.00	0.00	3A4
ATOM	1177	CA	GLN	199	41.636	-6.407	7.407	1.00	0.00	3A4
ATOM	1178	CB	GLN	199	41.900	-5.668	6.066	1.00	0.00	3A4
ATOM	1179	CG	GLN	199	41.001	-4.419	5.844	1.00	0.00	3A4
ATOM	1180	CD	GLN	199	41.471	-3.266	6.742	1.00	0.00	3A4
ATOM	1181	OE1	GLN	199	42.353	-2.503	6.348	1.00	0.00	3A4

ATOM	1182	NE2	GLN	199	40.885	-3.125	7.963	1.00	0.00	3A4
ATOM	1183	C	GLN	199	40.319	-7.071	7.338	1.00	0.00	3A4
ATOM	1184	O	GLN	199	39.374	-6.533	7.889	1.00	0.00	3A4
ATOM	1185	N	ASP	200	40.193	-8.262	6.717	1.00	0.00	3A4
ATOM	1186	CA	ASP	200	38.939	-8.983	6.597	1.00	0.00	3A4
ATOM	1187	CB	ASP	200	39.049	-10.138	5.538	1.00	0.00	3A4
ATOM	1188	CG	ASP	200	37.683	-10.693	5.079	1.00	0.00	3A4
ATOM	1189	OD1	ASP	200	37.459	-11.923	5.238	1.00	0.00	3A4
ATOM	1190	OD2	ASP	200	36.855	-9.893	4.566	1.00	0.00	3A4
ATOM	1191	C	ASP	200	38.347	-9.432	7.927	1.00	0.00	3A4
ATOM	1192	O	ASP	200	37.137	-9.315	8.099	1.00	0.00	3A4
ATOM	1193	N	PRO	201	39.155	-9.847	8.917	1.00	0.00	3A4
ATOM	1194	CA	PRO	201	38.699	-10.088	10.270	1.00	0.00	3A4
ATOM	1195	CD	PRO	201	40.343	-10.678	8.654	1.00	0.00	3A4
ATOM	1196	CB	PRO	201	39.936	-10.637	11.012	1.00	0.00	3A4
ATOM	1197	CG	PRO	201	40.633	-11.466	9.938	1.00	0.00	3A4
ATOM	1198	C	PRO	201	38.128	-8.916	10.997	1.00	0.00	3A4
ATOM	1199	O	PRO	201	37.076	-9.052	11.615	1.00	0.00	3A4
ATOM	1200	N	PHE	202	38.762	-7.733	10.872	1.00	0.00	3A4
ATOM	1201	CA	PHE	202	38.319	-6.521	11.530	1.00	0.00	3A4
ATOM	1202	CB	PHE	202	39.462	-5.473	11.494	1.00	0.00	3A4
ATOM	1203	CG	PHE	202	40.009	-5.259	12.888	1.00	0.00	3A4
ATOM	1204	CD1	PHE	202	40.365	-6.366	13.691	1.00	0.00	3A4
ATOM	1205	CD2	PHE	202	40.293	-3.968	13.372	1.00	0.00	3A4
ATOM	1206	CE1	PHE	202	40.856	-6.184	14.987	1.00	0.00	3A4
ATOM	1207	CE2	PHE	202	40.855	-3.790	14.647	1.00	0.00	3A4
ATOM	1208	CZ	PHE	202	41.107	-4.894	15.465	1.00	0.00	3A4
ATOM	1209	C	PHE	202	37.080	-5.964	10.887	1.00	0.00	3A4
ATOM	1210	O	PHE	202	36.208	-5.444	11.573	1.00	0.00	3A4
ATOM	1211	N	VAL	203	36.928	-6.145	9.554	1.00	0.00	3A4
ATOM	1212	CA	VAL	203	35.752	-5.762	8.799	1.00	0.00	3A4
ATOM	1213	CB	VAL	203	36.015	-5.808	7.287	1.00	0.00	3A4
ATOM	1214	CG1	VAL	203	34.738	-5.677	6.411	1.00	0.00	3A4
ATOM	1215	CG2	VAL	203	36.983	-4.648	6.954	1.00	0.00	3A4
ATOM	1216	C	VAL	203	34.545	-6.596	9.199	1.00	0.00	3A4
ATOM	1217	O	VAL	203	33.451	-6.068	9.364	1.00	0.00	3A4
ATOM	1218	N	GLU	204	34.736	-7.908	9.475	1.00	0.00	3A4
ATOM	1219	CA	GLU	204	33.684	-8.782	9.967	1.00	0.00	3A4
ATOM	1220	CB	GLU	204	34.114	-10.262	9.912	1.00	0.00	3A4
ATOM	1221	CG	GLU	204	34.199	-10.797	8.472	1.00	0.00	3A4
ATOM	1222	CD	GLU	204	34.793	-12.210	8.489	1.00	0.00	3A4
ATOM	1223	OE1	GLU	204	35.910	-12.394	7.934	1.00	0.00	3A4
ATOM	1224	OE2	GLU	204	34.137	-13.123	9.059	1.00	0.00	3A4
ATOM	1225	C	GLU	204	33.230	-8.440	11.373	1.00	0.00	3A4
ATOM	1226	O	GLU	204	32.042	-8.449	11.666	1.00	0.00	3A4
ATOM	1227	N	ASN	205	34.176	-8.057	12.259	1.00	0.00	3A4
ATOM	1228	CA	ASN	205	33.914	-7.660	13.628	1.00	0.00	3A4
ATOM	1229	CB	ASN	205	35.248	-7.438	14.383	1.00	0.00	3A4
ATOM	1230	CG	ASN	205	36.015	-8.751	14.628	1.00	0.00	3A4
ATOM	1231	OD1	ASN	205	37.233	-8.776	14.460	1.00	0.00	3A4
ATOM	1232	ND2	ASN	205	35.329	-9.842	15.069	1.00	0.00	3A4
ATOM	1233	C	ASN	205	33.087	-6.395	13.736	1.00	0.00	3A4
ATOM	1234	O	ASN	205	32.115	-6.344	14.487	1.00	0.00	3A4
ATOM	1235	N	THR	206	33.414	-5.376	12.903	1.00	0.00	3A4
ATOM	1236	CA	THR	206	32.762	-4.077	12.899	1.00	0.00	3A4
ATOM	1237	CB	THR	206	33.525	-3.007	12.102	1.00	0.00	3A4
ATOM	1238	OG1	THR	206	34.406	-3.549	11.139	1.00	0.00	3A4
ATOM	1239	CG2	THR	206	34.381	-2.246	13.141	1.00	0.00	3A4
ATOM	1240	C	THR	206	31.364	-4.178	12.322	1.00	0.00	3A4
ATOM	1241	O	THR	206	30.435	-3.581	12.843	1.00	0.00	3A4
ATOM	1242	N	LYS	207	31.178	-5.009	11.279	1.00	0.00	3A4
ATOM	1243	CA	LYS	207	29.905	-5.266	10.645	1.00	0.00	3A4
ATOM	1244	CB	LYS	207	30.122	-6.061	9.349	1.00	0.00	3A4
ATOM	1245	CG	LYS	207	28.927	-6.211	8.393	1.00	0.00	3A4
ATOM	1246	CD	LYS	207	29.306	-6.802	7.027	1.00	0.00	3A4
ATOM	1247	CE	LYS	207	29.832	-8.246	7.088	1.00	0.00	3A4
ATOM	1248	NZ	LYS	207	30.150	-8.750	5.731	1.00	0.00	3A4
ATOM	1249	C	LYS	207	28.938	-6.023	11.523	1.00	0.00	3A4
ATOM	1250	O	LYS	207	27.753	-5.736	11.533	1.00	0.00	3A4
ATOM	1251	N	LYS	208	29.441	-6.958	12.359	1.00	0.00	3A4
ATOM	1252	CA	LYS	208	28.646	-7.727	13.293	1.00	0.00	3A4
ATOM	1253	CB	LYS	208	29.443	-8.920	13.865	1.00	0.00	3A4

ATOM	1254	CG	LYS	208	28.627	-9.993	14.610	1.00	0.00	3A4
ATOM	1255	CD	LYS	208	29.414	-11.248	15.031	1.00	0.00	3A4
ATOM	1256	CE	LYS	208	29.894	-12.177	13.900	1.00	0.00	3A4
ATOM	1257	NZ	LYS	208	31.125	-11.677	13.236	1.00	0.00	3A4
ATOM	1258	C	LYS	208	28.094	-6.905	14.430	1.00	0.00	3A4
ATOM	1259	O	LYS	208	26.931	-7.047	14.780	1.00	0.00	3A4
ATOM	1260	N	LEU	209	28.886	-5.983	15.022	1.00	0.00	3A4
ATOM	1261	CA	LEU	209	28.454	-5.149	16.133	1.00	0.00	3A4
ATOM	1262	CB	LEU	209	29.656	-4.415	16.784	1.00	0.00	3A4
ATOM	1263	CG	LEU	209	29.353	-3.397	17.945	1.00	0.00	3A4
ATOM	1264	CD1	LEU	209	28.592	-4.009	19.146	1.00	0.00	3A4
ATOM	1265	CD2	LEU	209	30.596	-2.606	18.399	1.00	0.00	3A4
ATOM	1266	C	LEU	209	27.416	-4.112	15.737	1.00	0.00	3A4
ATOM	1267	O	LEU	209	26.515	-3.793	16.507	1.00	0.00	3A4
ATOM	1268	N	LEU	210	27.527	-3.561	14.510	1.00	0.00	3A4
ATOM	1269	CA	LEU	210	26.707	-2.449	14.080	1.00	0.00	3A4
ATOM	1270	CB	LEU	210	27.559	-1.343	13.418	1.00	0.00	3A4
ATOM	1271	CG	LEU	210	28.684	-0.850	14.384	1.00	0.00	3A4
ATOM	1272	CD1	LEU	210	29.655	0.113	13.699	1.00	0.00	3A4
ATOM	1273	CD2	LEU	210	28.176	-0.257	15.717	1.00	0.00	3A4
ATOM	1274	C	LEU	210	25.611	-2.862	13.145	1.00	0.00	3A4
ATOM	1275	O	LEU	210	24.465	-2.454	13.335	1.00	0.00	3A4
ATOM	1276	N	ARG	211	25.948	-3.571	12.035	1.00	0.00	3A4
ATOM	1277	CA	ARG	211	25.146	-3.650	10.816	1.00	0.00	3A4
ATOM	1278	CB	ARG	211	26.033	-3.592	9.539	1.00	0.00	3A4
ATOM	1279	CG	ARG	211	26.927	-2.337	9.503	1.00	0.00	3A4
ATOM	1280	CD	ARG	211	27.841	-2.220	8.274	1.00	0.00	3A4
ATOM	1281	NE	ARG	211	27.005	-2.107	7.024	1.00	0.00	3A4
ATOM	1282	CZ	ARG	211	26.814	-0.939	6.329	1.00	0.00	3A4
ATOM	1283	NH1	ARG	211	26.014	-0.951	5.223	1.00	0.00	3A4
ATOM	1284	NH2	ARG	211	27.397	0.236	6.711	1.00	0.00	3A4
ATOM	1285	C	ARG	211	24.236	-4.864	10.757	1.00	0.00	3A4
ATOM	1286	O	ARG	211	23.275	-4.868	9.989	1.00	0.00	3A4
ATOM	1287	N	PHE	212	24.496	-5.910	11.589	1.00	0.00	3A4
ATOM	1288	CA	PHE	212	23.555	-6.992	11.826	1.00	0.00	3A4
ATOM	1289	CB	PHE	212	23.730	-8.273	10.930	1.00	0.00	3A4
ATOM	1290	CG	PHE	212	25.061	-8.998	10.978	1.00	0.00	3A4
ATOM	1291	CD1	PHE	212	25.170	-10.224	11.667	1.00	0.00	3A4
ATOM	1292	CD2	PHE	212	26.182	-8.527	10.268	1.00	0.00	3A4
ATOM	1293	CE1	PHE	212	26.367	-10.954	11.660	1.00	0.00	3A4
ATOM	1294	CE2	PHE	212	27.380	-9.259	10.254	1.00	0.00	3A4
ATOM	1295	CZ	PHE	212	27.474	-10.469	10.952	1.00	0.00	3A4
ATOM	1296	C	PHE	212	23.608	-7.246	13.314	1.00	0.00	3A4
ATOM	1297	O	PHE	212	24.292	-8.143	13.802	1.00	0.00	3A4
ATOM	1298	N	ASP	213	22.863	-6.398	14.068	1.00	0.00	3A4
ATOM	1299	CA	ASP	213	22.843	-6.356	15.513	1.00	0.00	3A4
ATOM	1300	CB	ASP	213	23.642	-5.131	16.046	1.00	0.00	3A4
ATOM	1301	CG	ASP	213	23.916	-5.215	17.558	1.00	0.00	3A4
ATOM	1302	OD1	ASP	213	24.608	-6.179	17.982	1.00	0.00	3A4
ATOM	1303	OD2	ASP	213	23.444	-4.312	18.300	1.00	0.00	3A4
ATOM	1304	C	ASP	213	21.391	-6.281	15.902	1.00	0.00	3A4
ATOM	1305	O	ASP	213	20.714	-5.286	15.648	1.00	0.00	3A4
ATOM	1306	N	PHE	214	20.894	-7.371	16.533	1.00	0.00	3A4
ATOM	1307	CA	PHE	214	19.516	-7.516	16.941	1.00	0.00	3A4
ATOM	1308	CB	PHE	214	18.526	-7.900	15.776	1.00	0.00	3A4
ATOM	1309	CG	PHE	214	19.127	-8.826	14.734	1.00	0.00	3A4
ATOM	1310	CD1	PHE	214	19.610	-8.306	13.515	1.00	0.00	3A4
ATOM	1311	CD2	PHE	214	19.216	-10.215	14.950	1.00	0.00	3A4
ATOM	1312	CE1	PHE	214	20.186	-9.143	12.550	1.00	0.00	3A4
ATOM	1313	CE2	PHE	214	19.793	-11.058	13.987	1.00	0.00	3A4
ATOM	1314	CZ	PHE	214	20.280	-10.520	12.788	1.00	0.00	3A4
ATOM	1315	C	PHE	214	19.513	-8.554	18.034	1.00	0.00	3A4
ATOM	1316	O	PHE	214	20.344	-9.460	18.058	1.00	0.00	3A4
ATOM	1317	N	LEU	215	18.527	-8.428	18.956	1.00	0.00	3A4
ATOM	1318	CA	LEU	215	18.216	-9.384	19.995	1.00	0.00	3A4
ATOM	1319	CB	LEU	215	18.914	-9.072	21.353	1.00	0.00	3A4
ATOM	1320	CG	LEU	215	18.685	-10.089	22.505	1.00	0.00	3A4
ATOM	1321	CD1	LEU	215	19.075	-11.533	22.128	1.00	0.00	3A4
ATOM	1322	CD2	LEU	215	19.419	-9.639	23.783	1.00	0.00	3A4
ATOM	1323	C	LEU	215	16.716	-9.298	20.078	1.00	0.00	3A4
ATOM	1324	O	LEU	215	16.151	-8.667	20.970	1.00	0.00	3A4
ATOM	1325	N	ASP	216	16.046	-9.926	19.073	1.00	0.00	3A4

ATOM	1326	CA	ASP	216	14.627	-9.830	18.781	1.00	0.00	3A4
ATOM	1327	CB	ASP	216	14.369	-9.623	17.242	1.00	0.00	3A4
ATOM	1328	CG	ASP	216	14.915	-10.746	16.328	1.00	0.00	3A4
ATOM	1329	OD1	ASP	216	16.161	-10.914	16.241	1.00	0.00	3A4
ATOM	1330	OD2	ASP	216	14.075	-11.445	15.700	1.00	0.00	3A4
ATOM	1331	C	ASP	216	13.914	-11.069	19.316	1.00	0.00	3A4
ATOM	1332	O	ASP	216	14.578	-12.088	19.506	1.00	0.00	3A4
ATOM	1333	N	PRO	217	12.576	-11.062	19.553	1.00	0.00	3A4
ATOM	1334	CA	PRO	217	11.794	-12.227	19.974	1.00	0.00	3A4
ATOM	1335	CD	PRO	217	11.814	-9.819	19.695	1.00	0.00	3A4
ATOM	1336	CB	PRO	217	10.525	-11.614	20.611	1.00	0.00	3A4
ATOM	1337	CG	PRO	217	10.367	-10.231	19.970	1.00	0.00	3A4
ATOM	1338	C	PRO	217	11.504	-13.148	18.786	1.00	0.00	3A4
ATOM	1339	O	PRO	217	12.309	-14.043	18.527	1.00	0.00	3A4
ATOM	1340	N	PHE	218	10.374	-12.933	18.064	1.00	0.00	3A4
ATOM	1341	CA	PHE	218	10.004	-13.621	16.839	1.00	0.00	3A4
ATOM	1342	CB	PHE	218	8.877	-14.691	17.032	1.00	0.00	3A4
ATOM	1343	CG	PHE	218	9.294	-15.734	18.036	1.00	0.00	3A4
ATOM	1344	CD1	PHE	218	8.630	-15.831	19.273	1.00	0.00	3A4
ATOM	1345	CD2	PHE	218	10.354	-16.621	17.766	1.00	0.00	3A4
ATOM	1346	CE1	PHE	218	9.018	-16.783	20.225	1.00	0.00	3A4
ATOM	1347	CE2	PHE	218	10.751	-17.572	18.720	1.00	0.00	3A4
ATOM	1348	CZ	PHE	218	10.083	-17.651	19.950	1.00	0.00	3A4
ATOM	1349	C	PHE	218	9.495	-12.564	15.883	1.00	0.00	3A4
ATOM	1350	O	PHE	218	9.158	-12.860	14.737	1.00	0.00	3A4
ATOM	1351	N	PHE	219	9.400	-11.297	16.374	1.00	0.00	3A4
ATOM	1352	CA	PHE	219	8.762	-10.165	15.736	1.00	0.00	3A4
ATOM	1353	CB	PHE	219	7.558	-9.630	16.572	1.00	0.00	3A4
ATOM	1354	CG	PHE	219	6.443	-10.646	16.570	1.00	0.00	3A4
ATOM	1355	CD1	PHE	219	5.437	-10.600	15.587	1.00	0.00	3A4
ATOM	1356	CD2	PHE	219	6.389	-11.664	17.542	1.00	0.00	3A4
ATOM	1357	CE1	PHE	219	4.401	-11.546	15.576	1.00	0.00	3A4
ATOM	1358	CE2	PHE	219	5.356	-12.611	17.536	1.00	0.00	3A4
ATOM	1359	CZ	PHE	219	4.360	-12.551	16.553	1.00	0.00	3A4
ATOM	1360	C	PHE	219	9.798	-9.078	15.602	1.00	0.00	3A4
ATOM	1361	O	PHE	219	10.805	-9.068	16.307	1.00	0.00	3A4
ATOM	1362	N	LEU	220	9.547	-8.131	14.664	1.00	0.00	3A4
ATOM	1363	CA	LEU	220	10.447	-7.050	14.321	1.00	0.00	3A4
ATOM	1364	CB	LEU	220	11.550	-7.452	13.279	1.00	0.00	3A4
ATOM	1365	CG	LEU	220	11.130	-7.889	11.840	1.00	0.00	3A4
ATOM	1366	CD1	LEU	220	12.368	-7.938	10.924	1.00	0.00	3A4
ATOM	1367	CD2	LEU	220	10.365	-9.229	11.764	1.00	0.00	3A4
ATOM	1368	C	LEU	220	9.590	-5.908	13.825	1.00	0.00	3A4
ATOM	1369	O	LEU	220	8.366	-5.964	13.937	1.00	0.00	3A4
ATOM	1370	N	SER	221	10.268	-4.849	13.284	1.00	0.00	3A4
ATOM	1371	CA	SER	221	9.781	-3.584	12.735	1.00	0.00	3A4
ATOM	1372	CB	SER	221	8.270	-3.542	12.288	1.00	0.00	3A4
ATOM	1373	OG	SER	221	7.980	-2.485	11.376	1.00	0.00	3A4
ATOM	1374	C	SER	221	10.129	-2.514	13.764	1.00	0.00	3A4
ATOM	1375	O	SER	221	10.958	-2.740	14.646	1.00	0.00	3A4
ATOM	1376	N	ILE	222	9.495	-1.312	13.661	1.00	0.00	3A4
ATOM	1377	CA	ILE	222	9.692	-0.155	14.524	1.00	0.00	3A4
ATOM	1378	CB	ILE	222	9.886	1.145	13.735	1.00	0.00	3A4
ATOM	1379	CG2	ILE	222	11.258	1.038	13.025	1.00	0.00	3A4
ATOM	1380	CG1	ILE	222	8.727	1.449	12.741	1.00	0.00	3A4
ATOM	1381	CD	ILE	222	8.868	2.791	12.016	1.00	0.00	3A4
ATOM	1382	C	ILE	222	8.533	-0.038	15.500	1.00	0.00	3A4
ATOM	1383	O	ILE	222	8.631	0.670	16.501	1.00	0.00	3A4
ATOM	1384	N	THR	223	7.406	-0.746	15.215	1.00	0.00	3A4
ATOM	1385	CA	THR	223	6.225	-0.787	16.050	1.00	0.00	3A4
ATOM	1386	CB	THR	223	5.259	0.384	15.782	1.00	0.00	3A4
ATOM	1387	OG1	THR	223	4.159	0.414	16.691	1.00	0.00	3A4
ATOM	1388	CG2	THR	223	4.751	0.459	14.318	1.00	0.00	3A4
ATOM	1389	C	THR	223	5.633	-2.165	15.811	1.00	0.00	3A4
ATOM	1390	O	THR	223	5.360	-2.558	14.678	1.00	0.00	3A4
ATOM	1391	N	VAL	224	5.435	-2.927	16.918	1.00	0.00	3A4
ATOM	1392	CA	VAL	224	4.832	-4.244	16.917	1.00	0.00	3A4
ATOM	1393	CB	VAL	224	5.751	-5.354	16.379	1.00	0.00	3A4
ATOM	1394	CG1	VAL	224	7.065	-5.517	17.186	1.00	0.00	3A4
ATOM	1395	CG2	VAL	224	4.973	-6.679	16.198	1.00	0.00	3A4
ATOM	1396	C	VAL	224	4.397	-4.468	18.349	1.00	0.00	3A4
ATOM	1397	O	VAL	224	5.085	-4.071	19.290	1.00	0.00	3A4

ATOM	1398	N	PHE	225	3.212	-5.114	18.534	1.00	0.00	3A4
ATOM	1399	CA	PHE	225	2.568	-5.398	19.809	1.00	0.00	3A4
ATOM	1400	CB	PHE	225	1.025	-5.112	19.736	1.00	0.00	3A4
ATOM	1401	CG	PHE	225	0.345	-5.089	21.089	1.00	0.00	3A4
ATOM	1402	CD1	PHE	225	0.584	-4.036	21.993	1.00	0.00	3A4
ATOM	1403	CD2	PHE	225	-0.533	-6.123	21.470	1.00	0.00	3A4
ATOM	1404	CE1	PHE	225	-0.038	-4.017	23.251	1.00	0.00	3A4
ATOM	1405	CE2	PHE	225	-1.156	-6.107	22.726	1.00	0.00	3A4
ATOM	1406	CZ	PHE	225	-0.908	-5.053	23.617	1.00	0.00	3A4
ATOM	1407	C	PHE	225	2.898	-6.812	20.313	1.00	0.00	3A4
ATOM	1408	O	PHE	225	3.306	-6.885	21.472	1.00	0.00	3A4
ATOM	1409	N	PRO	226	2.776	-7.964	19.590	1.00	0.00	3A4
ATOM	1410	CA	PRO	226	3.087	-9.298	20.117	1.00	0.00	3A4
ATOM	1411	CD	PRO	226	2.027	-8.062	18.335	1.00	0.00	3A4
ATOM	1412	CB	PRO	226	2.324	-10.268	19.186	1.00	0.00	3A4
ATOM	1413	CG	PRO	226	2.191	-9.507	17.865	1.00	0.00	3A4
ATOM	1414	C	PRO	226	4.587	-9.598	20.127	1.00	0.00	3A4
ATOM	1415	O	PRO	226	5.346	-9.003	19.361	1.00	0.00	3A4
ATOM	1416	N	PHE	227	4.993	-10.544	21.009	1.00	0.00	3A4
ATOM	1417	CA	PHE	227	6.356	-10.995	21.212	1.00	0.00	3A4
ATOM	1418	CB	PHE	227	7.106	-10.254	22.376	1.00	0.00	3A4
ATOM	1419	CG	PHE	227	6.298	-10.129	23.651	1.00	0.00	3A4
ATOM	1420	CD1	PHE	227	5.437	-9.031	23.855	1.00	0.00	3A4
ATOM	1421	CD2	PHE	227	6.393	-11.105	24.663	1.00	0.00	3A4
ATOM	1422	CE1	PHE	227	4.677	-8.920	25.028	1.00	0.00	3A4
ATOM	1423	CE2	PHE	227	5.634	-10.999	25.838	1.00	0.00	3A4
ATOM	1424	CZ	PHE	227	4.775	-9.907	26.019	1.00	0.00	3A4
ATOM	1425	C	PHE	227	6.307	-12.495	21.429	1.00	0.00	3A4
ATOM	1426	O	PHE	227	7.291	-13.188	21.177	1.00	0.00	3A4
ATOM	1427	N	LEU	228	5.134	-13.001	21.925	1.00	0.00	3A4
ATOM	1428	CA	LEU	228	4.753	-14.389	22.186	1.00	0.00	3A4
ATOM	1429	CB	LEU	228	5.137	-15.381	21.024	1.00	0.00	3A4
ATOM	1430	CG	LEU	228	4.217	-16.607	20.757	1.00	0.00	3A4
ATOM	1431	CD1	LEU	228	4.267	-17.707	21.832	1.00	0.00	3A4
ATOM	1432	CD2	LEU	228	2.767	-16.215	20.406	1.00	0.00	3A4
ATOM	1433	C	LEU	228	5.274	-14.788	23.565	1.00	0.00	3A4
ATOM	1434	O	LEU	228	4.778	-14.291	24.575	1.00	0.00	3A4
ATOM	1435	N	ILE	229	6.316	-15.659	23.623	1.00	0.00	3A4
ATOM	1436	CA	ILE	229	7.097	-15.948	24.811	1.00	0.00	3A4
ATOM	1437	CB	ILE	229	6.457	-16.944	25.799	1.00	0.00	3A4
ATOM	1438	CG2	ILE	229	6.056	-18.311	25.188	1.00	0.00	3A4
ATOM	1439	CG1	ILE	229	7.185	-17.043	27.173	1.00	0.00	3A4
ATOM	1440	CD	ILE	229	8.372	-18.014	27.278	1.00	0.00	3A4
ATOM	1441	C	ILE	229	8.458	-16.351	24.252	1.00	0.00	3A4
ATOM	1442	O	ILE	229	8.631	-17.503	23.857	1.00	0.00	3A4
ATOM	1443	N	PRO	230	9.474	-15.455	24.157	1.00	0.00	3A4
ATOM	1444	CA	PRO	230	10.759	-15.735	23.519	1.00	0.00	3A4
ATOM	1445	CD	PRO	230	9.306	-14.022	24.410	1.00	0.00	3A4
ATOM	1446	CB	PRO	230	11.244	-14.349	23.055	1.00	0.00	3A4
ATOM	1447	CG	PRO	230	10.655	-13.376	24.082	1.00	0.00	3A4
ATOM	1448	C	PRO	230	11.749	-16.380	24.483	1.00	0.00	3A4
ATOM	1449	O	PRO	230	11.509	-16.422	25.691	1.00	0.00	3A4
ATOM	1450	N	ILE	231	12.894	-16.870	23.931	1.00	0.00	3A4
ATOM	1451	CA	ILE	231	13.997	-17.495	24.644	1.00	0.00	3A4
ATOM	1452	CB	ILE	231	14.463	-18.802	23.988	1.00	0.00	3A4
ATOM	1453	CG2	ILE	231	15.554	-19.489	24.852	1.00	0.00	3A4
ATOM	1454	CG1	ILE	231	13.275	-19.767	23.714	1.00	0.00	3A4
ATOM	1455	CD	ILE	231	12.502	-20.240	24.953	1.00	0.00	3A4
ATOM	1456	C	ILE	231	15.116	-16.473	24.709	1.00	0.00	3A4
ATOM	1457	O	ILE	231	15.691	-16.247	25.773	1.00	0.00	3A4
ATOM	1458	N	LEU	232	15.428	-15.844	23.533	1.00	0.00	3A4
ATOM	1459	CA	LEU	232	16.397	-14.778	23.277	1.00	0.00	3A4
ATOM	1460	CB	LEU	232	16.312	-13.552	24.250	1.00	0.00	3A4
ATOM	1461	CG	LEU	232	14.944	-12.824	24.269	1.00	0.00	3A4
ATOM	1462	CD1	LEU	232	14.900	-11.763	25.383	1.00	0.00	3A4
ATOM	1463	CD2	LEU	232	14.567	-12.203	22.908	1.00	0.00	3A4
ATOM	1464	C	LEU	232	17.814	-15.328	23.232	1.00	0.00	3A4
ATOM	1465	O	LEU	232	18.606	-15.133	24.154	1.00	0.00	3A4
ATOM	1466	N	GLU	233	18.131	-16.047	22.125	1.00	0.00	3A4
ATOM	1467	CA	GLU	233	19.390	-16.728	21.896	1.00	0.00	3A4
ATOM	1468	CB	GLU	233	19.269	-18.268	22.115	1.00	0.00	3A4
ATOM	1469	CG	GLU	233	18.095	-18.955	21.373	1.00	0.00	3A4

ATOM	1470	CD	GLU	233	18.120	-20.462	21.648	1.00	0.00	3A4
ATOM	1471	OE1	GLU	233	19.140	-21.114	21.295	1.00	0.00	3A4
ATOM	1472	OE2	GLU	233	17.118	-20.985	22.205	1.00	0.00	3A4
ATOM	1473	C	GLU	233	19.828	-16.395	20.489	1.00	0.00	3A4
ATOM	1474	O	GLU	233	20.256	-17.261	19.726	1.00	0.00	3A4
ATOM	1475	N	VAL	234	19.734	-15.088	20.125	1.00	0.00	3A4
ATOM	1476	CA	VAL	234	20.053	-14.558	18.815	1.00	0.00	3A4
ATOM	1477	CB	VAL	234	18.792	-14.275	17.987	1.00	0.00	3A4
ATOM	1478	CG1	VAL	234	17.739	-13.402	18.723	1.00	0.00	3A4
ATOM	1479	CG2	VAL	234	19.142	-13.768	16.568	1.00	0.00	3A4
ATOM	1480	C	VAL	234	20.960	-13.370	19.064	1.00	0.00	3A4
ATOM	1481	O	VAL	234	20.563	-12.209	18.984	1.00	0.00	3A4
ATOM	1482	N	LEU	235	22.242	-13.673	19.393	1.00	0.00	3A4
ATOM	1483	CA	LEU	235	23.270	-12.694	19.675	1.00	0.00	3A4
ATOM	1484	CB	LEU	235	23.137	-11.954	21.056	1.00	0.00	3A4
ATOM	1485	CG	LEU	235	23.294	-12.749	22.393	1.00	0.00	3A4
ATOM	1486	CD1	LEU	235	23.236	-11.785	23.594	1.00	0.00	3A4
ATOM	1487	CD2	LEU	235	22.289	-13.903	22.600	1.00	0.00	3A4
ATOM	1488	C	LEU	235	24.592	-13.413	19.593	1.00	0.00	3A4
ATOM	1489	O	LEU	235	24.703	-14.586	19.948	1.00	0.00	3A4
ATOM	1490	N	ASN	236	25.638	-12.684	19.128	1.00	0.00	3A4
ATOM	1491	CA	ASN	236	27.013	-13.135	19.089	1.00	0.00	3A4
ATOM	1492	CB	ASN	236	27.351	-13.966	17.803	1.00	0.00	3A4
ATOM	1493	CG	ASN	236	28.697	-14.706	17.931	1.00	0.00	3A4
ATOM	1494	OD1	ASN	236	28.818	-15.613	18.753	1.00	0.00	3A4
ATOM	1495	ND2	ASN	236	29.719	-14.326	17.115	1.00	0.00	3A4
ATOM	1496	C	ASN	236	27.795	-11.845	19.165	1.00	0.00	3A4
ATOM	1497	O	ASN	236	28.546	-11.489	18.259	1.00	0.00	3A4
ATOM	1498	N	ILE	237	27.590	-11.096	20.283	1.00	0.00	3A4
ATOM	1499	CA	ILE	237	28.074	-9.747	20.504	1.00	0.00	3A4
ATOM	1500	CB	ILE	237	26.980	-8.800	20.998	1.00	0.00	3A4
ATOM	1501	CG2	ILE	237	26.039	-8.584	19.789	1.00	0.00	3A4
ATOM	1502	CG1	ILE	237	26.203	-9.271	22.262	1.00	0.00	3A4
ATOM	1503	CD	ILE	237	25.059	-8.341	22.671	1.00	0.00	3A4
ATOM	1504	C	ILE	237	29.228	-9.798	21.461	1.00	0.00	3A4
ATOM	1505	O	ILE	237	30.202	-9.126	21.226	1.00	0.00	3A4
ATOM	1506	N	CYS	238	29.124	-10.614	22.532	1.00	0.00	3A4
ATOM	1507	CA	CYS	238	30.099	-10.834	23.576	1.00	0.00	3A4
ATOM	1508	CB	CYS	238	29.513	-11.689	24.739	1.00	0.00	3A4
ATOM	1509	SG	CYS	238	28.106	-10.870	25.526	1.00	0.00	3A4
ATOM	1510	C	CYS	238	31.307	-11.563	23.083	1.00	0.00	3A4
ATOM	1511	O	CYS	238	32.424	-11.278	23.493	1.00	0.00	3A4
ATOM	1512	N	VAL	239	31.138	-12.446	22.082	1.00	0.00	3A4
ATOM	1513	CA	VAL	239	32.219	-13.161	21.438	1.00	0.00	3A4
ATOM	1514	CB	VAL	239	31.700	-14.367	20.675	1.00	0.00	3A4
ATOM	1515	CG1	VAL	239	32.858	-15.308	20.247	1.00	0.00	3A4
ATOM	1516	CG2	VAL	239	30.715	-15.139	21.586	1.00	0.00	3A4
ATOM	1517	C	VAL	239	33.006	-12.283	20.505	1.00	0.00	3A4
ATOM	1518	O	VAL	239	34.228	-12.327	20.485	1.00	0.00	3A4
ATOM	1519	N	PHE	240	32.315	-11.420	19.731	1.00	0.00	3A4
ATOM	1520	CA	PHE	240	32.913	-10.422	18.870	1.00	0.00	3A4
ATOM	1521	CB	PHE	240	31.825	-9.669	18.040	1.00	0.00	3A4
ATOM	1522	CG	PHE	240	31.881	-8.134	17.899	1.00	0.00	3A4
ATOM	1523	CD1	PHE	240	32.913	-7.550	17.149	1.00	0.00	3A4
ATOM	1524	CD2	PHE	240	31.185	-7.320	18.812	1.00	0.00	3A4
ATOM	1525	CE1	PHE	240	33.312	-6.223	17.382	1.00	0.00	3A4
ATOM	1526	CE2	PHE	240	31.646	-6.034	19.117	1.00	0.00	3A4
ATOM	1527	CZ	PHE	240	32.709	-5.481	18.396	1.00	0.00	3A4
ATOM	1528	C	PHE	240	33.789	-9.440	19.608	1.00	0.00	3A4
ATOM	1529	O	PHE	240	34.906	-9.202	19.168	1.00	0.00	3A4
ATOM	1530	N	PRO	241	33.347	-8.835	20.727	1.00	0.00	3A4
ATOM	1531	CA	PRO	241	34.111	-7.940	21.493	1.00	0.00	3A4
ATOM	1532	CD	PRO	241	32.648	-9.345	21.724	1.00	0.00	3A4
ATOM	1533	CB	PRO	241	33.196	-7.358	22.578	1.00	0.00	3A4
ATOM	1534	CG	PRO	241	32.348	-8.435	22.936	1.00	0.00	3A4
ATOM	1535	C	PRO	241	35.347	-8.605	22.103	1.00	0.00	3A4
ATOM	1536	O	PRO	241	36.396	-7.992	22.029	1.00	0.00	3A4
ATOM	1537	N	ARG	242	35.316	-9.867	22.592	1.00	0.00	3A4
ATOM	1538	CA	ARG	242	36.450	-10.583	23.101	1.00	0.00	3A4
ATOM	1539	CB	ARG	242	35.986	-11.889	23.750	1.00	0.00	3A4
ATOM	1540	CG	ARG	242	35.213	-11.657	25.054	1.00	0.00	3A4
ATOM	1541	CD	ARG	242	34.515	-12.928	25.556	1.00	0.00	3A4

ATOM	1542	NE	ARG	242	33.717	-12.581	26.784	1.00	0.00	3A4
ATOM	1543	CZ	ARG	242	32.762	-13.412	27.314	1.00	0.00	3A4
ATOM	1544	NH1	ARG	242	32.114	-13.042	28.455	1.00	0.00	3A4
ATOM	1545	NH2	ARG	242	32.444	-14.603	26.725	1.00	0.00	3A4
ATOM	1546	C	ARG	242	37.483	-10.871	22.037	1.00	0.00	3A4
ATOM	1547	O	ARG	242	38.677	-10.761	22.298	1.00	0.00	3A4
ATOM	1548	N	GLU	243	37.044	-11.158	20.784	1.00	0.00	3A4
ATOM	1549	CA	GLU	243	37.911	-11.394	19.638	1.00	0.00	3A4
ATOM	1550	CB	GLU	243	37.126	-11.846	18.383	1.00	0.00	3A4
ATOM	1551	CG	GLU	243	36.626	-13.298	18.452	1.00	0.00	3A4
ATOM	1552	CD	GLU	243	35.759	-13.581	17.219	1.00	0.00	3A4
ATOM	1553	OE1	GLU	243	34.528	-13.792	17.385	1.00	0.00	3A4
ATOM	1554	OE2	GLU	243	36.319	-13.581	16.089	1.00	0.00	3A4
ATOM	1555	C	GLU	243	38.703	-10.164	19.275	1.00	0.00	3A4
ATOM	1556	O	GLU	243	39.908	-10.244	19.057	1.00	0.00	3A4
ATOM	1557	N	VAL	244	38.043	-8.981	19.287	1.00	0.00	3A4
ATOM	1558	CA	VAL	244	38.684	-7.714	18.990	1.00	0.00	3A4
ATOM	1559	CB	VAL	244	37.676	-6.607	18.731	1.00	0.00	3A4
ATOM	1560	CG1	VAL	244	38.391	-5.314	18.259	1.00	0.00	3A4
ATOM	1561	CG2	VAL	244	36.813	-7.052	17.545	1.00	0.00	3A4
ATOM	1562	C	VAL	244	39.649	-7.327	20.084	1.00	0.00	3A4
ATOM	1563	O	VAL	244	40.771	-6.912	19.811	1.00	0.00	3A4
ATOM	1564	N	THR	245	39.257	-7.535	21.357	1.00	0.00	3A4
ATOM	1565	CA	THR	245	40.070	-7.264	22.527	1.00	0.00	3A4
ATOM	1566	CB	THR	245	39.245	-7.434	23.795	1.00	0.00	3A4
ATOM	1567	OG1	THR	245	38.211	-6.455	23.817	1.00	0.00	3A4
ATOM	1568	CG2	THR	245	40.041	-7.330	25.127	1.00	0.00	3A4
ATOM	1569	C	THR	245	41.317	-8.113	22.572	1.00	0.00	3A4
ATOM	1570	O	THR	245	42.397	-7.605	22.842	1.00	0.00	3A4
ATOM	1571	N	ASN	246	41.225	-9.408	22.207	1.00	0.00	3A4
ATOM	1572	CA	ASN	246	42.344	-10.327	22.152	1.00	0.00	3A4
ATOM	1573	CB	ASN	246	41.877	-11.774	21.874	1.00	0.00	3A4
ATOM	1574	CG	ASN	246	41.116	-12.349	23.082	1.00	0.00	3A4
ATOM	1575	OD1	ASN	246	41.128	-11.808	24.187	1.00	0.00	3A4
ATOM	1576	ND2	ASN	246	40.427	-13.502	22.862	1.00	0.00	3A4
ATOM	1577	C	ASN	246	43.340	-9.950	21.088	1.00	0.00	3A4
ATOM	1578	O	ASN	246	44.544	-10.003	21.305	1.00	0.00	3A4
ATOM	1579	N	PHE	247	42.846	-9.491	19.921	1.00	0.00	3A4
ATOM	1580	CA	PHE	247	43.640	-9.006	18.820	1.00	0.00	3A4
ATOM	1581	CB	PHE	247	42.712	-8.691	17.625	1.00	0.00	3A4
ATOM	1582	CG	PHE	247	43.520	-8.335	16.378	1.00	0.00	3A4
ATOM	1583	CD1	PHE	247	44.084	-9.348	15.580	1.00	0.00	3A4
ATOM	1584	CD2	PHE	247	43.817	-6.990	16.065	1.00	0.00	3A4
ATOM	1585	CE1	PHE	247	44.943	-9.028	14.517	1.00	0.00	3A4
ATOM	1586	CE2	PHE	247	44.673	-6.665	15.008	1.00	0.00	3A4
ATOM	1587	CZ	PHE	247	45.245	-7.686	14.243	1.00	0.00	3A4
ATOM	1588	C	PHE	247	44.438	-7.768	19.171	1.00	0.00	3A4
ATOM	1589	O	PHE	247	45.631	-7.693	18.897	1.00	0.00	3A4
ATOM	1590	N	LEU	248	43.781	-6.766	19.795	1.00	0.00	3A4
ATOM	1591	CA	LEU	248	44.374	-5.480	20.131	1.00	0.00	3A4
ATOM	1592	CB	LEU	248	43.291	-4.473	20.599	1.00	0.00	3A4
ATOM	1593	CG	LEU	248	42.423	-3.985	19.422	1.00	0.00	3A4
ATOM	1594	CD1	LEU	248	41.143	-3.318	19.920	1.00	0.00	3A4
ATOM	1595	CD2	LEU	248	43.179	-3.055	18.448	1.00	0.00	3A4
ATOM	1596	C	LEU	248	45.407	-5.587	21.219	1.00	0.00	3A4
ATOM	1597	O	LEU	248	46.458	-4.959	21.175	1.00	0.00	3A4
ATOM	1598	N	ARG	249	45.152	-6.483	22.189	1.00	0.00	3A4
ATOM	1599	CA	ARG	249	46.055	-6.805	23.263	1.00	0.00	3A4
ATOM	1600	CB	ARG	249	45.402	-7.886	24.160	1.00	0.00	3A4
ATOM	1601	CG	ARG	249	44.526	-7.297	25.274	1.00	0.00	3A4
ATOM	1602	CD	ARG	249	45.372	-6.731	26.426	1.00	0.00	3A4
ATOM	1603	NE	ARG	249	44.462	-6.210	27.502	1.00	0.00	3A4
ATOM	1604	CZ	ARG	249	44.932	-5.795	28.722	1.00	0.00	3A4
ATOM	1605	NH1	ARG	249	44.068	-5.248	29.621	1.00	0.00	3A4
ATOM	1606	NH2	ARG	249	46.251	-5.917	29.056	1.00	0.00	3A4
ATOM	1607	C	ARG	249	47.418	-7.301	22.846	1.00	0.00	3A4
ATOM	1608	O	ARG	249	48.444	-6.897	23.385	1.00	0.00	3A4
ATOM	1609	N	LYS	250	47.456	-8.139	21.790	1.00	0.00	3A4
ATOM	1610	CA	LYS	250	48.664	-8.643	21.183	1.00	0.00	3A4
ATOM	1611	CB	LYS	250	48.353	-9.760	20.149	1.00	0.00	3A4
ATOM	1612	CG	LYS	250	47.735	-11.007	20.790	1.00	0.00	3A4
ATOM	1613	CD	LYS	250	47.184	-11.995	19.759	1.00	0.00	3A4

ATOM	1614	CE	LYS	250	46.472	-13.190	20.404	1.00	0.00	3A4
ATOM	1615	NZ	LYS	250	45.925	-14.102	19.372	1.00	0.00	3A4
ATOM	1616	C	LYS	250	49.481	-7.572	20.506	1.00	0.00	3A4
ATOM	1617	O	LYS	250	50.699	-7.572	20.583	1.00	0.00	3A4
ATOM	1618	N	SER	251	48.809	-6.584	19.881	1.00	0.00	3A4
ATOM	1619	CA	SER	251	49.413	-5.423	19.268	1.00	0.00	3A4
ATOM	1620	CB	SER	251	48.350	-4.598	18.498	1.00	0.00	3A4
ATOM	1621	OG	SER	251	47.705	-5.410	17.524	1.00	0.00	3A4
ATOM	1622	C	SER	251	50.056	-4.492	20.271	1.00	0.00	3A4
ATOM	1623	O	SER	251	51.163	-4.000	20.091	1.00	0.00	3A4
ATOM	1624	N	VAL	252	49.376	-4.275	21.416	1.00	0.00	3A4
ATOM	1625	CA	VAL	252	49.809	-3.398	22.495	1.00	0.00	3A4
ATOM	1626	CB	VAL	252	48.673	-3.198	23.486	1.00	0.00	3A4
ATOM	1627	CG1	VAL	252	49.132	-2.497	24.775	1.00	0.00	3A4
ATOM	1628	CG2	VAL	252	47.610	-2.462	22.625	1.00	0.00	3A4
ATOM	1629	C	VAL	252	51.052	-3.938	23.163	1.00	0.00	3A4
ATOM	1630	O	VAL	252	51.998	-3.206	23.419	1.00	0.00	3A4
ATOM	1631	N	LYS	253	51.108	-5.271	23.380	1.00	0.00	3A4
ATOM	1632	CA	LYS	253	52.243	-5.976	23.944	1.00	0.00	3A4
ATOM	1633	CB	LYS	253	51.887	-7.462	24.155	1.00	0.00	3A4
ATOM	1634	CG	LYS	253	52.903	-8.297	24.953	1.00	0.00	3A4
ATOM	1635	CD	LYS	253	52.410	-9.721	25.224	1.00	0.00	3A4
ATOM	1636	CE	LYS	253	53.418	-10.563	26.018	1.00	0.00	3A4
ATOM	1637	NZ	LYS	253	52.893	-11.929	26.256	1.00	0.00	3A4
ATOM	1638	C	LYS	253	53.481	-5.877	23.082	1.00	0.00	3A4
ATOM	1639	O	LYS	253	54.570	-5.578	23.557	1.00	0.00	3A4
ATOM	1640	N	ARG	254	53.316	-6.057	21.752	1.00	0.00	3A4
ATOM	1641	CA	ARG	254	54.372	-5.928	20.768	1.00	0.00	3A4
ATOM	1642	CB	ARG	254	53.887	-6.368	19.369	1.00	0.00	3A4
ATOM	1643	CG	ARG	254	53.631	-7.877	19.278	1.00	0.00	3A4
ATOM	1644	CD	ARG	254	52.822	-8.252	18.031	1.00	0.00	3A4
ATOM	1645	NE	ARG	254	52.473	-9.714	18.098	1.00	0.00	3A4
ATOM	1646	CZ	ARG	254	51.381	-10.256	17.466	1.00	0.00	3A4
ATOM	1647	NH1	ARG	254	51.133	-11.591	17.596	1.00	0.00	3A4
ATOM	1648	NH2	ARG	254	50.529	-9.490	16.721	1.00	0.00	3A4
ATOM	1649	C	ARG	254	54.899	-4.517	20.676	1.00	0.00	3A4
ATOM	1650	O	ARG	254	56.093	-4.310	20.498	1.00	0.00	3A4
ATOM	1651	N	MET	255	54.021	-3.508	20.844	1.00	0.00	3A4
ATOM	1652	CA	MET	255	54.372	-2.106	20.777	1.00	0.00	3A4
ATOM	1653	CB	MET	255	53.141	-1.258	20.406	1.00	0.00	3A4
ATOM	1654	CG	MET	255	52.816	-1.403	18.917	1.00	0.00	3A4
ATOM	1655	SD	MET	255	51.250	-0.639	18.447	1.00	0.00	3A4
ATOM	1656	CE	MET	255	51.470	-0.681	16.649	1.00	0.00	3A4
ATOM	1657	C	MET	255	55.008	-1.583	22.041	1.00	0.00	3A4
ATOM	1658	O	MET	255	55.687	-0.563	22.027	1.00	0.00	3A4
ATOM	1659	N	LYS	256	54.853	-2.296	23.174	1.00	0.00	3A4
ATOM	1660	CA	LYS	256	55.524	-1.998	24.424	1.00	0.00	3A4
ATOM	1661	CB	LYS	256	54.809	-2.661	25.623	1.00	0.00	3A4
ATOM	1662	CG	LYS	256	53.537	-1.942	26.076	1.00	0.00	3A4
ATOM	1663	CD	LYS	256	52.726	-2.649	27.168	1.00	0.00	3A4
ATOM	1664	CE	LYS	256	53.383	-2.616	28.556	1.00	0.00	3A4
ATOM	1665	NZ	LYS	256	52.487	-3.206	29.579	1.00	0.00	3A4
ATOM	1666	C	LYS	256	56.960	-2.488	24.397	1.00	0.00	3A4
ATOM	1667	O	LYS	256	57.837	-1.909	25.029	1.00	0.00	3A4
ATOM	1668	N	GLU	257	57.220	-3.565	23.619	1.00	0.00	3A4
ATOM	1669	CA	GLU	257	58.527	-4.164	23.444	1.00	0.00	3A4
ATOM	1670	CB	GLU	257	58.421	-5.661	23.058	1.00	0.00	3A4
ATOM	1671	CG	GLU	257	57.813	-6.520	24.182	1.00	0.00	3A4
ATOM	1672	CD	GLU	257	57.607	-7.953	23.679	1.00	0.00	3A4
ATOM	1673	OE1	GLU	257	56.428	-8.395	23.604	1.00	0.00	3A4
ATOM	1674	OE2	GLU	257	58.625	-8.625	23.363	1.00	0.00	3A4
ATOM	1675	C	GLU	257	59.381	-3.451	22.410	1.00	0.00	3A4
ATOM	1676	O	GLU	257	60.407	-2.870	22.760	1.00	0.00	3A4
ATOM	1677	N	SER	258	59.003	-3.527	21.108	1.00	0.00	3A4
ATOM	1678	CA	SER	258	59.766	-2.938	20.026	1.00	0.00	3A4
ATOM	1679	CB	SER	258	61.186	-3.589	19.807	1.00	0.00	3A4
ATOM	1680	OG	SER	258	62.002	-2.850	18.899	1.00	0.00	3A4
ATOM	1681	C	SER	258	58.938	-3.119	18.776	1.00	0.00	3A4
ATOM	1682	O	SER	258	58.503	-4.225	18.459	1.00	0.00	3A4
ATOM	1683	N	ARG	259	58.779	-2.011	18.007	1.00	0.00	3A4
ATOM	1684	CA	ARG	259	58.391	-2.013	16.612	1.00	0.00	3A4
ATOM	1685	CB	ARG	259	56.880	-1.758	16.329	1.00	0.00	3A4

ATOM	1686	CG	ARG	259	55.968	-2.939	16.688	1.00	0.00	3A4
ATOM	1687	CD	ARG	259	54.607	-2.858	15.987	1.00	0.00	3A4
ATOM	1688	NE	ARG	259	53.744	-4.000	16.458	1.00	0.00	3A4
ATOM	1689	CZ	ARG	259	52.617	-4.411	15.791	1.00	0.00	3A4
ATOM	1690	NH1	ARG	259	51.837	-5.390	16.332	1.00	0.00	3A4
ATOM	1691	NH2	ARG	259	52.247	-3.859	14.598	1.00	0.00	3A4
ATOM	1692	C	ARG	259	59.262	-0.943	16.000	1.00	0.00	3A4
ATOM	1693	O	ARG	259	60.401	-1.220	15.626	1.00	0.00	3A4
ATOM	1694	N	LEU	260	58.752	0.314	15.898	1.00	0.00	3A4
ATOM	1695	CA	LEU	260	59.502	1.436	15.373	1.00	0.00	3A4
ATOM	1696	CB	LEU	260	59.602	1.425	13.811	1.00	0.00	3A4
ATOM	1697	CG	LEU	260	60.595	2.428	13.175	1.00	0.00	3A4
ATOM	1698	CD1	LEU	260	62.054	2.163	13.599	1.00	0.00	3A4
ATOM	1699	CD2	LEU	260	60.467	2.427	11.640	1.00	0.00	3A4
ATOM	1700	C	LEU	260	58.790	2.670	15.874	1.00	0.00	3A4
ATOM	1701	O	LEU	260	58.005	3.291	15.159	1.00	0.00	3A4
ATOM	1702	N	GLU	261	59.062	3.038	17.155	1.00	0.00	3A4
ATOM	1703	CA	GLU	261	58.441	4.130	17.884	1.00	0.00	3A4
ATOM	1704	CB	GLU	261	57.742	3.683	19.213	1.00	0.00	3A4
ATOM	1705	CG	GLU	261	58.554	2.841	20.229	1.00	0.00	3A4
ATOM	1706	CD	GLU	261	58.717	1.386	19.761	1.00	0.00	3A4
ATOM	1707	OE1	GLU	261	59.884	0.942	19.589	1.00	0.00	3A4
ATOM	1708	OE2	GLU	261	57.675	0.701	19.572	1.00	0.00	3A4
ATOM	1709	C	GLU	261	59.482	5.186	18.166	1.00	0.00	3A4
ATOM	1710	O	GLU	261	60.619	4.877	18.523	1.00	0.00	3A4
ATOM	1711	N	ASP	262	59.067	6.478	17.991	1.00	0.00	3A4
ATOM	1712	CA	ASP	262	59.771	7.738	18.239	1.00	0.00	3A4
ATOM	1713	CB	ASP	262	60.392	7.859	19.674	1.00	0.00	3A4
ATOM	1714	CG	ASP	262	59.293	7.671	20.735	1.00	0.00	3A4
ATOM	1715	OD1	ASP	262	59.392	6.700	21.533	1.00	0.00	3A4
ATOM	1716	OD2	ASP	262	58.341	8.497	20.759	1.00	0.00	3A4
ATOM	1717	C	ASP	262	60.828	8.011	17.175	1.00	0.00	3A4
ATOM	1718	O	ASP	262	62.015	8.125	17.477	1.00	0.00	3A4
ATOM	1719	N	THR	263	60.385	8.087	15.889	1.00	0.00	3A4
ATOM	1720	CA	THR	263	61.231	8.151	14.709	1.00	0.00	3A4
ATOM	1721	CB	THR	263	61.257	6.828	13.922	1.00	0.00	3A4
ATOM	1722	OG1	THR	263	59.962	6.247	13.768	1.00	0.00	3A4
ATOM	1723	CG2	THR	263	62.163	5.831	14.677	1.00	0.00	3A4
ATOM	1724	C	THR	263	60.819	9.346	13.857	1.00	0.00	3A4
ATOM	1725	O	THR	263	61.248	10.466	14.127	1.00	0.00	3A4
ATOM	1726	N	GLN	264	60.017	9.120	12.773	1.00	0.00	3A4
ATOM	1727	CA	GLN	264	59.831	10.032	11.649	1.00	0.00	3A4
ATOM	1728	CB	GLN	264	59.812	9.263	10.288	1.00	0.00	3A4
ATOM	1729	CG	GLN	264	61.018	8.324	10.094	1.00	0.00	3A4
ATOM	1730	CD	GLN	264	60.951	7.671	8.710	1.00	0.00	3A4
ATOM	1731	OE1	GLN	264	61.775	7.968	7.846	1.00	0.00	3A4
ATOM	1732	NE2	GLN	264	59.961	6.763	8.489	1.00	0.00	3A4
ATOM	1733	C	GLN	264	58.564	10.861	11.768	1.00	0.00	3A4
ATOM	1734	O	GLN	264	57.907	10.891	12.808	1.00	0.00	3A4
ATOM	1735	N	LYS	265	58.214	11.556	10.645	1.00	0.00	3A4
ATOM	1736	CA	LYS	265	57.091	12.459	10.453	1.00	0.00	3A4
ATOM	1737	CB	LYS	265	57.471	13.608	9.470	1.00	0.00	3A4
ATOM	1738	CG	LYS	265	56.414	14.703	9.209	1.00	0.00	3A4
ATOM	1739	CD	LYS	265	55.986	15.485	10.458	1.00	0.00	3A4
ATOM	1740	CE	LYS	265	55.004	16.618	10.140	1.00	0.00	3A4
ATOM	1741	NZ	LYS	265	54.585	17.323	11.374	1.00	0.00	3A4
ATOM	1742	C	LYS	265	55.895	11.698	9.920	1.00	0.00	3A4
ATOM	1743	O	LYS	265	54.757	11.957	10.308	1.00	0.00	3A4
ATOM	1744	N	HIS	266	56.161	10.712	9.017	1.00	0.00	3A4
ATOM	1745	CA	HIS	266	55.192	9.789	8.453	1.00	0.00	3A4
ATOM	1746	ND1	HIS	266	53.213	11.484	6.555	1.00	0.00	3A4
ATOM	1747	CG	HIS	266	54.551	11.168	6.457	1.00	0.00	3A4
ATOM	1748	CB	HIS	266	55.138	9.857	6.906	1.00	0.00	3A4
ATOM	1749	NE2	HIS	266	54.234	13.294	5.769	1.00	0.00	3A4
ATOM	1750	CD2	HIS	266	55.161	12.287	5.977	1.00	0.00	3A4
ATOM	1751	CE1	HIS	266	53.080	12.764	6.128	1.00	0.00	3A4
ATOM	1752	C	HIS	266	55.520	8.402	8.961	1.00	0.00	3A4
ATOM	1753	O	HIS	266	55.595	7.432	8.208	1.00	0.00	3A4
ATOM	1754	N	ARG	267	55.681	8.319	10.306	1.00	0.00	3A4
ATOM	1755	CA	ARG	267	55.787	7.112	11.088	1.00	0.00	3A4
ATOM	1756	CB	ARG	267	57.206	6.450	11.025	1.00	0.00	3A4
ATOM	1757	CG	ARG	267	57.342	5.024	11.602	1.00	0.00	3A4

ATOM	1758	CD	ARG	267	56.433	3.983	10.915	1.00	0.00	3A4
ATOM	1759	NE	ARG	267	56.515	2.666	11.644	1.00	0.00	3A4
ATOM	1760	CZ	ARG	267	55.718	2.342	12.715	1.00	0.00	3A4
ATOM	1761	NH1	ARG	267	55.829	1.104	13.280	1.00	0.00	3A4
ATOM	1762	NH2	ARG	267	54.819	3.229	13.235	1.00	0.00	3A4
ATOM	1763	C	ARG	267	55.443	7.575	12.488	1.00	0.00	3A4
ATOM	1764	O	ARG	267	55.403	8.776	12.757	1.00	0.00	3A4
ATOM	1765	N	VAL	268	55.180	6.600	13.409	1.00	0.00	3A4
ATOM	1766	CA	VAL	268	54.850	6.700	14.830	1.00	0.00	3A4
ATOM	1767	CB	VAL	268	55.608	7.738	15.672	1.00	0.00	3A4
ATOM	1768	CG1	VAL	268	55.286	7.564	17.181	1.00	0.00	3A4
ATOM	1769	CG2	VAL	268	57.124	7.555	15.459	1.00	0.00	3A4
ATOM	1770	C	VAL	268	53.347	6.859	14.949	1.00	0.00	3A4
ATOM	1771	O	VAL	268	52.814	7.966	14.876	1.00	0.00	3A4
ATOM	1772	N	ASP	269	52.650	5.703	15.128	1.00	0.00	3A4
ATOM	1773	CA	ASP	269	51.217	5.484	15.039	1.00	0.00	3A4
ATOM	1774	CB	ASP	269	50.952	4.008	14.629	1.00	0.00	3A4
ATOM	1775	CG	ASP	269	51.584	2.963	15.562	1.00	0.00	3A4
ATOM	1776	OD1	ASP	269	52.585	2.329	15.136	1.00	0.00	3A4
ATOM	1777	OD2	ASP	269	51.040	2.734	16.671	1.00	0.00	3A4
ATOM	1778	C	ASP	269	50.513	5.855	16.322	1.00	0.00	3A4
ATOM	1779	O	ASP	269	51.163	6.144	17.324	1.00	0.00	3A4
ATOM	1780	N	PHE	270	49.161	5.834	16.331	1.00	0.00	3A4
ATOM	1781	CA	PHE	270	48.362	6.204	17.490	1.00	0.00	3A4
ATOM	1782	CB	PHE	270	46.855	6.258	17.148	1.00	0.00	3A4
ATOM	1783	CG	PHE	270	45.990	6.766	18.282	1.00	0.00	3A4
ATOM	1784	CD1	PHE	270	45.280	5.854	19.081	1.00	0.00	3A4
ATOM	1785	CD2	PHE	270	46.020	8.114	18.661	1.00	0.00	3A4
ATOM	1786	CE1	PHE	270	44.531	6.282	20.177	1.00	0.00	3A4
ATOM	1787	CE2	PHE	270	45.309	8.546	19.789	1.00	0.00	3A4
ATOM	1788	CZ	PHE	270	44.542	7.634	20.522	1.00	0.00	3A4
ATOM	1789	C	PHE	270	48.565	5.305	18.696	1.00	0.00	3A4
ATOM	1790	O	PHE	270	48.623	5.789	19.822	1.00	0.00	3A4
ATOM	1791	N	LEU	271	48.707	3.980	18.488	1.00	0.00	3A4
ATOM	1792	CA	LEU	271	48.911	3.039	19.569	1.00	0.00	3A4
ATOM	1793	CB	LEU	271	48.798	1.584	19.058	1.00	0.00	3A4
ATOM	1794	CG	LEU	271	47.377	1.034	18.852	1.00	0.00	3A4
ATOM	1795	CD1	LEU	271	47.422	-0.399	18.277	1.00	0.00	3A4
ATOM	1796	CD2	LEU	271	46.550	1.035	20.150	1.00	0.00	3A4
ATOM	1797	C	LEU	271	50.247	3.247	20.287	1.00	0.00	3A4
ATOM	1798	O	LEU	271	50.309	3.283	21.510	1.00	0.00	3A4
ATOM	1799	N	GLN	272	51.325	3.513	19.518	1.00	0.00	3A4
ATOM	1800	CA	GLN	272	52.641	3.856	20.018	1.00	0.00	3A4
ATOM	1801	CB	GLN	272	53.651	3.973	18.871	1.00	0.00	3A4
ATOM	1802	CG	GLN	272	53.989	2.568	18.334	1.00	0.00	3A4
ATOM	1803	CD	GLN	272	54.908	2.656	17.119	1.00	0.00	3A4
ATOM	1804	OE1	GLN	272	55.225	3.735	16.626	1.00	0.00	3A4
ATOM	1805	NE2	GLN	272	55.347	1.475	16.611	1.00	0.00	3A4
ATOM	1806	C	GLN	272	52.646	5.136	20.813	1.00	0.00	3A4
ATOM	1807	O	GLN	272	53.254	5.214	21.874	1.00	0.00	3A4
ATOM	1808	N	LEU	273	51.883	6.155	20.356	1.00	0.00	3A4
ATOM	1809	CA	LEU	273	51.695	7.415	21.048	1.00	0.00	3A4
ATOM	1810	CB	LEU	273	50.926	8.433	20.166	1.00	0.00	3A4
ATOM	1811	CG	LEU	273	51.785	8.888	18.948	1.00	0.00	3A4
ATOM	1812	CD1	LEU	273	50.959	9.439	17.771	1.00	0.00	3A4
ATOM	1813	CD2	LEU	273	52.899	9.882	19.332	1.00	0.00	3A4
ATOM	1814	C	LEU	273	50.983	7.274	22.346	1.00	0.00	3A4
ATOM	1815	O	LEU	273	51.365	7.895	23.329	1.00	0.00	3A4
ATOM	1816	N	MET	274	49.964	6.395	22.412	1.00	0.00	3A4
ATOM	1817	CA	MET	274	49.244	6.073	23.621	1.00	0.00	3A4
ATOM	1818	CB	MET	274	47.977	5.254	23.316	1.00	0.00	3A4
ATOM	1819	CG	MET	274	46.828	6.090	22.751	1.00	0.00	3A4
ATOM	1820	SD	MET	274	45.317	6.067	23.770	1.00	0.00	3A4
ATOM	1821	CE	MET	274	45.991	6.940	25.218	1.00	0.00	3A4
ATOM	1822	C	MET	274	50.109	5.325	24.619	1.00	0.00	3A4
ATOM	1823	O	MET	274	50.038	5.567	25.819	1.00	0.00	3A4
ATOM	1824	N	ILE	275	50.988	4.417	24.131	1.00	0.00	3A4
ATOM	1825	CA	ILE	275	51.851	3.564	24.931	1.00	0.00	3A4
ATOM	1826	CB	ILE	275	52.467	2.441	24.078	1.00	0.00	3A4
ATOM	1827	CG2	ILE	275	53.965	2.545	23.648	1.00	0.00	3A4
ATOM	1828	CG1	ILE	275	52.209	1.038	24.643	1.00	0.00	3A4
ATOM	1829	CD	ILE	275	51.787	0.081	23.536	1.00	0.00	3A4

ATOM	1830	C	ILE	275	52.925	4.329	25.660	1.00	0.00	3A4
ATOM	1831	O	ILE	275	53.323	3.975	26.764	1.00	0.00	3A4
ATOM	1832	N	ASP	276	53.392	5.425	25.033	1.00	0.00	3A4
ATOM	1833	CA	ASP	276	54.488	6.233	25.491	1.00	0.00	3A4
ATOM	1834	CB	ASP	276	55.375	6.635	24.263	1.00	0.00	3A4
ATOM	1835	CG	ASP	276	56.766	7.177	24.648	1.00	0.00	3A4
ATOM	1836	OD1	ASP	276	57.527	6.432	25.323	1.00	0.00	3A4
ATOM	1837	OD2	ASP	276	57.080	8.336	24.266	1.00	0.00	3A4
ATOM	1838	C	ASP	276	53.994	7.467	26.229	1.00	0.00	3A4
ATOM	1839	O	ASP	276	54.738	8.023	27.029	1.00	0.00	3A4
ATOM	1840	N	SER	277	52.734	7.918	25.959	1.00	0.00	3A4
ATOM	1841	CA	SER	277	51.962	9.005	26.574	1.00	0.00	3A4
ATOM	1842	CB	SER	277	51.494	8.689	28.034	1.00	0.00	3A4
ATOM	1843	OG	SER	277	52.536	8.498	28.989	1.00	0.00	3A4
ATOM	1844	C	SER	277	52.586	10.401	26.477	1.00	0.00	3A4
ATOM	1845	O	SER	277	53.547	10.719	27.177	1.00	0.00	3A4
ATOM	1846	N	GLN	278	52.027	11.259	25.584	1.00	0.00	3A4
ATOM	1847	CA	GLN	278	52.576	12.557	25.230	1.00	0.00	3A4
ATOM	1848	CB	GLN	278	53.079	12.585	23.748	1.00	0.00	3A4
ATOM	1849	CG	GLN	278	52.289	11.752	22.708	1.00	0.00	3A4
ATOM	1850	CD	GLN	278	50.896	12.317	22.436	1.00	0.00	3A4
ATOM	1851	OE1	GLN	278	49.896	11.703	22.807	1.00	0.00	3A4
ATOM	1852	NE2	GLN	278	50.821	13.500	21.767	1.00	0.00	3A4
ATOM	1853	C	GLN	278	51.568	13.647	25.534	1.00	0.00	3A4
ATOM	1854	O	GLN	278	51.306	14.524	24.712	1.00	0.00	3A4
ATOM	1855	N	ASN	279	51.016	13.632	26.775	1.00	0.00	3A4
ATOM	1856	CA	ASN	279	50.193	14.697	27.310	1.00	0.00	3A4
ATOM	1857	CB	ASN	279	48.716	14.690	26.781	1.00	0.00	3A4
ATOM	1858	CG	ASN	279	47.973	15.999	27.107	1.00	0.00	3A4
ATOM	1859	OD1	ASN	279	47.305	16.089	28.136	1.00	0.00	3A4
ATOM	1860	ND2	ASN	279	48.086	17.026	26.221	1.00	0.00	3A4
ATOM	1861	C	ASN	279	50.239	14.505	28.808	1.00	0.00	3A4
ATOM	1862	O	ASN	279	50.626	15.409	29.546	1.00	0.00	3A4
ATOM	1863	N	SER	280	49.821	13.295	29.277	1.00	0.00	3A4
ATOM	1864	CA	SER	280	49.736	12.901	30.674	1.00	0.00	3A4
ATOM	1865	CB	SER	280	48.334	12.330	31.056	1.00	0.00	3A4
ATOM	1866	OG	SER	280	47.313	13.268	30.740	1.00	0.00	3A4
ATOM	1867	C	SER	280	50.810	11.870	30.942	1.00	0.00	3A4
ATOM	1868	O	SER	280	51.635	11.569	30.079	1.00	0.00	3A4
ATOM	1869	N	LYS	281	50.813	11.317	32.183	1.00	0.00	3A4
ATOM	1870	CA	LYS	281	51.810	10.412	32.724	1.00	0.00	3A4
ATOM	1871	CB	LYS	281	52.318	10.863	34.135	1.00	0.00	3A4
ATOM	1872	CG	LYS	281	51.368	10.740	35.357	1.00	0.00	3A4
ATOM	1873	CD	LYS	281	50.099	11.612	35.328	1.00	0.00	3A4
ATOM	1874	CE	LYS	281	49.241	11.508	36.598	1.00	0.00	3A4
ATOM	1875	NZ	LYS	281	48.695	10.139	36.770	1.00	0.00	3A4
ATOM	1876	C	LYS	281	51.259	9.009	32.800	1.00	0.00	3A4
ATOM	1877	O	LYS	281	50.051	8.792	32.725	1.00	0.00	3A4
ATOM	1878	N	GLU	282	52.179	8.025	33.003	1.00	0.00	3A4
ATOM	1879	CA	GLU	282	51.902	6.623	33.252	1.00	0.00	3A4
ATOM	1880	CB	GLU	282	52.839	5.684	32.439	1.00	0.00	3A4
ATOM	1881	CG	GLU	282	54.355	5.905	32.633	1.00	0.00	3A4
ATOM	1882	CD	GLU	282	55.125	5.055	31.617	1.00	0.00	3A4
ATOM	1883	OE1	GLU	282	54.983	5.322	30.393	1.00	0.00	3A4
ATOM	1884	OE2	GLU	282	55.866	4.133	32.049	1.00	0.00	3A4
ATOM	1885	C	GLU	282	52.026	6.378	34.739	1.00	0.00	3A4
ATOM	1886	O	GLU	282	52.842	7.002	35.416	1.00	0.00	3A4
ATOM	1887	N	THR	283	51.169	5.468	35.281	1.00	0.00	3A4
ATOM	1888	CA	THR	283	50.949	5.262	36.708	1.00	0.00	3A4
ATOM	1889	CB	THR	283	49.462	5.076	37.037	1.00	0.00	3A4
ATOM	1890	OG1	THR	283	48.843	4.071	36.236	1.00	0.00	3A4
ATOM	1891	CG2	THR	283	48.746	6.425	36.797	1.00	0.00	3A4
ATOM	1892	C	THR	283	51.786	4.117	37.266	1.00	0.00	3A4
ATOM	1893	O	THR	283	51.843	3.935	38.481	1.00	0.00	3A4
ATOM	1894	N	GLU	284	52.457	3.329	36.385	1.00	0.00	3A4
ATOM	1895	CA	GLU	284	53.336	2.253	36.792	1.00	0.00	3A4
ATOM	1896	CB	GLU	284	52.583	0.907	37.025	1.00	0.00	3A4
ATOM	1897	CG	GLU	284	53.427	-0.211	37.670	1.00	0.00	3A4
ATOM	1898	CD	GLU	284	52.553	-1.452	37.873	1.00	0.00	3A4
ATOM	1899	OE1	GLU	284	52.075	-2.014	36.851	1.00	0.00	3A4
ATOM	1900	OE2	GLU	284	52.352	-1.855	39.051	1.00	0.00	3A4
ATOM	1901	C	GLU	284	54.393	2.152	35.719	1.00	0.00	3A4

ATOM	1902	O	GLU	284	55.397	2.861	35.770	1.00	0.00	3A4
ATOM	1903	N	SER	285	54.186	1.256	34.721	1.00	0.00	3A4
ATOM	1904	CA	SER	285	55.139	0.973	33.669	1.00	0.00	3A4
ATOM	1905	CB	SER	285	56.281	-0.008	34.108	1.00	0.00	3A4
ATOM	1906	OG	SER	285	55.800	-1.171	34.781	1.00	0.00	3A4
ATOM	1907	C	SER	285	54.331	0.438	32.510	1.00	0.00	3A4
ATOM	1908	O	SER	285	54.522	-0.694	32.066	1.00	0.00	3A4
ATOM	1909	N	HIS	286	53.396	1.275	31.998	1.00	0.00	3A4
ATOM	1910	CA	HIS	286	52.522	0.926	30.901	1.00	0.00	3A4
ATOM	1911	ND1	HIS	286	49.824	1.672	32.816	1.00	0.00	3A4
ATOM	1912	CG	HIS	286	50.594	0.542	32.645	1.00	0.00	3A4
ATOM	1913	CB	HIS	286	51.264	0.113	31.356	1.00	0.00	3A4
ATOM	1914	NE2	HIS	286	49.782	0.592	34.753	1.00	0.00	3A4
ATOM	1915	CD2	HIS	286	50.557	-0.106	33.843	1.00	0.00	3A4
ATOM	1916	CE1	HIS	286	49.366	1.652	34.090	1.00	0.00	3A4
ATOM	1917	C	HIS	286	52.192	2.222	30.200	1.00	0.00	3A4
ATOM	1918	O	HIS	286	53.089	2.937	29.758	1.00	0.00	3A4
ATOM	1919	N	LYS	287	50.878	2.537	30.069	1.00	0.00	3A4
ATOM	1920	CA	LYS	287	50.317	3.652	29.338	1.00	0.00	3A4
ATOM	1921	CB	LYS	287	49.136	3.180	28.453	1.00	0.00	3A4
ATOM	1922	CG	LYS	287	49.553	2.209	27.349	1.00	0.00	3A4
ATOM	1923	CD	LYS	287	48.717	2.529	26.095	1.00	0.00	3A4
ATOM	1924	CE	LYS	287	48.931	1.795	24.736	1.00	0.00	3A4
ATOM	1925	NZ	LYS	287	47.885	2.079	23.732	1.00	0.00	3A4
ATOM	1926	C	LYS	287	49.794	4.698	30.287	1.00	0.00	3A4
ATOM	1927	O	LYS	287	49.872	4.548	31.504	1.00	0.00	3A4
ATOM	1928	N	ALA	288	49.185	5.771	29.701	1.00	0.00	3A4
ATOM	1929	CA	ALA	288	48.374	6.783	30.350	1.00	0.00	3A4
ATOM	1930	CB	ALA	288	48.615	8.202	29.810	1.00	0.00	3A4
ATOM	1931	C	ALA	288	46.906	6.403	30.192	1.00	0.00	3A4
ATOM	1932	O	ALA	288	46.333	6.618	29.125	1.00	0.00	3A4
ATOM	1933	N	LEU	289	46.245	5.810	31.226	1.00	0.00	3A4
ATOM	1934	CA	LEU	289	46.774	5.489	32.535	1.00	0.00	3A4
ATOM	1935	CB	LEU	289	46.349	6.484	33.668	1.00	0.00	3A4
ATOM	1936	CG	LEU	289	44.839	6.740	33.920	1.00	0.00	3A4
ATOM	1937	CD1	LEU	289	44.604	7.179	35.378	1.00	0.00	3A4
ATOM	1938	CD2	LEU	289	44.221	7.776	32.951	1.00	0.00	3A4
ATOM	1939	C	LEU	289	46.475	4.056	32.878	1.00	0.00	3A4
ATOM	1940	O	LEU	289	46.614	3.704	34.048	1.00	0.00	3A4
ATOM	1941	N	SER	290	46.131	3.176	31.880	1.00	0.00	3A4
ATOM	1942	CA	SER	290	46.112	1.765	32.148	1.00	0.00	3A4
ATOM	1943	CB	SER	290	45.026	1.325	33.179	1.00	0.00	3A4
ATOM	1944	OG	SER	290	43.728	1.835	32.895	1.00	0.00	3A4
ATOM	1945	C	SER	290	45.931	1.008	30.867	1.00	0.00	3A4
ATOM	1946	O	SER	290	45.432	1.483	29.847	1.00	0.00	3A4
ATOM	1947	N	ASP	291	46.293	-0.287	30.944	1.00	0.00	3A4
ATOM	1948	CA	ASP	291	46.226	-1.223	29.856	1.00	0.00	3A4
ATOM	1949	CB	ASP	291	46.894	-2.555	30.218	1.00	0.00	3A4
ATOM	1950	CG	ASP	291	48.385	-2.331	30.513	1.00	0.00	3A4
ATOM	1951	OD1	ASP	291	49.127	-1.982	29.555	1.00	0.00	3A4
ATOM	1952	OD2	ASP	291	48.800	-2.508	31.690	1.00	0.00	3A4
ATOM	1953	C	ASP	291	44.820	-1.495	29.390	1.00	0.00	3A4
ATOM	1954	O	ASP	291	44.578	-1.735	28.227	1.00	0.00	3A4
ATOM	1955	N	LEU	292	43.831	-1.426	30.296	1.00	0.00	3A4
ATOM	1956	CA	LEU	292	42.433	-1.624	29.999	1.00	0.00	3A4
ATOM	1957	CB	LEU	292	41.659	-1.848	31.312	1.00	0.00	3A4
ATOM	1958	CG	LEU	292	41.910	-3.218	31.978	1.00	0.00	3A4
ATOM	1959	CD1	LEU	292	41.502	-3.197	33.463	1.00	0.00	3A4
ATOM	1960	CD2	LEU	292	41.193	-4.362	31.230	1.00	0.00	3A4
ATOM	1961	C	LEU	292	41.827	-0.445	29.268	1.00	0.00	3A4
ATOM	1962	O	LEU	292	41.078	-0.602	28.309	1.00	0.00	3A4
ATOM	1963	N	GLU	293	42.216	0.784	29.669	1.00	0.00	3A4
ATOM	1964	CA	GLU	293	41.794	2.025	29.064	1.00	0.00	3A4
ATOM	1965	CB	GLU	293	42.258	3.233	29.892	1.00	0.00	3A4
ATOM	1966	CG	GLU	293	41.403	3.396	31.163	1.00	0.00	3A4
ATOM	1967	CD	GLU	293	41.950	4.520	32.046	1.00	0.00	3A4
ATOM	1968	OE1	GLU	293	41.285	4.842	33.067	1.00	0.00	3A4
ATOM	1969	OE2	GLU	293	43.037	5.066	31.722	1.00	0.00	3A4
ATOM	1970	C	GLU	293	42.286	2.186	27.666	1.00	0.00	3A4
ATOM	1971	O	GLU	293	41.540	2.607	26.793	1.00	0.00	3A4
ATOM	1972	N	LEU	294	43.547	1.769	27.420	1.00	0.00	3A4
ATOM	1973	CA	LEU	294	44.175	1.802	26.122	1.00	0.00	3A4

ATOM	1974	CB	LEU	294	45.633	1.380	26.208	1.00	0.00	3A4
ATOM	1975	CG	LEU	294	46.091	-0.086	26.051	1.00	0.00	3A4
ATOM	1976	CD1	LEU	294	46.203	-0.637	24.643	1.00	0.00	3A4
ATOM	1977	CD2	LEU	294	47.365	-0.436	26.810	1.00	0.00	3A4
ATOM	1978	C	LEU	294	43.443	0.944	25.134	1.00	0.00	3A4
ATOM	1979	O	LEU	294	43.172	1.361	24.020	1.00	0.00	3A4
ATOM	1980	N	VAL	295	43.044	-0.282	25.551	1.00	0.00	3A4
ATOM	1981	CA	VAL	295	42.358	-1.242	24.721	1.00	0.00	3A4
ATOM	1982	CB	VAL	295	42.271	-2.600	25.380	1.00	0.00	3A4
ATOM	1983	CG1	VAL	295	41.397	-3.622	24.599	1.00	0.00	3A4
ATOM	1984	CG2	VAL	295	43.701	-3.178	25.429	1.00	0.00	3A4
ATOM	1985	C	VAL	295	40.980	-0.762	24.357	1.00	0.00	3A4
ATOM	1986	O	VAL	295	40.584	-0.846	23.207	1.00	0.00	3A4
ATOM	1987	N	ALA	296	40.252	-0.146	25.306	1.00	0.00	3A4
ATOM	1988	CA	ALA	296	38.945	0.439	25.074	1.00	0.00	3A4
ATOM	1989	CB	ALA	296	38.344	0.902	26.408	1.00	0.00	3A4
ATOM	1990	C	ALA	296	38.944	1.619	24.132	1.00	0.00	3A4
ATOM	1991	O	ALA	296	38.032	1.797	23.342	1.00	0.00	3A4
ATOM	1992	N	GLN	297	40.018	2.430	24.170	1.00	0.00	3A4
ATOM	1993	CA	GLN	297	40.228	3.546	23.284	1.00	0.00	3A4
ATOM	1994	CB	GLN	297	41.379	4.436	23.773	1.00	0.00	3A4
ATOM	1995	CG	GLN	297	40.914	5.233	25.008	1.00	0.00	3A4
ATOM	1996	CD	GLN	297	42.099	5.887	25.715	1.00	0.00	3A4
ATOM	1997	OE1	GLN	297	43.052	5.222	26.114	1.00	0.00	3A4
ATOM	1998	NE2	GLN	297	42.034	7.228	25.902	1.00	0.00	3A4
ATOM	1999	C	GLN	297	40.505	3.108	21.882	1.00	0.00	3A4
ATOM	2000	O	GLN	297	39.872	3.572	20.943	1.00	0.00	3A4
ATOM	2001	N	SER	298	41.403	2.117	21.715	1.00	0.00	3A4
ATOM	2002	CA	SER	298	41.744	1.546	20.434	1.00	0.00	3A4
ATOM	2003	CB	SER	298	42.925	0.563	20.529	1.00	0.00	3A4
ATOM	2004	OG	SER	298	42.771	-0.519	21.435	1.00	0.00	3A4
ATOM	2005	C	SER	298	40.584	0.872	19.755	1.00	0.00	3A4
ATOM	2006	O	SER	298	40.435	0.977	18.546	1.00	0.00	3A4
ATOM	2007	N	ILE	299	39.688	0.228	20.542	1.00	0.00	3A4
ATOM	2008	CA	ILE	299	38.438	-0.363	20.098	1.00	0.00	3A4
ATOM	2009	CB	ILE	299	37.670	-1.032	21.291	1.00	0.00	3A4
ATOM	2010	CG2	ILE	299	36.134	-1.268	21.098	1.00	0.00	3A4
ATOM	2011	CG1	ILE	299	38.328	-2.333	21.803	1.00	0.00	3A4
ATOM	2012	CD	ILE	299	37.787	-3.619	21.185	1.00	0.00	3A4
ATOM	2013	C	ILE	299	37.515	0.677	19.534	1.00	0.00	3A4
ATOM	2014	O	ILE	299	36.949	0.525	18.457	1.00	0.00	3A4
ATOM	2015	N	ILE	300	37.374	1.799	20.268	1.00	0.00	3A4
ATOM	2016	CA	ILE	300	36.494	2.883	19.921	1.00	0.00	3A4
ATOM	2017	CB	ILE	300	36.290	3.798	21.113	1.00	0.00	3A4
ATOM	2018	CG2	ILE	300	36.292	5.340	20.897	1.00	0.00	3A4
ATOM	2019	CG1	ILE	300	34.906	3.296	21.637	1.00	0.00	3A4
ATOM	2020	CD	ILE	300	34.503	3.642	23.050	1.00	0.00	3A4
ATOM	2021	C	ILE	300	36.962	3.618	18.712	1.00	0.00	3A4
ATOM	2022	O	ILE	300	36.161	3.994	17.872	1.00	0.00	3A4
ATOM	2023	N	PHE	301	38.279	3.774	18.515	1.00	0.00	3A4
ATOM	2024	CA	PHE	301	38.819	4.525	17.406	1.00	0.00	3A4
ATOM	2025	CB	PHE	301	40.332	4.745	17.663	1.00	0.00	3A4
ATOM	2026	CG	PHE	301	40.520	5.958	18.535	1.00	0.00	3A4
ATOM	2027	CD1	PHE	301	41.157	5.931	19.784	1.00	0.00	3A4
ATOM	2028	CD2	PHE	301	39.913	7.144	18.106	1.00	0.00	3A4
ATOM	2029	CE1	PHE	301	41.032	7.015	20.660	1.00	0.00	3A4
ATOM	2030	CE2	PHE	301	39.784	8.213	18.969	1.00	0.00	3A4
ATOM	2031	CZ	PHE	301	40.300	8.142	20.259	1.00	0.00	3A4
ATOM	2032	C	PHE	301	38.633	3.743	16.111	1.00	0.00	3A4
ATOM	2033	O	PHE	301	38.332	4.306	15.062	1.00	0.00	3A4
ATOM	2034	N	ILE	302	38.742	2.401	16.178	1.00	0.00	3A4
ATOM	2035	CA	ILE	302	38.511	1.491	15.076	1.00	0.00	3A4
ATOM	2036	CB	ILE	302	39.005	0.104	15.470	1.00	0.00	3A4
ATOM	2037	CG2	ILE	302	38.482	-1.056	14.570	1.00	0.00	3A4
ATOM	2038	CG1	ILE	302	40.563	0.105	15.527	1.00	0.00	3A4
ATOM	2039	CD	ILE	302	41.293	0.195	14.178	1.00	0.00	3A4
ATOM	2040	C	ILE	302	37.054	1.462	14.656	1.00	0.00	3A4
ATOM	2041	O	ILE	302	36.732	1.682	13.491	1.00	0.00	3A4
ATOM	2042	N	PHE	303	36.126	1.231	15.610	1.00	0.00	3A4
ATOM	2043	CA	PHE	303	34.711	1.090	15.324	1.00	0.00	3A4
ATOM	2044	CB	PHE	303	34.008	0.159	16.395	1.00	0.00	3A4
ATOM	2045	CG	PHE	303	33.072	0.735	17.449	1.00	0.00	3A4

ATOM	2046	CD1	PHE	303	31.783	1.209	17.127	1.00	0.00	3A4
ATOM	2047	CD2	PHE	303	33.443	0.706	18.808	1.00	0.00	3A4
ATOM	2048	CE1	PHE	303	30.911	1.674	18.121	1.00	0.00	3A4
ATOM	2049	CE2	PHE	303	32.572	1.155	19.810	1.00	0.00	3A4
ATOM	2050	CZ	PHE	303	31.307	1.647	19.465	1.00	0.00	3A4
ATOM	2051	C	PHE	303	34.016	2.407	14.993	1.00	0.00	3A4
ATOM	2052	O	PHE	303	33.183	2.472	14.092	1.00	0.00	3A4
ATOM	2053	N	ALA	304	34.391	3.513	15.679	1.00	0.00	3A4
ATOM	2054	CA	ALA	304	33.814	4.831	15.484	1.00	0.00	3A4
ATOM	2055	CB	ALA	304	34.124	5.826	16.638	1.00	0.00	3A4
ATOM	2056	C	ALA	304	34.221	5.470	14.208	1.00	0.00	3A4
ATOM	2057	O	ALA	304	33.449	6.196	13.589	1.00	0.00	3A4
ATOM	2058	N	GLY	305	35.466	5.191	13.787	1.00	0.00	3A4
ATOM	2059	CA	GLY	305	36.037	5.755	12.599	1.00	0.00	3A4
ATOM	2060	C	GLY	305	35.766	5.044	11.304	1.00	0.00	3A4
ATOM	2061	O	GLY	305	36.028	5.603	10.243	1.00	0.00	3A4
ATOM	2062	N	TYR	306	35.257	3.789	11.337	1.00	0.00	3A4
ATOM	2063	CA	TYR	306	35.125	2.982	10.139	1.00	0.00	3A4
ATOM	2064	CB	TYR	306	35.531	1.484	10.389	1.00	0.00	3A4
ATOM	2065	CG	TYR	306	35.403	0.528	9.206	1.00	0.00	3A4
ATOM	2066	CD1	TYR	306	35.378	0.950	7.858	1.00	0.00	3A4
ATOM	2067	CD2	TYR	306	35.195	-0.835	9.469	1.00	0.00	3A4
ATOM	2068	CE1	TYR	306	35.009	0.064	6.843	1.00	0.00	3A4
ATOM	2069	CE2	TYR	306	34.885	-1.738	8.441	1.00	0.00	3A4
ATOM	2070	CZ	TYR	306	34.766	-1.281	7.125	1.00	0.00	3A4
ATOM	2071	OH	TYR	306	34.383	-2.159	6.089	1.00	0.00	3A4
ATOM	2072	C	TYR	306	33.741	3.132	9.572	1.00	0.00	3A4
ATOM	2073	O	TYR	306	33.566	3.553	8.431	1.00	0.00	3A4
ATOM	2074	N	GLU	307	32.692	2.781	10.344	1.00	0.00	3A4
ATOM	2075	CA	GLU	307	31.384	2.639	9.745	1.00	0.00	3A4
ATOM	2076	CB	GLU	307	30.517	1.553	10.437	1.00	0.00	3A4
ATOM	2077	CG	GLU	307	31.119	0.127	10.329	1.00	0.00	3A4
ATOM	2078	CD	GLU	307	31.130	-0.460	8.905	1.00	0.00	3A4
ATOM	2079	OE1	GLU	307	30.600	0.159	7.942	1.00	0.00	3A4
ATOM	2080	OE2	GLU	307	31.670	-1.592	8.778	1.00	0.00	3A4
ATOM	2081	C	GLU	307	30.630	3.933	9.563	1.00	0.00	3A4
ATOM	2082	O	GLU	307	29.605	3.926	8.924	1.00	0.00	3A4
ATOM	2083	N	THR	308	31.140	5.089	10.026	1.00	0.00	3A4
ATOM	2084	CA	THR	308	30.556	6.394	9.788	1.00	0.00	3A4
ATOM	2085	CB	THR	308	30.866	7.363	10.932	1.00	0.00	3A4
ATOM	2086	OG1	THR	308	32.255	7.423	11.254	1.00	0.00	3A4
ATOM	2087	CG2	THR	308	30.088	6.935	12.191	1.00	0.00	3A4
ATOM	2088	C	THR	308	31.006	6.957	8.463	1.00	0.00	3A4
ATOM	2089	O	THR	308	30.202	7.360	7.632	1.00	0.00	3A4
ATOM	2090	N	THR	309	32.332	6.929	8.226	1.00	0.00	3A4
ATOM	2091	CA	THR	309	32.979	7.436	7.038	1.00	0.00	3A4
ATOM	2092	CB	THR	309	34.479	7.445	7.204	1.00	0.00	3A4
ATOM	2093	OG1	THR	309	34.937	6.213	7.743	1.00	0.00	3A4
ATOM	2094	CG2	THR	309	34.867	8.555	8.200	1.00	0.00	3A4
ATOM	2095	C	THR	309	32.600	6.684	5.779	1.00	0.00	3A4
ATOM	2096	O	THR	309	32.349	7.278	4.741	1.00	0.00	3A4
ATOM	2097	N	SER	310	32.484	5.339	5.875	1.00	0.00	3A4
ATOM	2098	CA	SER	310	32.052	4.458	4.809	1.00	0.00	3A4
ATOM	2099	CB	SER	310	31.996	2.990	5.310	1.00	0.00	3A4
ATOM	2100	OG	SER	310	33.306	2.563	5.646	1.00	0.00	3A4
ATOM	2101	C	SER	310	30.666	4.763	4.322	1.00	0.00	3A4
ATOM	2102	O	SER	310	30.413	4.886	3.131	1.00	0.00	3A4
ATOM	2103	N	SER	311	29.728	4.960	5.261	1.00	0.00	3A4
ATOM	2104	CA	SER	311	28.351	5.245	4.950	1.00	0.00	3A4
ATOM	2105	CB	SER	311	27.509	5.056	6.222	1.00	0.00	3A4
ATOM	2106	OG	SER	311	27.701	3.739	6.719	1.00	0.00	3A4
ATOM	2107	C	SER	311	28.153	6.627	4.389	1.00	0.00	3A4
ATOM	2108	O	SER	311	27.316	6.833	3.523	1.00	0.00	3A4
ATOM	2109	N	VAL	312	28.984	7.609	4.813	1.00	0.00	3A4
ATOM	2110	CA	VAL	312	28.964	8.970	4.310	1.00	0.00	3A4
ATOM	2111	CB	VAL	312	29.781	9.902	5.173	1.00	0.00	3A4
ATOM	2112	CG1	VAL	312	29.980	11.315	4.570	1.00	0.00	3A4
ATOM	2113	CG2	VAL	312	28.894	10.077	6.433	1.00	0.00	3A4
ATOM	2114	C	VAL	312	29.408	9.072	2.884	1.00	0.00	3A4
ATOM	2115	O	VAL	312	28.751	9.739	2.103	1.00	0.00	3A4
ATOM	2116	N	LEU	313	30.463	8.328	2.495	1.00	0.00	3A4
ATOM	2117	CA	LEU	313	30.996	8.277	1.150	1.00	0.00	3A4

ATOM	2118	CB	LEU	313	32.294	7.466	1.085	1.00	0.00	3A4
ATOM	2119	CG	LEU	313	33.512	8.219	1.649	1.00	0.00	3A4
ATOM	2120	CD1	LEU	313	34.492	8.511	0.499	1.00	0.00	3A4
ATOM	2121	CD2	LEU	313	33.322	9.485	2.496	1.00	0.00	3A4
ATOM	2122	C	LEU	313	30.017	7.696	0.167	1.00	0.00	3A4
ATOM	2123	O	LEU	313	29.808	8.229	-0.917	1.00	0.00	3A4
ATOM	2124	N	SER	314	29.309	6.624	0.579	1.00	0.00	3A4
ATOM	2125	CA	SER	314	28.305	5.981	-0.243	1.00	0.00	3A4
ATOM	2126	CB	SER	314	27.992	4.570	0.299	1.00	0.00	3A4
ATOM	2127	OG	SER	314	29.195	3.821	0.397	1.00	0.00	3A4
ATOM	2128	C	SER	314	27.070	6.845	-0.420	1.00	0.00	3A4
ATOM	2129	O	SER	314	26.505	6.909	-1.507	1.00	0.00	3A4
ATOM	2130	N	PHE	315	26.702	7.636	0.625	1.00	0.00	3A4
ATOM	2131	CA	PHE	315	25.595	8.572	0.583	1.00	0.00	3A4
ATOM	2132	CB	PHE	315	25.181	9.076	2.015	1.00	0.00	3A4
ATOM	2133	CG	PHE	315	23.897	8.407	2.456	1.00	0.00	3A4
ATOM	2134	CD1	PHE	315	23.856	7.678	3.662	1.00	0.00	3A4
ATOM	2135	CD2	PHE	315	22.732	8.451	1.660	1.00	0.00	3A4
ATOM	2136	CE1	PHE	315	22.683	7.024	4.067	1.00	0.00	3A4
ATOM	2137	CE2	PHE	315	21.568	7.770	2.047	1.00	0.00	3A4
ATOM	2138	CZ	PHE	315	21.542	7.061	3.254	1.00	0.00	3A4
ATOM	2139	C	PHE	315	25.938	9.760	-0.291	1.00	0.00	3A4
ATOM	2140	O	PHE	315	25.075	10.250	-1.011	1.00	0.00	3A4
ATOM	2141	N	ILE	316	27.230	10.200	-0.328	1.00	0.00	3A4
ATOM	2142	CA	ILE	316	27.669	11.286	-1.202	1.00	0.00	3A4
ATOM	2143	CB	ILE	316	29.119	11.864	-1.060	1.00	0.00	3A4
ATOM	2144	CG2	ILE	316	29.128	13.291	-1.688	1.00	0.00	3A4
ATOM	2145	CG1	ILE	316	29.687	11.833	0.371	1.00	0.00	3A4
ATOM	2146	CD	ILE	316	30.950	12.629	0.687	1.00	0.00	3A4
ATOM	2147	C	ILE	316	27.559	10.926	-2.666	1.00	0.00	3A4
ATOM	2148	O	ILE	316	27.111	11.726	-3.476	1.00	0.00	3A4
ATOM	2149	N	MET	317	27.919	9.671	-3.009	1.00	0.00	3A4
ATOM	2150	CA	MET	317	27.868	9.137	-4.351	1.00	0.00	3A4
ATOM	2151	CB	MET	317	28.640	7.803	-4.441	1.00	0.00	3A4
ATOM	2152	CG	MET	317	30.148	8.007	-4.191	1.00	0.00	3A4
ATOM	2153	SD	MET	317	31.027	6.548	-3.550	1.00	0.00	3A4
ATOM	2154	CE	MET	317	32.475	7.489	-2.987	1.00	0.00	3A4
ATOM	2155	C	MET	317	26.449	8.978	-4.853	1.00	0.00	3A4
ATOM	2156	O	MET	317	26.139	9.327	-5.986	1.00	0.00	3A4
ATOM	2157	N	TYR	318	25.516	8.539	-3.981	1.00	0.00	3A4
ATOM	2158	CA	TYR	318	24.101	8.458	-4.293	1.00	0.00	3A4
ATOM	2159	CB	TYR	318	23.333	7.794	-3.134	1.00	0.00	3A4
ATOM	2160	CG	TYR	318	21.822	7.683	-3.312	1.00	0.00	3A4
ATOM	2161	CD1	TYR	318	21.269	7.039	-4.436	1.00	0.00	3A4
ATOM	2162	CD2	TYR	318	20.950	8.269	-2.372	1.00	0.00	3A4
ATOM	2163	CE1	TYR	318	19.881	6.987	-4.624	1.00	0.00	3A4
ATOM	2164	CE2	TYR	318	19.560	8.209	-2.548	1.00	0.00	3A4
ATOM	2165	CZ	TYR	318	19.024	7.566	-3.675	1.00	0.00	3A4
ATOM	2166	OH	TYR	318	17.625	7.498	-3.855	1.00	0.00	3A4
ATOM	2167	C	TYR	318	23.501	9.814	-4.592	1.00	0.00	3A4
ATOM	2168	O	TYR	318	22.759	9.967	-5.553	1.00	0.00	3A4
ATOM	2169	N	GLU	319	23.864	10.847	-3.796	1.00	0.00	3A4
ATOM	2170	CA	GLU	319	23.389	12.203	-3.970	1.00	0.00	3A4
ATOM	2171	CB	GLU	319	23.703	13.127	-2.775	1.00	0.00	3A4
ATOM	2172	CG	GLU	319	22.849	12.760	-1.559	1.00	0.00	3A4
ATOM	2173	CD	GLU	319	23.038	13.838	-0.506	1.00	0.00	3A4
ATOM	2174	OE1	GLU	319	24.202	14.049	-0.085	1.00	0.00	3A4
ATOM	2175	OE2	GLU	319	22.027	14.476	-0.119	1.00	0.00	3A4
ATOM	2176	C	GLU	319	23.894	12.847	-5.231	1.00	0.00	3A4
ATOM	2177	O	GLU	319	23.132	13.474	-5.951	1.00	0.00	3A4
ATOM	2178	N	LEU	320	25.170	12.641	-5.595	1.00	0.00	3A4
ATOM	2179	CA	LEU	320	25.713	13.161	-6.828	1.00	0.00	3A4
ATOM	2180	CB	LEU	320	27.239	13.059	-6.841	1.00	0.00	3A4
ATOM	2181	CG	LEU	320	27.880	14.027	-5.843	1.00	0.00	3A4
ATOM	2182	CD1	LEU	320	29.380	13.757	-5.709	1.00	0.00	3A4
ATOM	2183	CD2	LEU	320	27.611	15.489	-6.192	1.00	0.00	3A4
ATOM	2184	C	LEU	320	25.160	12.475	-8.048	1.00	0.00	3A4
ATOM	2185	O	LEU	320	24.977	13.105	-9.083	1.00	0.00	3A4
ATOM	2186	N	ALA	321	24.818	11.177	-7.933	1.00	0.00	3A4
ATOM	2187	CA	ALA	321	24.215	10.397	-8.990	1.00	0.00	3A4
ATOM	2188	CB	ALA	321	24.217	8.897	-8.645	1.00	0.00	3A4
ATOM	2189	C	ALA	321	22.802	10.861	-9.259	1.00	0.00	3A4

ATOM	2190	O	ALA	321	22.338	10.884	-10.397	1.00	0.00	3A4
ATOM	2191	N	THR	322	22.103	11.305	-8.194	1.00	0.00	3A4
ATOM	2192	CA	THR	322	20.743	11.780	-8.258	1.00	0.00	3A4
ATOM	2193	CB	THR	322	19.981	11.519	-6.972	1.00	0.00	3A4
ATOM	2194	OG1	THR	322	20.610	11.999	-5.794	1.00	0.00	3A4
ATOM	2195	CG2	THR	322	19.745	9.994	-6.849	1.00	0.00	3A4
ATOM	2196	C	THR	322	20.627	13.242	-8.642	1.00	0.00	3A4
ATOM	2197	O	THR	322	19.555	13.704	-9.018	1.00	0.00	3A4
ATOM	2198	N	HIS	323	21.731	14.006	-8.558	1.00	0.00	3A4
ATOM	2199	CA	HIS	323	21.740	15.416	-8.856	1.00	0.00	3A4
ATOM	2200	ND1	HIS	323	20.544	15.212	-5.650	1.00	0.00	3A4
ATOM	2201	CG	HIS	323	20.676	16.147	-6.653	1.00	0.00	3A4
ATOM	2202	CB	HIS	323	21.859	16.259	-7.581	1.00	0.00	3A4
ATOM	2203	NE2	HIS	323	18.715	16.470	-5.582	1.00	0.00	3A4
ATOM	2204	CD2	HIS	323	19.549	16.908	-6.595	1.00	0.00	3A4
ATOM	2205	CE1	HIS	323	19.356	15.449	-5.043	1.00	0.00	3A4
ATOM	2206	C	HIS	323	22.892	15.711	-9.775	1.00	0.00	3A4
ATOM	2207	O	HIS	323	23.883	16.309	-9.352	1.00	0.00	3A4
ATOM	2208	N	PRO	324	22.833	15.378	-11.076	1.00	0.00	3A4
ATOM	2209	CA	PRO	324	23.958	15.508	-12.002	1.00	0.00	3A4
ATOM	2210	CD	PRO	324	21.602	14.983	-11.765	1.00	0.00	3A4
ATOM	2211	CB	PRO	324	23.420	14.910	-13.300	1.00	0.00	3A4
ATOM	2212	CG	PRO	324	21.905	15.129	-13.255	1.00	0.00	3A4
ATOM	2213	C	PRO	324	24.415	16.938	-12.213	1.00	0.00	3A4
ATOM	2214	O	PRO	324	25.575	17.158	-12.534	1.00	0.00	3A4
ATOM	2215	N	ASP	325	23.561	17.950	-11.949	1.00	0.00	3A4
ATOM	2216	CA	ASP	325	23.917	19.351	-12.002	1.00	0.00	3A4
ATOM	2217	CB	ASP	325	22.668	20.245	-11.821	1.00	0.00	3A4
ATOM	2218	CG	ASP	325	21.653	19.933	-12.931	1.00	0.00	3A4
ATOM	2219	OD1	ASP	325	21.991	20.159	-14.125	1.00	0.00	3A4
ATOM	2220	OD2	ASP	325	20.531	19.463	-12.600	1.00	0.00	3A4
ATOM	2221	C	ASP	325	24.927	19.731	-10.944	1.00	0.00	3A4
ATOM	2222	O	ASP	325	25.817	20.547	-11.169	1.00	0.00	3A4
ATOM	2223	N	VAL	326	24.835	19.071	-9.767	1.00	0.00	3A4
ATOM	2224	CA	VAL	326	25.742	19.249	-8.647	1.00	0.00	3A4
ATOM	2225	CB	VAL	326	25.198	18.672	-7.341	1.00	0.00	3A4
ATOM	2226	CG1	VAL	326	26.201	18.872	-6.173	1.00	0.00	3A4
ATOM	2227	CG2	VAL	326	23.874	19.402	-7.034	1.00	0.00	3A4
ATOM	2228	C	VAL	326	27.083	18.648	-8.960	1.00	0.00	3A4
ATOM	2229	O	VAL	326	28.106	19.288	-8.782	1.00	0.00	3A4
ATOM	2230	N	GLN	327	27.089	17.427	-9.528	1.00	0.00	3A4
ATOM	2231	CA	GLN	327	28.281	16.718	-9.931	1.00	0.00	3A4
ATOM	2232	CB	GLN	327	27.899	15.340	-10.487	1.00	0.00	3A4
ATOM	2233	CG	GLN	327	29.062	14.350	-10.683	1.00	0.00	3A4
ATOM	2234	CD	GLN	327	28.538	12.991	-11.166	1.00	0.00	3A4
ATOM	2235	OE1	GLN	327	27.336	12.728	-11.186	1.00	0.00	3A4
ATOM	2236	NE2	GLN	327	29.475	12.091	-11.572	1.00	0.00	3A4
ATOM	2237	C	GLN	327	29.088	17.459	-10.960	1.00	0.00	3A4
ATOM	2238	O	GLN	327	30.301	17.551	-10.855	1.00	0.00	3A4
ATOM	2239	N	GLN	328	28.408	18.092	-11.941	1.00	0.00	3A4
ATOM	2240	CA	GLN	328	29.023	18.879	-12.995	1.00	0.00	3A4
ATOM	2241	CB	GLN	328	27.977	19.321	-14.041	1.00	0.00	3A4
ATOM	2242	CG	GLN	328	27.544	18.163	-14.957	1.00	0.00	3A4
ATOM	2243	CD	GLN	328	26.423	18.643	-15.885	1.00	0.00	3A4
ATOM	2244	OE1	GLN	328	26.675	19.426	-16.800	1.00	0.00	3A4
ATOM	2245	NE2	GLN	328	25.164	18.178	-15.654	1.00	0.00	3A4
ATOM	2246	C	GLN	328	29.711	20.106	-12.470	1.00	0.00	3A4
ATOM	2247	O	GLN	328	30.827	20.429	-12.855	1.00	0.00	3A4
ATOM	2248	N	LYS	329	29.068	20.782	-11.501	1.00	0.00	3A4
ATOM	2249	CA	LYS	329	29.597	21.931	-10.807	1.00	0.00	3A4
ATOM	2250	CB	LYS	329	28.515	22.465	-9.850	1.00	0.00	3A4
ATOM	2251	CG	LYS	329	28.752	23.857	-9.250	1.00	0.00	3A4
ATOM	2252	CD	LYS	329	27.533	24.347	-8.460	1.00	0.00	3A4
ATOM	2253	CE	LYS	329	27.679	25.785	-7.953	1.00	0.00	3A4
ATOM	2254	NZ	LYS	329	26.477	26.210	-7.202	1.00	0.00	3A4
ATOM	2255	C	LYS	329	30.884	21.621	-10.052	1.00	0.00	3A4
ATOM	2256	O	LYS	329	31.860	22.366	-10.101	1.00	0.00	3A4
ATOM	2257	N	LEU	330	30.952	20.423	-9.426	1.00	0.00	3A4
ATOM	2258	CA	LEU	330	32.100	19.968	-8.670	1.00	0.00	3A4
ATOM	2259	CB	LEU	330	31.814	18.742	-7.797	1.00	0.00	3A4
ATOM	2260	CG	LEU	330	30.502	18.756	-7.038	1.00	0.00	3A4
ATOM	2261	CD1	LEU	330	30.541	17.732	-5.920	1.00	0.00	3A4

ATOM	2262	CD2	LEU	330	29.986	20.145	-6.584	1.00	0.00	3A4
ATOM	2263	C	LEU	330	33.250	19.598	-9.579	1.00	0.00	3A4
ATOM	2264	O	LEU	330	34.410	19.864	-9.296	1.00	0.00	3A4
ATOM	2265	N	GLN	331	32.931	18.993	-10.741	1.00	0.00	3A4
ATOM	2266	CA	GLN	331	33.881	18.627	-11.762	1.00	0.00	3A4
ATOM	2267	CB	GLN	331	33.229	17.787	-12.880	1.00	0.00	3A4
ATOM	2268	CG	GLN	331	32.942	16.354	-12.389	1.00	0.00	3A4
ATOM	2269	CD	GLN	331	32.147	15.568	-13.437	1.00	0.00	3A4
ATOM	2270	OE1	GLN	331	31.063	15.988	-13.839	1.00	0.00	3A4
ATOM	2271	NE2	GLN	331	32.677	14.396	-13.885	1.00	0.00	3A4
ATOM	2272	C	GLN	331	34.500	19.817	-12.447	1.00	0.00	3A4
ATOM	2273	O	GLN	331	35.682	19.821	-12.771	1.00	0.00	3A4
ATOM	2274	N	GLU	332	33.723	20.913	-12.594	1.00	0.00	3A4
ATOM	2275	CA	GLU	332	34.188	22.185	-13.099	1.00	0.00	3A4
ATOM	2276	CB	GLU	332	33.019	23.173	-13.413	1.00	0.00	3A4
ATOM	2277	CG	GLU	332	32.212	22.808	-14.675	1.00	0.00	3A4
ATOM	2278	CD	GLU	332	33.080	22.951	-15.931	1.00	0.00	3A4
ATOM	2279	OE1	GLU	332	33.533	24.092	-16.217	1.00	0.00	3A4
ATOM	2280	OE2	GLU	332	33.301	21.919	-16.622	1.00	0.00	3A4
ATOM	2281	C	GLU	332	35.190	22.869	-12.182	1.00	0.00	3A4
ATOM	2282	O	GLU	332	35.834	23.799	-12.629	1.00	0.00	3A4
ATOM	2283	N	GLU	333	35.484	22.350	-10.947	1.00	0.00	3A4
ATOM	2284	CA	GLU	333	36.662	22.661	-10.132	1.00	0.00	3A4
ATOM	2285	CB	GLU	333	36.449	22.284	-8.639	1.00	0.00	3A4
ATOM	2286	CG	GLU	333	35.228	22.936	-7.985	1.00	0.00	3A4
ATOM	2287	CD	GLU	333	35.046	22.273	-6.620	1.00	0.00	3A4
ATOM	2288	OE1	GLU	333	35.918	22.455	-5.730	1.00	0.00	3A4
ATOM	2289	OE2	GLU	333	34.038	21.540	-6.462	1.00	0.00	3A4
ATOM	2290	C	GLU	333	37.923	21.912	-10.581	1.00	0.00	3A4
ATOM	2291	O	GLU	333	38.425	21.038	-9.874	1.00	0.00	3A4
ATOM	2292	N	ILE	334	38.469	22.262	-11.773	1.00	0.00	3A4
ATOM	2293	CA	ILE	334	39.710	21.726	-12.300	1.00	0.00	3A4
ATOM	2294	CB	ILE	334	39.559	20.353	-12.973	1.00	0.00	3A4
ATOM	2295	CG2	ILE	334	38.582	20.368	-14.182	1.00	0.00	3A4
ATOM	2296	CG1	ILE	334	40.932	19.687	-13.257	1.00	0.00	3A4
ATOM	2297	CD	ILE	334	40.838	18.213	-13.660	1.00	0.00	3A4
ATOM	2298	C	ILE	334	40.231	22.836	-13.189	1.00	0.00	3A4
ATOM	2299	O	ILE	334	40.570	22.658	-14.358	1.00	0.00	3A4
ATOM	2300	N	ASP	335	40.294	24.063	-12.600	1.00	0.00	3A4
ATOM	2301	CA	ASP	335	40.593	25.320	-13.260	1.00	0.00	3A4
ATOM	2302	CB	ASP	335	39.726	26.490	-12.699	1.00	0.00	3A4
ATOM	2303	CG	ASP	335	38.240	26.203	-12.943	1.00	0.00	3A4
ATOM	2304	OD1	ASP	335	37.854	26.015	-14.129	1.00	0.00	3A4
ATOM	2305	OD2	ASP	335	37.469	26.175	-11.947	1.00	0.00	3A4
ATOM	2306	C	ASP	335	42.054	25.655	-13.079	1.00	0.00	3A4
ATOM	2307	O	ASP	335	42.537	25.781	-11.956	1.00	0.00	3A4
ATOM	2308	N	ALA	336	42.772	25.816	-14.223	1.00	0.00	3A4
ATOM	2309	CA	ALA	336	44.168	26.192	-14.316	1.00	0.00	3A4
ATOM	2310	CB	ALA	336	45.027	25.116	-15.028	1.00	0.00	3A4
ATOM	2311	C	ALA	336	44.207	27.500	-15.065	1.00	0.00	3A4
ATOM	2312	O	ALA	336	44.428	27.544	-16.275	1.00	0.00	3A4
ATOM	2313	N	VAL	337	43.963	28.609	-14.313	1.00	0.00	3A4
ATOM	2314	CA	VAL	337	43.815	29.978	-14.773	1.00	0.00	3A4
ATOM	2315	CB	VAL	337	42.641	30.686	-14.085	1.00	0.00	3A4
ATOM	2316	CG1	VAL	337	42.436	32.130	-14.612	1.00	0.00	3A4
ATOM	2317	CG2	VAL	337	41.367	29.847	-14.326	1.00	0.00	3A4
ATOM	2318	C	VAL	337	45.115	30.696	-14.492	1.00	0.00	3A4
ATOM	2319	O	VAL	337	45.661	30.605	-13.394	1.00	0.00	3A4
ATOM	2320	N	LEU	338	45.621	31.439	-15.517	1.00	0.00	3A4
ATOM	2321	CA	LEU	338	46.821	32.257	-15.500	1.00	0.00	3A4
ATOM	2322	CB	LEU	338	47.678	32.088	-16.799	1.00	0.00	3A4
ATOM	2323	CG	LEU	338	48.507	30.778	-16.897	1.00	0.00	3A4
ATOM	2324	CD1	LEU	338	47.680	29.494	-17.124	1.00	0.00	3A4
ATOM	2325	CD2	LEU	338	49.592	30.909	-17.984	1.00	0.00	3A4
ATOM	2326	C	LEU	338	46.355	33.705	-15.361	1.00	0.00	3A4
ATOM	2327	O	LEU	338	45.265	34.009	-15.844	1.00	0.00	3A4
ATOM	2328	N	PRO	339	47.103	34.638	-14.719	1.00	0.00	3A4
ATOM	2329	CA	PRO	339	46.612	35.949	-14.286	1.00	0.00	3A4
ATOM	2330	CD	PRO	339	48.443	34.363	-14.196	1.00	0.00	3A4
ATOM	2331	CB	PRO	339	47.610	36.376	-13.189	1.00	0.00	3A4
ATOM	2332	CG	PRO	339	48.922	35.669	-13.552	1.00	0.00	3A4
ATOM	2333	C	PRO	339	46.561	36.955	-15.437	1.00	0.00	3A4

ATOM	2334	O	PRO	339	47.465	36.980	-16.272	1.00	0.00	3A4
ATOM	2335	N	ASN	340	45.491	37.790	-15.465	1.00	0.00	3A4
ATOM	2336	CA	ASN	340	45.246	38.810	-16.464	1.00	0.00	3A4
ATOM	2337	CB	ASN	340	44.189	38.343	-17.523	1.00	0.00	3A4
ATOM	2338	CG	ASN	340	44.036	39.320	-18.704	1.00	0.00	3A4
ATOM	2339	OD1	ASN	340	42.986	39.942	-18.858	1.00	0.00	3A4
ATOM	2340	ND2	ASN	340	45.094	39.457	-19.550	1.00	0.00	3A4
ATOM	2341	C	ASN	340	44.785	40.012	-15.672	1.00	0.00	3A4
ATOM	2342	O	ASN	340	45.452	41.045	-15.645	1.00	0.00	3A4
ATOM	2343	N	LYS	341	43.617	39.870	-14.997	1.00	0.00	3A4
ATOM	2344	CA	LYS	341	43.059	40.852	-14.095	1.00	0.00	3A4
ATOM	2345	CB	LYS	341	42.250	41.970	-14.822	1.00	0.00	3A4
ATOM	2346	CG	LYS	341	41.892	43.181	-13.936	1.00	0.00	3A4
ATOM	2347	CD	LYS	341	41.220	44.359	-14.664	1.00	0.00	3A4
ATOM	2348	CE	LYS	341	39.708	44.212	-14.924	1.00	0.00	3A4
ATOM	2349	NZ	LYS	341	39.409	43.231	-15.994	1.00	0.00	3A4
ATOM	2350	C	LYS	341	42.197	40.042	-13.158	1.00	0.00	3A4
ATOM	2351	O	LYS	341	40.991	40.258	-13.036	1.00	0.00	3A4
ATOM	2352	N	ALA	342	42.834	39.053	-12.482	1.00	0.00	3A4
ATOM	2353	CA	ALA	342	42.189	38.131	-11.577	1.00	0.00	3A4
ATOM	2354	CB	ALA	342	41.316	37.064	-12.306	1.00	0.00	3A4
ATOM	2355	C	ALA	342	43.313	37.430	-10.839	1.00	0.00	3A4
ATOM	2356	O	ALA	342	44.413	37.344	-11.386	1.00	0.00	3A4
ATOM	2357	N	PRO	343	43.106	36.880	-9.614	1.00	0.00	3A4
ATOM	2358	CA	PRO	343	44.072	36.050	-8.891	1.00	0.00	3A4
ATOM	2359	CD	PRO	343	41.953	37.220	-8.779	1.00	0.00	3A4
ATOM	2360	CB	PRO	343	43.605	36.121	-7.421	1.00	0.00	3A4
ATOM	2361	CG	PRO	343	42.097	36.392	-7.496	1.00	0.00	3A4
ATOM	2362	C	PRO	343	44.071	34.607	-9.441	1.00	0.00	3A4
ATOM	2363	O	PRO	343	42.970	34.083	-9.619	1.00	0.00	3A4
ATOM	2364	N	PRO	344	45.209	33.930	-9.727	1.00	0.00	3A4
ATOM	2365	CA	PRO	344	45.259	32.659	-10.448	1.00	0.00	3A4
ATOM	2366	CD	PRO	344	46.542	34.509	-9.559	1.00	0.00	3A4
ATOM	2367	CB	PRO	344	46.678	32.636	-11.047	1.00	0.00	3A4
ATOM	2368	CG	PRO	344	47.532	33.459	-10.077	1.00	0.00	3A4
ATOM	2369	C	PRO	344	45.002	31.473	-9.520	1.00	0.00	3A4
ATOM	2370	O	PRO	344	45.522	31.443	-8.404	1.00	0.00	3A4
ATOM	2371	N	THR	345	44.206	30.483	-10.004	1.00	0.00	3A4
ATOM	2372	CA	THR	345	43.860	29.247	-9.324	1.00	0.00	3A4
ATOM	2373	CB	THR	345	42.343	29.124	-9.107	1.00	0.00	3A4
ATOM	2374	OG1	THR	345	41.981	27.994	-8.315	1.00	0.00	3A4
ATOM	2375	CG2	THR	345	41.532	29.140	-10.430	1.00	0.00	3A4
ATOM	2376	C	THR	345	44.457	28.142	-10.173	1.00	0.00	3A4
ATOM	2377	O	THR	345	44.489	28.242	-11.397	1.00	0.00	3A4
ATOM	2378	N	TYR	346	44.964	27.063	-9.521	1.00	0.00	3A4
ATOM	2379	CA	TYR	346	45.601	25.934	-10.173	1.00	0.00	3A4
ATOM	2380	CB	TYR	346	47.162	25.970	-10.121	1.00	0.00	3A4
ATOM	2381	CG	TYR	346	47.679	27.135	-10.925	1.00	0.00	3A4
ATOM	2382	CD1	TYR	346	48.250	28.252	-10.287	1.00	0.00	3A4
ATOM	2383	CD2	TYR	346	47.581	27.136	-12.331	1.00	0.00	3A4
ATOM	2384	CE1	TYR	346	48.713	29.345	-11.032	1.00	0.00	3A4
ATOM	2385	CE2	TYR	346	48.037	28.229	-13.082	1.00	0.00	3A4
ATOM	2386	CZ	TYR	346	48.606	29.335	-12.431	1.00	0.00	3A4
ATOM	2387	OH	TYR	346	49.065	30.442	-13.178	1.00	0.00	3A4
ATOM	2388	C	TYR	346	45.106	24.709	-9.453	1.00	0.00	3A4
ATOM	2389	O	TYR	346	45.423	24.491	-8.285	1.00	0.00	3A4
ATOM	2390	N	ASP	347	44.302	23.879	-10.168	1.00	0.00	3A4
ATOM	2391	CA	ASP	347	43.715	22.647	-9.683	1.00	0.00	3A4
ATOM	2392	CB	ASP	347	42.187	22.761	-9.384	1.00	0.00	3A4
ATOM	2393	CG	ASP	347	41.948	23.760	-8.248	1.00	0.00	3A4
ATOM	2394	OD1	ASP	347	41.329	24.825	-8.516	1.00	0.00	3A4
ATOM	2395	OD2	ASP	347	42.386	23.474	-7.102	1.00	0.00	3A4
ATOM	2396	C	ASP	347	43.937	21.639	-10.781	1.00	0.00	3A4
ATOM	2397	O	ASP	347	43.549	21.862	-11.927	1.00	0.00	3A4
ATOM	2398	N	THR	348	44.581	20.493	-10.427	1.00	0.00	3A4
ATOM	2399	CA	THR	348	44.908	19.388	-11.314	1.00	0.00	3A4
ATOM	2400	CB	THR	348	46.416	19.199	-11.501	1.00	0.00	3A4
ATOM	2401	OG1	THR	348	46.987	20.401	-12.006	1.00	0.00	3A4
ATOM	2402	CG2	THR	348	46.725	18.051	-12.500	1.00	0.00	3A4
ATOM	2403	C	THR	348	44.258	18.178	-10.688	1.00	0.00	3A4
ATOM	2404	O	THR	348	43.393	17.548	-11.293	1.00	0.00	3A4
ATOM	2405	N	VAL	349	44.670	17.854	-9.434	1.00	0.00	3A4

ATOM	2406	CA	VAL	349	44.059	16.848	-8.590	1.00	0.00	3A4
ATOM	2407	CB	VAL	349	44.630	15.437	-8.788	1.00	0.00	3A4
ATOM	2408	CG1	VAL	349	46.169	15.347	-8.617	1.00	0.00	3A4
ATOM	2409	CG2	VAL	349	43.834	14.402	-7.958	1.00	0.00	3A4
ATOM	2410	C	VAL	349	44.175	17.435	-7.201	1.00	0.00	3A4
ATOM	2411	O	VAL	349	44.934	16.990	-6.341	1.00	0.00	3A4
ATOM	2412	N	LEU	350	43.387	18.518	-6.988	1.00	0.00	3A4
ATOM	2413	CA	LEU	350	43.440	19.369	-5.824	1.00	0.00	3A4
ATOM	2414	CB	LEU	350	44.479	20.520	-6.024	1.00	0.00	3A4
ATOM	2415	CG	LEU	350	44.847	21.374	-4.785	1.00	0.00	3A4
ATOM	2416	CD1	LEU	350	45.497	20.539	-3.662	1.00	0.00	3A4
ATOM	2417	CD2	LEU	350	45.743	22.560	-5.187	1.00	0.00	3A4
ATOM	2418	C	LEU	350	42.042	19.913	-5.672	1.00	0.00	3A4
ATOM	2419	O	LEU	350	41.270	19.945	-6.631	1.00	0.00	3A4
ATOM	2420	N	GLN	351	41.689	20.372	-4.436	1.00	0.00	3A4
ATOM	2421	CA	GLN	351	40.404	20.942	-4.059	1.00	0.00	3A4
ATOM	2422	CB	GLN	351	40.005	20.645	-2.573	1.00	0.00	3A4
ATOM	2423	CG	GLN	351	40.814	21.289	-1.417	1.00	0.00	3A4
ATOM	2424	CD	GLN	351	42.269	20.816	-1.386	1.00	0.00	3A4
ATOM	2425	OE1	GLN	351	43.177	21.634	-1.520	1.00	0.00	3A4
ATOM	2426	NE2	GLN	351	42.505	19.487	-1.200	1.00	0.00	3A4
ATOM	2427	C	GLN	351	40.390	22.432	-4.305	1.00	0.00	3A4
ATOM	2428	O	GLN	351	41.399	23.112	-4.117	1.00	0.00	3A4
ATOM	2429	N	MET	352	39.214	22.962	-4.740	1.00	0.00	3A4
ATOM	2430	CA	MET	352	38.994	24.368	-5.014	1.00	0.00	3A4
ATOM	2431	CB	MET	352	38.436	24.632	-6.438	1.00	0.00	3A4
ATOM	2432	CG	MET	352	38.472	26.097	-6.900	1.00	0.00	3A4
ATOM	2433	SD	MET	352	37.969	26.316	-8.633	1.00	0.00	3A4
ATOM	2434	CE	MET	352	38.075	28.129	-8.608	1.00	0.00	3A4
ATOM	2435	C	MET	352	38.113	24.911	-3.914	1.00	0.00	3A4
ATOM	2436	O	MET	352	38.636	25.287	-2.866	1.00	0.00	3A4
ATOM	2437	N	GLU	353	36.765	25.000	-4.117	1.00	0.00	3A4
ATOM	2438	CA	GLU	353	35.914	25.749	-3.211	1.00	0.00	3A4
ATOM	2439	CB	GLU	353	35.689	27.217	-3.688	1.00	0.00	3A4
ATOM	2440	CG	GLU	353	36.922	28.142	-3.627	1.00	0.00	3A4
ATOM	2441	CD	GLU	353	36.543	29.540	-4.126	1.00	0.00	3A4
ATOM	2442	OE1	GLU	353	36.622	30.504	-3.318	1.00	0.00	3A4
ATOM	2443	OE2	GLU	353	36.171	29.660	-5.325	1.00	0.00	3A4
ATOM	2444	C	GLU	353	34.592	25.102	-2.984	1.00	0.00	3A4
ATOM	2445	O	GLU	353	34.078	25.104	-1.864	1.00	0.00	3A4
ATOM	2446	N	TYR	354	33.979	24.537	-4.047	1.00	0.00	3A4
ATOM	2447	CA	TYR	354	32.629	24.016	-3.996	1.00	0.00	3A4
ATOM	2448	CB	TYR	354	31.928	24.005	-5.369	1.00	0.00	3A4
ATOM	2449	CG	TYR	354	31.880	25.395	-5.954	1.00	0.00	3A4
ATOM	2450	CD1	TYR	354	32.962	25.916	-6.691	1.00	0.00	3A4
ATOM	2451	CD2	TYR	354	30.740	26.199	-5.783	1.00	0.00	3A4
ATOM	2452	CE1	TYR	354	32.917	27.212	-7.224	1.00	0.00	3A4
ATOM	2453	CE2	TYR	354	30.683	27.496	-6.314	1.00	0.00	3A4
ATOM	2454	CZ	TYR	354	31.774	28.004	-7.035	1.00	0.00	3A4
ATOM	2455	OH	TYR	354	31.722	29.310	-7.571	1.00	0.00	3A4
ATOM	2456	C	TYR	354	32.592	22.628	-3.428	1.00	0.00	3A4
ATOM	2457	O	TYR	354	31.575	22.220	-2.892	1.00	0.00	3A4
ATOM	2458	N	LEU	355	33.710	21.867	-3.466	1.00	0.00	3A4
ATOM	2459	CA	LEU	355	33.715	20.493	-2.996	1.00	0.00	3A4
ATOM	2460	CB	LEU	355	34.970	19.771	-3.512	1.00	0.00	3A4
ATOM	2461	CG	LEU	355	34.521	18.784	-4.631	1.00	0.00	3A4
ATOM	2462	CD1	LEU	355	35.547	18.525	-5.749	1.00	0.00	3A4
ATOM	2463	CD2	LEU	355	33.945	17.479	-4.064	1.00	0.00	3A4
ATOM	2464	C	LEU	355	33.573	20.380	-1.485	1.00	0.00	3A4
ATOM	2465	O	LEU	355	32.806	19.570	-0.980	1.00	0.00	3A4
ATOM	2466	N	ASP	356	34.225	21.283	-0.721	1.00	0.00	3A4
ATOM	2467	CA	ASP	356	34.070	21.466	0.714	1.00	0.00	3A4
ATOM	2468	CB	ASP	356	34.921	22.723	1.144	1.00	0.00	3A4
ATOM	2469	CG	ASP	356	35.819	22.461	2.358	1.00	0.00	3A4
ATOM	2470	OD1	ASP	356	35.262	22.182	3.454	1.00	0.00	3A4
ATOM	2471	OD2	ASP	356	37.067	22.560	2.214	1.00	0.00	3A4
ATOM	2472	C	ASP	356	32.651	21.700	1.182	1.00	0.00	3A4
ATOM	2473	O	ASP	356	32.180	21.110	2.149	1.00	0.00	3A4
ATOM	2474	N	MET	357	31.928	22.551	0.423	1.00	0.00	3A4
ATOM	2475	CA	MET	357	30.540	22.879	0.616	1.00	0.00	3A4
ATOM	2476	CB	MET	357	30.168	24.100	-0.239	1.00	0.00	3A4
ATOM	2477	CG	MET	357	29.601	25.250	0.627	1.00	0.00	3A4

ATOM	2478	SD	MET	357	30.612	26.763	0.665	1.00	0.00	3A4
ATOM	2479	CE	MET	357	29.381	27.754	1.562	1.00	0.00	3A4
ATOM	2480	C	MET	357	29.622	21.737	0.289	1.00	0.00	3A4
ATOM	2481	O	MET	357	28.618	21.519	0.952	1.00	0.00	3A4
ATOM	2482	N	VAL	358	29.995	20.909	-0.714	1.00	0.00	3A4
ATOM	2483	CA	VAL	358	29.302	19.693	-1.096	1.00	0.00	3A4
ATOM	2484	CB	VAL	358	29.848	19.071	-2.374	1.00	0.00	3A4
ATOM	2485	CG1	VAL	358	29.224	17.667	-2.681	1.00	0.00	3A4
ATOM	2486	CG2	VAL	358	29.530	20.074	-3.459	1.00	0.00	3A4
ATOM	2487	C	VAL	358	29.376	18.671	0.012	1.00	0.00	3A4
ATOM	2488	O	VAL	358	28.364	18.076	0.363	1.00	0.00	3A4
ATOM	2489	N	VAL	359	30.567	18.479	0.633	1.00	0.00	3A4
ATOM	2490	CA	VAL	359	30.783	17.579	1.758	1.00	0.00	3A4
ATOM	2491	CB	VAL	359	32.264	17.531	2.146	1.00	0.00	3A4
ATOM	2492	CG1	VAL	359	32.553	16.768	3.459	1.00	0.00	3A4
ATOM	2493	CG2	VAL	359	33.043	16.854	1.004	1.00	0.00	3A4
ATOM	2494	C	VAL	359	29.954	17.977	2.962	1.00	0.00	3A4
ATOM	2495	O	VAL	359	29.303	17.151	3.591	1.00	0.00	3A4
ATOM	2496	N	ASN	360	29.903	19.287	3.263	1.00	0.00	3A4
ATOM	2497	CA	ASN	360	29.117	19.830	4.350	1.00	0.00	3A4
ATOM	2498	CB	ASN	360	29.412	21.328	4.537	1.00	0.00	3A4
ATOM	2499	CG	ASN	360	30.795	21.548	5.189	1.00	0.00	3A4
ATOM	2500	OD1	ASN	360	31.725	20.750	5.080	1.00	0.00	3A4
ATOM	2501	ND2	ASN	360	30.946	22.706	5.890	1.00	0.00	3A4
ATOM	2502	C	ASN	360	27.624	19.645	4.147	1.00	0.00	3A4
ATOM	2503	O	ASN	360	26.891	19.274	5.060	1.00	0.00	3A4
ATOM	2504	N	GLU	361	27.149	19.820	2.890	1.00	0.00	3A4
ATOM	2505	CA	GLU	361	25.768	19.606	2.527	1.00	0.00	3A4
ATOM	2506	CB	GLU	361	25.458	20.211	1.139	1.00	0.00	3A4
ATOM	2507	CG	GLU	361	24.026	19.998	0.629	1.00	0.00	3A4
ATOM	2508	CD	GLU	361	22.935	20.638	1.489	1.00	0.00	3A4
ATOM	2509	OE1	GLU	361	23.253	21.306	2.504	1.00	0.00	3A4
ATOM	2510	OE2	GLU	361	21.740	20.442	1.143	1.00	0.00	3A4
ATOM	2511	C	GLU	361	25.372	18.147	2.553	1.00	0.00	3A4
ATOM	2512	O	GLU	361	24.258	17.809	2.941	1.00	0.00	3A4
ATOM	2513	N	THR	362	26.285	17.210	2.205	1.00	0.00	3A4
ATOM	2514	CA	THR	362	26.034	15.779	2.269	1.00	0.00	3A4
ATOM	2515	CB	THR	362	27.109	14.973	1.573	1.00	0.00	3A4
ATOM	2516	OG1	THR	362	27.154	15.360	0.208	1.00	0.00	3A4
ATOM	2517	CG2	THR	362	26.766	13.462	1.673	1.00	0.00	3A4
ATOM	2518	C	THR	362	25.886	15.303	3.702	1.00	0.00	3A4
ATOM	2519	O	THR	362	24.990	14.527	4.020	1.00	0.00	3A4
ATOM	2520	N	LEU	363	26.722	15.835	4.611	1.00	0.00	3A4
ATOM	2521	CA	LEU	363	26.677	15.555	6.026	1.00	0.00	3A4
ATOM	2522	CB	LEU	363	27.934	16.102	6.729	1.00	0.00	3A4
ATOM	2523	CG	LEU	363	29.216	15.310	6.428	1.00	0.00	3A4
ATOM	2524	CD1	LEU	363	30.434	16.188	6.740	1.00	0.00	3A4
ATOM	2525	CD2	LEU	363	29.238	13.981	7.211	1.00	0.00	3A4
ATOM	2526	C	LEU	363	25.448	16.157	6.698	1.00	0.00	3A4
ATOM	2527	O	LEU	363	24.956	15.614	7.681	1.00	0.00	3A4
ATOM	2528	N	ARG	364	24.890	17.274	6.163	1.00	0.00	3A4
ATOM	2529	CA	ARG	364	23.659	17.879	6.633	1.00	0.00	3A4
ATOM	2530	CB	ARG	364	23.446	19.303	6.082	1.00	0.00	3A4
ATOM	2531	CG	ARG	364	22.238	20.031	6.676	1.00	0.00	3A4
ATOM	2532	CD	ARG	364	22.212	21.544	6.417	1.00	0.00	3A4
ATOM	2533	NE	ARG	364	21.256	22.182	7.393	1.00	0.00	3A4
ATOM	2534	CZ	ARG	364	21.624	22.741	8.595	1.00	0.00	3A4
ATOM	2535	NH1	ARG	364	20.663	23.251	9.418	1.00	0.00	3A4
ATOM	2536	NH2	ARG	364	22.925	22.809	8.992	1.00	0.00	3A4
ATOM	2537	C	ARG	364	22.463	17.060	6.233	1.00	0.00	3A4
ATOM	2538	O	ARG	364	21.622	16.711	7.049	1.00	0.00	3A4
ATOM	2539	N	LEU	365	22.393	16.685	4.940	1.00	0.00	3A4
ATOM	2540	CA	LEU	365	21.267	15.979	4.384	1.00	0.00	3A4
ATOM	2541	CB	LEU	365	21.247	16.050	2.848	1.00	0.00	3A4
ATOM	2542	CG	LEU	365	19.879	16.592	2.326	1.00	0.00	3A4
ATOM	2543	CD1	LEU	365	19.837	16.585	0.811	1.00	0.00	3A4
ATOM	2544	CD2	LEU	365	18.607	15.874	2.828	1.00	0.00	3A4
ATOM	2545	C	LEU	365	21.135	14.540	4.810	1.00	0.00	3A4
ATOM	2546	O	LEU	365	20.029	14.082	5.089	1.00	0.00	3A4
ATOM	2547	N	PHE	366	22.252	13.787	4.904	1.00	0.00	3A4
ATOM	2548	CA	PHE	366	22.226	12.409	5.376	1.00	0.00	3A4
ATOM	2549	CB	PHE	366	22.642	11.385	4.273	1.00	0.00	3A4

ATOM	2550	CG	PHE	366	21.503	11.244	3.297	1.00	0.00	3A4
ATOM	2551	CD1	PHE	366	21.538	11.861	2.035	1.00	0.00	3A4
ATOM	2552	CD2	PHE	366	20.363	10.498	3.651	1.00	0.00	3A4
ATOM	2553	CE1	PHE	366	20.455	11.742	1.150	1.00	0.00	3A4
ATOM	2554	CE2	PHE	366	19.278	10.377	2.773	1.00	0.00	3A4
ATOM	2555	CZ	PHE	366	19.325	11.000	1.520	1.00	0.00	3A4
ATOM	2556	C	PHE	366	23.116	12.273	6.585	1.00	0.00	3A4
ATOM	2557	O	PHE	366	24.165	11.637	6.497	1.00	0.00	3A4
ATOM	2558	N	PRO	367	22.732	12.795	7.772	1.00	0.00	3A4
ATOM	2559	CA	PRO	367	23.466	12.674	9.011	1.00	0.00	3A4
ATOM	2560	CD	PRO	367	21.498	13.517	7.993	1.00	0.00	3A4
ATOM	2561	CB	PRO	367	22.894	13.739	9.935	1.00	0.00	3A4
ATOM	2562	CG	PRO	367	21.461	13.878	9.463	1.00	0.00	3A4
ATOM	2563	C	PRO	367	23.332	11.269	9.536	1.00	0.00	3A4
ATOM	2564	O	PRO	367	22.246	10.779	9.824	1.00	0.00	3A4
ATOM	2565	N	ILE	368	24.476	10.572	9.569	1.00	0.00	3A4
ATOM	2566	CA	ILE	368	24.602	9.143	9.718	1.00	0.00	3A4
ATOM	2567	CB	ILE	368	25.992	8.818	9.131	1.00	0.00	3A4
ATOM	2568	CG2	ILE	368	27.160	9.306	10.024	1.00	0.00	3A4
ATOM	2569	CG1	ILE	368	26.230	7.413	8.553	1.00	0.00	3A4
ATOM	2570	CD	ILE	368	26.421	6.268	9.546	1.00	0.00	3A4
ATOM	2571	C	ILE	368	24.406	8.654	11.153	1.00	0.00	3A4
ATOM	2572	O	ILE	368	24.024	7.515	11.392	1.00	0.00	3A4
ATOM	2573	N	ALA	369	24.661	9.530	12.146	1.00	0.00	3A4
ATOM	2574	CA	ALA	369	24.719	9.183	13.542	1.00	0.00	3A4
ATOM	2575	CB	ALA	369	26.067	9.640	14.141	1.00	0.00	3A4
ATOM	2576	C	ALA	369	23.654	9.859	14.360	1.00	0.00	3A4
ATOM	2577	O	ALA	369	23.267	10.991	14.104	1.00	0.00	3A4
ATOM	2578	N	MET	370	23.265	9.221	15.511	1.00	0.00	3A4
ATOM	2579	CA	MET	370	22.422	9.803	16.560	1.00	0.00	3A4
ATOM	2580	CB	MET	370	20.964	9.264	16.470	1.00	0.00	3A4
ATOM	2581	CG	MET	370	19.910	10.113	17.209	1.00	0.00	3A4
ATOM	2582	SD	MET	370	18.173	9.663	16.885	1.00	0.00	3A4
ATOM	2583	CE	MET	370	18.081	10.195	15.146	1.00	0.00	3A4
ATOM	2584	C	MET	370	23.062	9.512	17.921	1.00	0.00	3A4
ATOM	2585	O	MET	370	23.884	8.603	18.029	1.00	0.00	3A4
ATOM	2586	N	ARG	371	22.711	10.299	18.992	1.00	0.00	3A4
ATOM	2587	CA	ARG	371	23.356	10.277	20.307	1.00	0.00	3A4
ATOM	2588	CB	ARG	371	24.430	11.405	20.437	1.00	0.00	3A4
ATOM	2589	CG	ARG	371	23.944	12.828	20.099	1.00	0.00	3A4
ATOM	2590	CD	ARG	371	25.049	13.888	20.216	1.00	0.00	3A4
ATOM	2591	NE	ARG	371	24.503	15.208	19.738	1.00	0.00	3A4
ATOM	2592	CZ	ARG	371	25.012	16.428	20.108	1.00	0.00	3A4
ATOM	2593	NH1	ARG	371	24.468	17.561	19.575	1.00	0.00	3A4
ATOM	2594	NH2	ARG	371	26.049	16.546	20.988	1.00	0.00	3A4
ATOM	2595	C	ARG	371	22.333	10.392	21.438	1.00	0.00	3A4
ATOM	2596	O	ARG	371	21.181	10.760	21.216	1.00	0.00	3A4
ATOM	2597	N	LEU	372	22.776	10.045	22.692	1.00	0.00	3A4
ATOM	2598	CA	LEU	372	22.016	9.951	23.936	1.00	0.00	3A4
ATOM	2599	CB	LEU	372	21.964	8.482	24.512	1.00	0.00	3A4
ATOM	2600	CG	LEU	372	21.345	7.343	23.661	1.00	0.00	3A4
ATOM	2601	CD1	LEU	372	19.908	7.641	23.227	1.00	0.00	3A4
ATOM	2602	CD2	LEU	372	22.216	6.816	22.501	1.00	0.00	3A4
ATOM	2603	C	LEU	372	22.693	10.771	25.005	1.00	0.00	3A4
ATOM	2604	O	LEU	372	23.899	11.003	24.975	1.00	0.00	3A4
ATOM	2605	N	GLU	373	21.900	11.155	26.021	1.00	0.00	3A4
ATOM	2606	CA	GLU	373	22.322	11.807	27.237	1.00	0.00	3A4
ATOM	2607	CB	GLU	373	22.131	13.344	27.172	1.00	0.00	3A4
ATOM	2608	CG	GLU	373	23.197	14.057	26.329	1.00	0.00	3A4
ATOM	2609	CD	GLU	373	23.009	15.577	26.343	1.00	0.00	3A4
ATOM	2610	OE1	GLU	373	23.722	16.250	25.553	1.00	0.00	3A4
ATOM	2611	OE2	GLU	373	22.167	16.090	27.128	1.00	0.00	3A4
ATOM	2612	C	GLU	373	21.466	11.241	28.351	1.00	0.00	3A4
ATOM	2613	O	GLU	373	20.387	10.695	28.121	1.00	0.00	3A4
ATOM	2614	N	ARG	374	21.930	11.386	29.612	1.00	0.00	3A4
ATOM	2615	CA	ARG	374	21.138	11.043	30.774	1.00	0.00	3A4
ATOM	2616	CB	ARG	374	21.532	9.678	31.420	1.00	0.00	3A4
ATOM	2617	CG	ARG	374	22.371	9.595	32.715	1.00	0.00	3A4
ATOM	2618	CD	ARG	374	21.558	9.546	34.018	1.00	0.00	3A4
ATOM	2619	NE	ARG	374	22.476	9.916	35.152	1.00	0.00	3A4
ATOM	2620	CZ	ARG	374	22.249	9.595	36.465	1.00	0.00	3A4
ATOM	2621	NH1	ARG	374	23.147	10.010	37.405	1.00	0.00	3A4

ATOM	2622	NH2	ARG	374	21.156	8.879	36.860	1.00	0.00	3A4
ATOM	2623	C	ARG	374	21.272	12.200	31.721	1.00	0.00	3A4
ATOM	2624	O	ARG	374	22.360	12.720	31.947	1.00	0.00	3A4
ATOM	2625	N	VAL	375	20.152	12.629	32.340	1.00	0.00	3A4
ATOM	2626	CA	VAL	375	20.085	13.742	33.272	1.00	0.00	3A4
ATOM	2627	CB	VAL	375	18.651	14.239	33.344	1.00	0.00	3A4
ATOM	2628	CG1	VAL	375	18.283	15.175	34.420	1.00	0.00	3A4
ATOM	2629	CG2	VAL	375	18.394	14.888	31.964	1.00	0.00	3A4
ATOM	2630	C	VAL	375	20.606	13.314	34.625	1.00	0.00	3A4
ATOM	2631	O	VAL	375	20.173	12.325	35.197	1.00	0.00	3A4
ATOM	2632	N	CYS	376	21.593	14.058	35.166	1.00	0.00	3A4
ATOM	2633	CA	CYS	376	22.269	13.722	36.404	1.00	0.00	3A4
ATOM	2634	CB	CYS	376	23.708	14.284	36.408	1.00	0.00	3A4
ATOM	2635	SG	CYS	376	24.721	13.423	35.165	1.00	0.00	3A4
ATOM	2636	C	CYS	376	21.525	14.230	37.618	1.00	0.00	3A4
ATOM	2637	O	CYS	376	21.699	13.713	38.720	1.00	0.00	3A4
ATOM	2638	N	LYS	377	20.691	15.268	37.426	1.00	0.00	3A4
ATOM	2639	CA	LYS	377	19.982	15.944	38.480	1.00	0.00	3A4
ATOM	2640	CB	LYS	377	20.773	17.167	38.996	1.00	0.00	3A4
ATOM	2641	CG	LYS	377	22.008	16.876	39.867	1.00	0.00	3A4
ATOM	2642	CD	LYS	377	21.695	16.179	41.198	1.00	0.00	3A4
ATOM	2643	CE	LYS	377	22.947	15.957	42.056	1.00	0.00	3A4
ATOM	2644	NZ	LYS	377	22.604	15.293	43.336	1.00	0.00	3A4
ATOM	2645	C	LYS	377	18.735	16.448	37.827	1.00	0.00	3A4
ATOM	2646	O	LYS	377	18.689	16.603	36.617	1.00	0.00	3A4
ATOM	2647	N	LYS	378	17.690	16.839	38.593	1.00	0.00	3A4
ATOM	2648	CA	LYS	378	16.465	17.414	38.063	1.00	0.00	3A4
ATOM	2649	CB	LYS	378	15.419	17.607	39.177	1.00	0.00	3A4
ATOM	2650	CG	LYS	378	15.088	16.287	39.895	1.00	0.00	3A4
ATOM	2651	CD	LYS	378	14.017	16.418	40.984	1.00	0.00	3A4
ATOM	2652	CE	LYS	378	13.613	15.082	41.625	1.00	0.00	3A4
ATOM	2653	NZ	LYS	378	14.747	14.462	42.352	1.00	0.00	3A4
ATOM	2654	C	LYS	378	16.741	18.741	37.382	1.00	0.00	3A4
ATOM	2655	O	LYS	378	17.545	19.524	37.877	1.00	0.00	3A4
ATOM	2656	N	ASP	379	16.172	18.960	36.183	1.00	0.00	3A4
ATOM	2657	CA	ASP	379	16.483	20.125	35.394	1.00	0.00	3A4
ATOM	2658	CB	ASP	379	17.706	19.925	34.443	1.00	0.00	3A4
ATOM	2659	CG	ASP	379	17.527	19.059	33.183	1.00	0.00	3A4
ATOM	2660	OD1	ASP	379	17.455	17.817	33.330	1.00	0.00	3A4
ATOM	2661	OD2	ASP	379	17.475	19.634	32.063	1.00	0.00	3A4
ATOM	2662	C	ASP	379	15.250	20.543	34.652	1.00	0.00	3A4
ATOM	2663	O	ASP	379	14.333	19.776	34.415	1.00	0.00	3A4
ATOM	2664	N	VAL	380	15.216	21.819	34.247	1.00	0.00	3A4
ATOM	2665	CA	VAL	380	14.098	22.398	33.548	1.00	0.00	3A4
ATOM	2666	CB	VAL	380	13.450	23.491	34.376	1.00	0.00	3A4
ATOM	2667	CG1	VAL	380	12.212	24.040	33.665	1.00	0.00	3A4
ATOM	2668	CG2	VAL	380	13.057	22.943	35.763	1.00	0.00	3A4
ATOM	2669	C	VAL	380	14.659	22.869	32.227	1.00	0.00	3A4
ATOM	2670	O	VAL	380	15.521	23.743	32.201	1.00	0.00	3A4
ATOM	2671	N	GLU	381	14.219	22.259	31.107	1.00	0.00	3A4
ATOM	2672	CA	GLU	381	14.653	22.560	29.760	1.00	0.00	3A4
ATOM	2673	CB	GLU	381	15.044	21.298	28.989	1.00	0.00	3A4
ATOM	2674	CG	GLU	381	15.995	21.611	27.810	1.00	0.00	3A4
ATOM	2675	CD	GLU	381	16.331	20.375	26.965	1.00	0.00	3A4
ATOM	2676	OE1	GLU	381	17.063	20.564	25.958	1.00	0.00	3A4
ATOM	2677	OE2	GLU	381	15.873	19.246	27.284	1.00	0.00	3A4
ATOM	2678	C	GLU	381	13.495	23.231	29.052	1.00	0.00	3A4
ATOM	2679	O	GLU	381	12.355	22.802	29.042	1.00	0.00	3A4
ATOM	2680	N	ILE	382	13.715	24.405	28.468	1.00	0.00	3A4
ATOM	2681	CA	ILE	382	12.690	25.313	27.960	1.00	0.00	3A4
ATOM	2682	CB	ILE	382	11.956	24.945	26.638	1.00	0.00	3A4
ATOM	2683	CG2	ILE	382	10.525	25.549	26.472	1.00	0.00	3A4
ATOM	2684	CG1	ILE	382	12.874	25.434	25.467	1.00	0.00	3A4
ATOM	2685	CD	ILE	382	12.229	25.497	24.082	1.00	0.00	3A4
ATOM	2686	C	ILE	382	11.919	25.809	29.163	1.00	0.00	3A4
ATOM	2687	O	ILE	382	12.497	26.469	29.990	1.00	0.00	3A4
ATOM	2688	N	ASN	383	10.722	25.435	29.490	1.00	0.00	3A4
ATOM	2689	CA	ASN	383	10.349	25.838	30.866	1.00	0.00	3A4
ATOM	2690	CB	ASN	383	9.806	27.330	30.959	1.00	0.00	3A4
ATOM	2691	CG	ASN	383	9.693	27.860	32.407	1.00	0.00	3A4
ATOM	2692	OD1	ASN	383	8.596	28.169	32.869	1.00	0.00	3A4
ATOM	2693	ND2	ASN	383	10.843	27.967	33.129	1.00	0.00	3A4

ATOM	2694	C	ASN	383	9.349	24.945	31.284	1.00	0.00	3A4
ATOM	2695	O	ASN	383	8.160	25.107	30.993	1.00	0.00	3A4
ATOM	2696	N	GLY	384	9.485	23.892	32.102	1.00	0.00	3A4
ATOM	2697	CA	GLY	384	8.315	22.984	32.156	1.00	0.00	3A4
ATOM	2698	C	GLY	384	8.276	22.292	30.798	1.00	0.00	3A4
ATOM	2699	O	GLY	384	7.285	21.764	30.297	1.00	0.00	3A4
ATOM	2700	N	MET	385	9.600	22.252	30.331	1.00	0.00	3A4
ATOM	2701	CA	MET	385	9.904	20.858	30.491	1.00	0.00	3A4
ATOM	2702	CB	MET	385	10.648	20.273	29.245	1.00	0.00	3A4
ATOM	2703	CG	MET	385	10.078	18.932	28.749	1.00	0.00	3A4
ATOM	2704	SD	MET	385	10.271	17.522	29.885	1.00	0.00	3A4
ATOM	2705	CE	MET	385	8.674	16.747	29.504	1.00	0.00	3A4
ATOM	2706	C	MET	385	10.673	20.574	31.772	1.00	0.00	3A4
ATOM	2707	O	MET	385	11.823	20.957	31.867	1.00	0.00	3A4
ATOM	2708	N	PHE	386	10.077	19.903	32.767	1.00	0.00	3A4
ATOM	2709	CA	PHE	386	10.786	19.416	33.933	1.00	0.00	3A4
ATOM	2710	CB	PHE	386	9.854	19.471	35.160	1.00	0.00	3A4
ATOM	2711	CG	PHE	386	10.561	19.327	36.492	1.00	0.00	3A4
ATOM	2712	CD1	PHE	386	10.905	20.467	37.242	1.00	0.00	3A4
ATOM	2713	CD2	PHE	386	10.861	18.057	37.026	1.00	0.00	3A4
ATOM	2714	CE1	PHE	386	11.556	20.349	38.477	1.00	0.00	3A4
ATOM	2715	CE2	PHE	386	11.512	17.931	38.260	1.00	0.00	3A4
ATOM	2716	CZ	PHE	386	11.859	19.080	38.985	1.00	0.00	3A4
ATOM	2717	C	PHE	386	11.245	17.997	33.650	1.00	0.00	3A4
ATOM	2718	O	PHE	386	10.434	17.097	33.442	1.00	0.00	3A4
ATOM	2719	N	ILE	387	12.579	17.797	33.622	1.00	0.00	3A4
ATOM	2720	CA	ILE	387	13.234	16.542	33.348	1.00	0.00	3A4
ATOM	2721	CB	ILE	387	14.381	16.682	32.335	1.00	0.00	3A4
ATOM	2722	CG2	ILE	387	14.760	15.256	31.874	1.00	0.00	3A4
ATOM	2723	CG1	ILE	387	13.940	17.566	31.142	1.00	0.00	3A4
ATOM	2724	CD	ILE	387	14.996	17.732	30.052	1.00	0.00	3A4
ATOM	2725	C	ILE	387	13.712	16.037	34.699	1.00	0.00	3A4
ATOM	2726	O	ILE	387	14.542	16.701	35.311	1.00	0.00	3A4
ATOM	2727	N	PRO	388	13.230	14.898	35.231	1.00	0.00	3A4
ATOM	2728	CA	PRO	388	13.741	14.297	36.449	1.00	0.00	3A4
ATOM	2729	CD	PRO	388	11.827	14.522	35.038	1.00	0.00	3A4
ATOM	2730	CB	PRO	388	12.685	13.264	36.864	1.00	0.00	3A4
ATOM	2731	CG	PRO	388	11.381	13.833	36.327	1.00	0.00	3A4
ATOM	2732	C	PRO	388	15.090	13.656	36.297	1.00	0.00	3A4
ATOM	2733	O	PRO	388	15.481	13.246	35.212	1.00	0.00	3A4
ATOM	2734	N	LYS	389	15.825	13.516	37.416	1.00	0.00	3A4
ATOM	2735	CA	LYS	389	17.102	12.839	37.479	1.00	0.00	3A4
ATOM	2736	CB	LYS	389	17.661	12.891	38.918	1.00	0.00	3A4
ATOM	2737	CG	LYS	389	16.754	12.453	40.092	1.00	0.00	3A4
ATOM	2738	CD	LYS	389	16.878	10.984	40.532	1.00	0.00	3A4
ATOM	2739	CE	LYS	389	16.079	10.653	41.802	1.00	0.00	3A4
ATOM	2740	NZ	LYS	389	14.624	10.849	41.589	1.00	0.00	3A4
ATOM	2741	C	LYS	389	16.984	11.412	37.009	1.00	0.00	3A4
ATOM	2742	O	LYS	389	15.997	10.745	37.301	1.00	0.00	3A4
ATOM	2743	N	GLY	390	17.932	10.973	36.172	1.00	0.00	3A4
ATOM	2744	CA	GLY	390	17.963	9.654	35.593	1.00	0.00	3A4
ATOM	2745	C	GLY	390	17.174	9.470	34.332	1.00	0.00	3A4
ATOM	2746	O	GLY	390	17.046	8.351	33.839	1.00	0.00	3A4
ATOM	2747	N	TRP	391	16.619	10.571	33.769	1.00	0.00	3A4
ATOM	2748	CA	TRP	391	15.850	10.544	32.546	1.00	0.00	3A4
ATOM	2749	CB	TRP	391	14.930	11.760	32.448	1.00	0.00	3A4
ATOM	2750	CG	TRP	391	13.571	11.608	33.100	1.00	0.00	3A4
ATOM	2751	CD2	TRP	391	13.050	10.792	34.187	1.00	0.00	3A4
ATOM	2752	CD1	TRP	391	12.458	12.068	32.439	1.00	0.00	3A4
ATOM	2753	NE1	TRP	391	11.305	11.618	33.025	1.00	0.00	3A4
ATOM	2754	CE2	TRP	391	11.634	10.839	34.102	1.00	0.00	3A4
ATOM	2755	CE3	TRP	391	13.655	10.032	35.188	1.00	0.00	3A4
ATOM	2756	CZ2	TRP	391	10.825	10.153	35.005	1.00	0.00	3A4
ATOM	2757	CZ3	TRP	391	12.843	9.345	36.102	1.00	0.00	3A4
ATOM	2758	CH2	TRP	391	11.446	9.404	36.011	1.00	0.00	3A4
ATOM	2759	C	TRP	391	16.783	10.563	31.369	1.00	0.00	3A4
ATOM	2760	O	TRP	391	17.769	11.289	31.371	1.00	0.00	3A4
ATOM	2761	N	VAL	392	16.466	9.736	30.350	1.00	0.00	3A4
ATOM	2762	CA	VAL	392	17.263	9.564	29.159	1.00	0.00	3A4
ATOM	2763	CB	VAL	392	17.270	8.105	28.700	1.00	0.00	3A4
ATOM	2764	CG1	VAL	392	17.957	7.898	27.322	1.00	0.00	3A4
ATOM	2765	CG2	VAL	392	17.984	7.270	29.787	1.00	0.00	3A4

ATOM	2766	C	VAL	392	16.723	10.497	28.110	1.00	0.00	3A4
ATOM	2767	O	VAL	392	15.519	10.598	27.908	1.00	0.00	3A4
ATOM	2768	N	VAL	393	17.636	11.234	27.453	1.00	0.00	3A4
ATOM	2769	CA	VAL	393	17.333	12.226	26.455	1.00	0.00	3A4
ATOM	2770	CB	VAL	393	17.828	13.610	26.868	1.00	0.00	3A4
ATOM	2771	CG1	VAL	393	17.556	14.652	25.780	1.00	0.00	3A4
ATOM	2772	CG2	VAL	393	17.145	14.023	28.194	1.00	0.00	3A4
ATOM	2773	C	VAL	393	17.993	11.735	25.192	1.00	0.00	3A4
ATOM	2774	O	VAL	393	19.147	11.327	25.196	1.00	0.00	3A4
ATOM	2775	N	MET	394	17.251	11.776	24.072	1.00	0.00	3A4
ATOM	2776	CA	MET	394	17.726	11.439	22.757	1.00	0.00	3A4
ATOM	2777	CB	MET	394	16.799	10.393	22.065	1.00	0.00	3A4
ATOM	2778	CG	MET	394	16.558	9.106	22.860	1.00	0.00	3A4
ATOM	2779	SD	MET	394	15.673	7.800	21.946	1.00	0.00	3A4
ATOM	2780	CE	MET	394	16.910	7.426	20.666	1.00	0.00	3A4
ATOM	2781	C	MET	394	17.772	12.724	21.991	1.00	0.00	3A4
ATOM	2782	O	MET	394	16.799	13.464	21.947	1.00	0.00	3A4
ATOM	2783	N	ILE	395	18.916	13.023	21.347	1.00	0.00	3A4
ATOM	2784	CA	ILE	395	19.139	14.208	20.554	1.00	0.00	3A4
ATOM	2785	CB	ILE	395	20.476	14.837	20.956	1.00	0.00	3A4
ATOM	2786	CG2	ILE	395	21.095	15.840	19.965	1.00	0.00	3A4
ATOM	2787	CG1	ILE	395	20.413	15.442	22.374	1.00	0.00	3A4
ATOM	2788	CD	ILE	395	20.802	14.496	23.518	1.00	0.00	3A4
ATOM	2789	C	ILE	395	19.146	13.747	19.102	1.00	0.00	3A4
ATOM	2790	O	ILE	395	20.160	13.239	18.627	1.00	0.00	3A4
ATOM	2791	N	PRO	396	18.048	13.907	18.342	1.00	0.00	3A4
ATOM	2792	CA	PRO	396	18.027	13.792	16.906	1.00	0.00	3A4
ATOM	2793	CD	PRO	396	16.755	13.448	18.870	1.00	0.00	3A4
ATOM	2794	CB	PRO	396	16.531	13.829	16.546	1.00	0.00	3A4
ATOM	2795	CG	PRO	396	15.857	13.097	17.687	1.00	0.00	3A4
ATOM	2796	C	PRO	396	18.776	14.889	16.173	1.00	0.00	3A4
ATOM	2797	O	PRO	396	18.239	15.950	15.861	1.00	0.00	3A4
ATOM	2798	N	SER	397	20.048	14.601	15.825	1.00	0.00	3A4
ATOM	2799	CA	SER	397	20.904	15.470	15.055	1.00	0.00	3A4
ATOM	2800	CB	SER	397	22.360	14.989	15.079	1.00	0.00	3A4
ATOM	2801	OG	SER	397	22.500	13.601	14.800	1.00	0.00	3A4
ATOM	2802	C	SER	397	20.417	15.595	13.635	1.00	0.00	3A4
ATOM	2803	O	SER	397	20.522	16.640	13.023	1.00	0.00	3A4
ATOM	2804	N	TYR	398	19.766	14.539	13.106	1.00	0.00	3A4
ATOM	2805	CA	TYR	398	19.026	14.496	11.862	1.00	0.00	3A4
ATOM	2806	CB	TYR	398	18.323	13.079	11.799	1.00	0.00	3A4
ATOM	2807	CG	TYR	398	18.447	12.353	10.483	1.00	0.00	3A4
ATOM	2808	CD1	TYR	398	19.004	11.056	10.456	1.00	0.00	3A4
ATOM	2809	CD2	TYR	398	18.041	12.935	9.266	1.00	0.00	3A4
ATOM	2810	CE1	TYR	398	19.153	10.357	9.251	1.00	0.00	3A4
ATOM	2811	CE2	TYR	398	18.216	12.249	8.058	1.00	0.00	3A4
ATOM	2812	CZ	TYR	398	18.763	10.958	8.048	1.00	0.00	3A4
ATOM	2813	OH	TYR	398	18.924	10.266	6.829	1.00	0.00	3A4
ATOM	2814	C	TYR	398	17.923	15.540	11.741	1.00	0.00	3A4
ATOM	2815	O	TYR	398	17.730	16.207	10.728	1.00	0.00	3A4
ATOM	2816	N	ALA	399	17.184	15.730	12.853	1.00	0.00	3A4
ATOM	2817	CA	ALA	399	16.116	16.686	12.969	1.00	0.00	3A4
ATOM	2818	CB	ALA	399	15.263	16.409	14.206	1.00	0.00	3A4
ATOM	2819	C	ALA	399	16.594	18.122	13.028	1.00	0.00	3A4
ATOM	2820	O	ALA	399	15.939	19.008	12.501	1.00	0.00	3A4
ATOM	2821	N	LEU	400	17.795	18.377	13.599	1.00	0.00	3A4
ATOM	2822	CA	LEU	400	18.426	19.687	13.645	1.00	0.00	3A4
ATOM	2823	CB	LEU	400	19.762	19.647	14.448	1.00	0.00	3A4
ATOM	2824	CG	LEU	400	19.694	19.664	15.956	1.00	0.00	3A4
ATOM	2825	CD1	LEU	400	20.663	20.773	16.433	1.00	0.00	3A4
ATOM	2826	CD2	LEU	400	18.244	19.759	16.433	1.00	0.00	3A4
ATOM	2827	C	LEU	400	18.832	20.202	12.285	1.00	0.00	3A4
ATOM	2828	O	LEU	400	18.639	21.368	11.954	1.00	0.00	3A4
ATOM	2829	N	HIS	401	19.402	19.298	11.465	1.00	0.00	3A4
ATOM	2830	CA	HIS	401	19.852	19.556	10.124	1.00	0.00	3A4
ATOM	2831	ND1	HIS	401	22.332	16.943	10.714	1.00	0.00	3A4
ATOM	2832	CG	HIS	401	21.917	18.117	10.143	1.00	0.00	3A4
ATOM	2833	CB	HIS	401	20.572	18.319	9.559	1.00	0.00	3A4
ATOM	2834	NE2	HIS	401	24.123	18.219	10.505	1.00	0.00	3A4
ATOM	2835	CD2	HIS	401	23.023	18.893	10.033	1.00	0.00	3A4
ATOM	2836	CE1	HIS	401	23.659	17.057	10.914	1.00	0.00	3A4
ATOM	2837	C	HIS	401	18.745	19.836	9.125	1.00	0.00	3A4

ATOM	2838	O	HIS	401	18.970	20.398	8.056	1.00	0.00	3A4
ATOM	2839	N	ARG	402	17.513	19.410	9.474	1.00	0.00	3A4
ATOM	2840	CA	ARG	402	16.350	19.558	8.644	1.00	0.00	3A4
ATOM	2841	CB	ARG	402	15.632	18.220	8.410	1.00	0.00	3A4
ATOM	2842	CG	ARG	402	16.476	17.220	7.607	1.00	0.00	3A4
ATOM	2843	CD	ARG	402	15.663	15.992	7.176	1.00	0.00	3A4
ATOM	2844	NE	ARG	402	16.519	15.105	6.308	1.00	0.00	3A4
ATOM	2845	CZ	ARG	402	16.028	14.373	5.254	1.00	0.00	3A4
ATOM	2846	NH1	ARG	402	16.860	13.518	4.593	1.00	0.00	3A4
ATOM	2847	NH2	ARG	402	14.725	14.465	4.853	1.00	0.00	3A4
ATOM	2848	C	ARG	402	15.378	20.553	9.211	1.00	0.00	3A4
ATOM	2849	O	ARG	402	14.224	20.625	8.790	1.00	0.00	3A4
ATOM	2850	N	ASP	403	15.839	21.391	10.171	1.00	0.00	3A4
ATOM	2851	CA	ASP	403	15.031	22.422	10.772	1.00	0.00	3A4
ATOM	2852	CB	ASP	403	15.642	22.973	12.085	1.00	0.00	3A4
ATOM	2853	CG	ASP	403	14.530	23.734	12.847	1.00	0.00	3A4
ATOM	2854	OD1	ASP	403	14.116	24.806	12.394	1.00	0.00	3A4
ATOM	2855	OD2	ASP	403	13.981	23.160	13.823	1.00	0.00	3A4
ATOM	2856	C	ASP	403	14.822	23.549	9.771	1.00	0.00	3A4
ATOM	2857	O	ASP	403	15.805	24.148	9.348	1.00	0.00	3A4
ATOM	2858	N	PRO	404	13.575	23.872	9.387	1.00	0.00	3A4
ATOM	2859	CA	PRO	404	13.256	24.866	8.377	1.00	0.00	3A4
ATOM	2860	CD	PRO	404	12.350	23.288	9.945	1.00	0.00	3A4
ATOM	2861	CB	PRO	404	11.749	24.727	8.133	1.00	0.00	3A4
ATOM	2862	CG	PRO	404	11.195	24.161	9.445	1.00	0.00	3A4
ATOM	2863	C	PRO	404	13.582	26.287	8.784	1.00	0.00	3A4
ATOM	2864	O	PRO	404	13.786	27.122	7.915	1.00	0.00	3A4
ATOM	2865	N	LYS	405	13.702	26.594	10.092	1.00	0.00	3A4
ATOM	2866	CA	LYS	405	14.102	27.890	10.588	1.00	0.00	3A4
ATOM	2867	CB	LYS	405	13.708	28.082	12.078	1.00	0.00	3A4
ATOM	2868	CG	LYS	405	12.230	27.779	12.361	1.00	0.00	3A4
ATOM	2869	CD	LYS	405	11.862	27.931	13.843	1.00	0.00	3A4
ATOM	2870	CE	LYS	405	10.437	27.465	14.181	1.00	0.00	3A4
ATOM	2871	NZ	LYS	405	9.420	28.274	13.467	1.00	0.00	3A4
ATOM	2872	C	LYS	405	15.589	28.111	10.451	1.00	0.00	3A4
ATOM	2873	O	LYS	405	16.040	29.247	10.435	1.00	0.00	3A4
ATOM	2874	N	TYR	406	16.387	27.031	10.326	1.00	0.00	3A4
ATOM	2875	CA	TYR	406	17.828	27.082	10.196	1.00	0.00	3A4
ATOM	2876	CB	TYR	406	18.501	25.978	11.073	1.00	0.00	3A4
ATOM	2877	CG	TYR	406	18.818	26.481	12.466	1.00	0.00	3A4
ATOM	2878	CD1	TYR	406	17.845	27.049	13.316	1.00	0.00	3A4
ATOM	2879	CD2	TYR	406	20.123	26.324	12.973	1.00	0.00	3A4
ATOM	2880	CE1	TYR	406	18.180	27.502	14.601	1.00	0.00	3A4
ATOM	2881	CE2	TYR	406	20.465	26.758	14.261	1.00	0.00	3A4
ATOM	2882	CZ	TYR	406	19.493	27.354	15.076	1.00	0.00	3A4
ATOM	2883	OH	TYR	406	19.831	27.781	16.379	1.00	0.00	3A4
ATOM	2884	C	TYR	406	18.238	26.911	8.742	1.00	0.00	3A4
ATOM	2885	O	TYR	406	19.185	27.556	8.293	1.00	0.00	3A4
ATOM	2886	N	TRP	407	17.542	26.030	7.986	1.00	0.00	3A4
ATOM	2887	CA	TRP	407	17.869	25.728	6.609	1.00	0.00	3A4
ATOM	2888	CB	TRP	407	18.602	24.364	6.460	1.00	0.00	3A4
ATOM	2889	CG	TRP	407	19.890	24.534	5.666	1.00	0.00	3A4
ATOM	2890	CD2	TRP	407	20.082	24.159	4.293	1.00	0.00	3A4
ATOM	2891	CD1	TRP	407	21.050	25.141	6.063	1.00	0.00	3A4
ATOM	2892	NE1	TRP	407	21.981	25.110	5.052	1.00	0.00	3A4
ATOM	2893	CE2	TRP	407	21.405	24.521	3.948	1.00	0.00	3A4
ATOM	2894	CE3	TRP	407	19.231	23.566	3.365	1.00	0.00	3A4
ATOM	2895	CZ2	TRP	407	21.902	24.280	2.673	1.00	0.00	3A4
ATOM	2896	CZ3	TRP	407	19.728	23.326	2.076	1.00	0.00	3A4
ATOM	2897	CH2	TRP	407	21.046	23.678	1.741	1.00	0.00	3A4
ATOM	2898	C	TRP	407	16.592	25.684	5.809	1.00	0.00	3A4
ATOM	2899	O	TRP	407	15.735	24.831	6.029	1.00	0.00	3A4
ATOM	2900	N	THR	408	16.454	26.581	4.791	1.00	0.00	3A4
ATOM	2901	CA	THR	408	15.311	26.691	3.895	1.00	0.00	3A4
ATOM	2902	CB	THR	408	15.211	28.071	3.263	1.00	0.00	3A4
ATOM	2903	OG1	THR	408	16.432	28.505	2.662	1.00	0.00	3A4
ATOM	2904	CG2	THR	408	14.818	29.070	4.376	1.00	0.00	3A4
ATOM	2905	C	THR	408	15.392	25.598	2.839	1.00	0.00	3A4
ATOM	2906	O	THR	408	16.472	25.245	2.376	1.00	0.00	3A4
ATOM	2907	N	GLU	409	14.235	24.987	2.499	1.00	0.00	3A4
ATOM	2908	CA	GLU	409	14.103	23.803	1.664	1.00	0.00	3A4
ATOM	2909	CB	GLU	409	14.330	24.118	0.167	1.00	0.00	3A4

ATOM	2910	CG	GLU	409	13.370	25.190	-0.379	1.00	0.00	3A4
ATOM	2911	CD	GLU	409	13.625	25.385	-1.878	1.00	0.00	3A4
ATOM	2912	OE1	GLU	409	12.698	25.099	-2.683	1.00	0.00	3A4
ATOM	2913	OE2	GLU	409	14.752	25.821	-2.236	1.00	0.00	3A4
ATOM	2914	C	GLU	409	15.001	22.657	2.097	1.00	0.00	3A4
ATOM	2915	O	GLU	409	15.858	22.218	1.334	1.00	0.00	3A4
ATOM	2916	N	PRO	410	14.886	22.233	3.369	1.00	0.00	3A4
ATOM	2917	CA	PRO	410	15.857	21.388	4.073	1.00	0.00	3A4
ATOM	2918	CD	PRO	410	13.663	22.414	4.165	1.00	0.00	3A4
ATOM	2919	CB	PRO	410	15.298	21.307	5.504	1.00	0.00	3A4
ATOM	2920	CG	PRO	410	13.783	21.467	5.357	1.00	0.00	3A4
ATOM	2921	C	PRO	410	16.013	20.007	3.463	1.00	0.00	3A4
ATOM	2922	O	PRO	410	17.048	19.368	3.620	1.00	0.00	3A4
ATOM	2923	N	GLU	411	15.001	19.530	2.723	1.00	0.00	3A4
ATOM	2924	CA	GLU	411	15.007	18.249	2.086	1.00	0.00	3A4
ATOM	2925	CB	GLU	411	13.575	17.671	2.041	1.00	0.00	3A4
ATOM	2926	CG	GLU	411	12.398	18.662	1.868	1.00	0.00	3A4
ATOM	2927	CD	GLU	411	12.395	19.342	0.498	1.00	0.00	3A4
ATOM	2928	OE1	GLU	411	12.459	20.600	0.464	1.00	0.00	3A4
ATOM	2929	OE2	GLU	411	12.316	18.616	-0.530	1.00	0.00	3A4
ATOM	2930	C	GLU	411	15.637	18.272	0.712	1.00	0.00	3A4
ATOM	2931	O	GLU	411	15.745	17.227	0.076	1.00	0.00	3A4
ATOM	2932	N	LYS	412	16.093	19.439	0.214	1.00	0.00	3A4
ATOM	2933	CA	LYS	412	16.747	19.560	-1.069	1.00	0.00	3A4
ATOM	2934	CB	LYS	412	16.319	20.855	-1.798	1.00	0.00	3A4
ATOM	2935	CG	LYS	412	14.842	20.918	-2.228	1.00	0.00	3A4
ATOM	2936	CD	LYS	412	14.489	20.264	-3.577	1.00	0.00	3A4
ATOM	2937	CE	LYS	412	14.483	18.726	-3.601	1.00	0.00	3A4
ATOM	2938	NZ	LYS	412	13.990	18.220	-4.904	1.00	0.00	3A4
ATOM	2939	C	LYS	412	18.246	19.556	-0.876	1.00	0.00	3A4
ATOM	2940	O	LYS	412	18.788	20.180	0.031	1.00	0.00	3A4
ATOM	2941	N	PHE	413	18.970	18.849	-1.771	1.00	0.00	3A4
ATOM	2942	CA	PHE	413	20.413	18.790	-1.784	1.00	0.00	3A4
ATOM	2943	CB	PHE	413	20.897	17.450	-2.401	1.00	0.00	3A4
ATOM	2944	CG	PHE	413	22.398	17.294	-2.423	1.00	0.00	3A4
ATOM	2945	CD1	PHE	413	23.168	17.227	-1.254	1.00	0.00	3A4
ATOM	2946	CD2	PHE	413	23.046	17.095	-3.661	1.00	0.00	3A4
ATOM	2947	CE1	PHE	413	24.550	16.999	-1.315	1.00	0.00	3A4
ATOM	2948	CE2	PHE	413	24.421	16.834	-3.726	1.00	0.00	3A4
ATOM	2949	CZ	PHE	413	25.177	16.794	-2.550	1.00	0.00	3A4
ATOM	2950	C	PHE	413	20.891	19.968	-2.586	1.00	0.00	3A4
ATOM	2951	O	PHE	413	20.724	20.009	-3.801	1.00	0.00	3A4
ATOM	2952	N	LEU	414	21.483	20.957	-1.901	1.00	0.00	3A4
ATOM	2953	CA	LEU	414	21.933	22.177	-2.522	1.00	0.00	3A4
ATOM	2954	CB	LEU	414	20.902	23.301	-2.306	1.00	0.00	3A4
ATOM	2955	CG	LEU	414	21.169	24.700	-2.902	1.00	0.00	3A4
ATOM	2956	CD1	LEU	414	21.261	24.685	-4.441	1.00	0.00	3A4
ATOM	2957	CD2	LEU	414	20.079	25.663	-2.388	1.00	0.00	3A4
ATOM	2958	C	LEU	414	23.275	22.553	-1.966	1.00	0.00	3A4
ATOM	2959	O	LEU	414	23.343	23.031	-0.834	1.00	0.00	3A4
ATOM	2960	N	PRO	415	24.394	22.396	-2.681	1.00	0.00	3A4
ATOM	2961	CA	PRO	415	25.721	22.710	-2.165	1.00	0.00	3A4
ATOM	2962	CD	PRO	415	24.457	21.932	-4.069	1.00	0.00	3A4
ATOM	2963	CB	PRO	415	26.676	22.158	-3.227	1.00	0.00	3A4
ATOM	2964	CG	PRO	415	25.882	22.244	-4.535	1.00	0.00	3A4
ATOM	2965	C	PRO	415	25.978	24.200	-1.983	1.00	0.00	3A4
ATOM	2966	O	PRO	415	26.655	24.548	-1.013	1.00	0.00	3A4
ATOM	2967	N	GLU	416	25.547	25.077	-2.937	1.00	0.00	3A4
ATOM	2968	CA	GLU	416	25.810	26.505	-2.951	1.00	0.00	3A4
ATOM	2969	CB	GLU	416	27.244	26.943	-3.438	1.00	0.00	3A4
ATOM	2970	CG	GLU	416	28.338	26.841	-2.361	1.00	0.00	3A4
ATOM	2971	CD	GLU	416	29.636	27.541	-2.784	1.00	0.00	3A4
ATOM	2972	OE1	GLU	416	29.584	28.756	-3.114	1.00	0.00	3A4
ATOM	2973	OE2	GLU	416	30.704	26.872	-2.759	1.00	0.00	3A4
ATOM	2974	C	GLU	416	24.818	27.126	-3.902	1.00	0.00	3A4
ATOM	2975	O	GLU	416	24.357	26.500	-4.855	1.00	0.00	3A4
ATOM	2976	N	ARG	417	24.555	28.429	-3.633	1.00	0.00	3A4
ATOM	2977	CA	ARG	417	23.940	29.448	-4.465	1.00	0.00	3A4
ATOM	2978	CB	ARG	417	22.623	29.089	-5.229	1.00	0.00	3A4
ATOM	2979	CG	ARG	417	21.420	28.657	-4.370	1.00	0.00	3A4
ATOM	2980	CD	ARG	417	20.160	28.317	-5.191	1.00	0.00	3A4
ATOM	2981	NE	ARG	417	19.654	29.550	-5.895	1.00	0.00	3A4

ATOM	2982	CZ	ARG	417	18.836	30.485	-5.308	1.00	0.00	3A4
ATOM	2983	NH1	ARG	417	18.453	31.575	-6.033	1.00	0.00	3A4
ATOM	2984	NH2	ARG	417	18.396	30.357	-4.021	1.00	0.00	3A4
ATOM	2985	C	ARG	417	23.675	30.614	-3.534	1.00	0.00	3A4
ATOM	2986	O	ARG	417	23.277	31.695	-3.966	1.00	0.00	3A4
ATOM	2987	N	PHE	418	23.883	30.380	-2.207	1.00	0.00	3A4
ATOM	2988	CA	PHE	418	23.598	31.253	-1.087	1.00	0.00	3A4
ATOM	2989	CB	PHE	418	22.842	30.493	0.064	1.00	0.00	3A4
ATOM	2990	CG	PHE	418	23.400	29.109	0.354	1.00	0.00	3A4
ATOM	2991	CD1	PHE	418	24.479	28.931	1.245	1.00	0.00	3A4
ATOM	2992	CD2	PHE	418	22.845	27.967	-0.262	1.00	0.00	3A4
ATOM	2993	CE1	PHE	418	25.002	27.653	1.496	1.00	0.00	3A4
ATOM	2994	CE2	PHE	418	23.361	26.688	-0.007	1.00	0.00	3A4
ATOM	2995	CZ	PHE	418	24.442	26.532	0.869	1.00	0.00	3A4
ATOM	2996	C	PHE	418	24.891	31.865	-0.589	1.00	0.00	3A4
ATOM	2997	O	PHE	418	25.978	31.337	-0.822	1.00	0.00	3A4
ATOM	2998	N	SER	419	24.764	33.010	0.130	1.00	0.00	3A4
ATOM	2999	CA	SER	419	25.850	33.749	0.742	1.00	0.00	3A4
ATOM	3000	CB	SER	419	26.168	35.084	0.003	1.00	0.00	3A4
ATOM	3001	OG	SER	419	26.610	34.824	-1.323	1.00	0.00	3A4
ATOM	3002	C	SER	419	25.419	34.042	2.158	1.00	0.00	3A4
ATOM	3003	O	SER	419	24.254	33.869	2.516	1.00	0.00	3A4
ATOM	3004	N	LYS	420	26.380	34.507	2.995	1.00	0.00	3A4
ATOM	3005	CA	LYS	420	26.162	34.853	4.383	1.00	0.00	3A4
ATOM	3006	CB	LYS	420	26.449	33.660	5.338	1.00	0.00	3A4
ATOM	3007	CG	LYS	420	26.041	33.882	6.806	1.00	0.00	3A4
ATOM	3008	CD	LYS	420	25.973	32.611	7.673	1.00	0.00	3A4
ATOM	3009	CE	LYS	420	27.316	31.947	8.025	1.00	0.00	3A4
ATOM	3010	NZ	LYS	420	27.897	31.201	6.884	1.00	0.00	3A4
ATOM	3011	C	LYS	420	27.070	36.024	4.656	1.00	0.00	3A4
ATOM	3012	O	LYS	420	28.205	36.070	4.182	1.00	0.00	3A4
ATOM	3013	N	LYS	421	26.554	37.018	5.432	1.00	0.00	3A4
ATOM	3014	CA	LYS	421	27.150	38.319	5.697	1.00	0.00	3A4
ATOM	3015	CB	LYS	421	26.041	39.410	5.739	1.00	0.00	3A4
ATOM	3016	CG	LYS	421	26.518	40.872	5.751	1.00	0.00	3A4
ATOM	3017	CD	LYS	421	25.360	41.868	5.629	1.00	0.00	3A4
ATOM	3018	CE	LYS	421	25.821	43.332	5.619	1.00	0.00	3A4
ATOM	3019	NZ	LYS	421	24.664	44.251	5.492	1.00	0.00	3A4
ATOM	3020	C	LYS	421	27.940	38.313	6.992	1.00	0.00	3A4
ATOM	3021	O	LYS	421	28.871	39.099	7.165	1.00	0.00	3A4
ATOM	3022	N	ASN	422	27.572	37.398	7.933	1.00	0.00	3A4
ATOM	3023	CA	ASN	422	28.154	37.237	9.255	1.00	0.00	3A4
ATOM	3024	CB	ASN	422	27.020	37.047	10.319	1.00	0.00	3A4
ATOM	3025	CG	ASN	422	27.499	37.210	11.776	1.00	0.00	3A4
ATOM	3026	OD1	ASN	422	27.456	36.260	12.556	1.00	0.00	3A4
ATOM	3027	ND2	ASN	422	27.964	38.434	12.149	1.00	0.00	3A4
ATOM	3028	C	ASN	422	29.107	36.052	9.222	1.00	0.00	3A4
ATOM	3029	O	ASN	422	29.035	35.203	8.335	1.00	0.00	3A4
ATOM	3030	N	LYS	423	30.033	35.989	10.220	1.00	0.00	3A4
ATOM	3031	CA	LYS	423	31.052	34.968	10.382	1.00	0.00	3A4
ATOM	3032	CB	LYS	423	32.450	35.576	10.704	1.00	0.00	3A4
ATOM	3033	CG	LYS	423	33.030	36.450	9.575	1.00	0.00	3A4
ATOM	3034	CD	LYS	423	33.266	35.769	8.209	1.00	0.00	3A4
ATOM	3035	CE	LYS	423	34.431	34.762	8.142	1.00	0.00	3A4
ATOM	3036	NZ	LYS	423	34.107	33.470	8.794	1.00	0.00	3A4
ATOM	3037	C	LYS	423	30.631	34.032	11.491	1.00	0.00	3A4
ATOM	3038	O	LYS	423	30.939	34.245	12.663	1.00	0.00	3A4
ATOM	3039	N	ASP	424	29.907	32.953	11.101	1.00	0.00	3A4
ATOM	3040	CA	ASP	424	29.457	31.893	11.976	1.00	0.00	3A4
ATOM	3041	CB	ASP	424	28.060	32.147	12.651	1.00	0.00	3A4
ATOM	3042	CG	ASP	424	26.909	32.519	11.687	1.00	0.00	3A4
ATOM	3043	OD1	ASP	424	25.944	31.714	11.589	1.00	0.00	3A4
ATOM	3044	OD2	ASP	424	26.973	33.604	11.051	1.00	0.00	3A4
ATOM	3045	C	ASP	424	29.495	30.648	11.123	1.00	0.00	3A4
ATOM	3046	O	ASP	424	28.470	30.043	10.811	1.00	0.00	3A4
ATOM	3047	N	ASN	425	30.728	30.251	10.724	1.00	0.00	3A4
ATOM	3048	CA	ASN	425	30.999	29.112	9.872	1.00	0.00	3A4
ATOM	3049	CB	ASN	425	30.910	29.449	8.339	1.00	0.00	3A4
ATOM	3050	CG	ASN	425	31.718	30.701	7.912	1.00	0.00	3A4
ATOM	3051	OD1	ASN	425	32.894	30.588	7.570	1.00	0.00	3A4
ATOM	3052	ND2	ASN	425	31.085	31.907	7.916	1.00	0.00	3A4
ATOM	3053	C	ASN	425	32.363	28.587	10.270	1.00	0.00	3A4

ATOM	3054	O	ASN	425	33.092	28.033	9.449	1.00	0.00	3A4
ATOM	3055	N	ILE	426	32.734	28.773	11.570	1.00	0.00	3A4
ATOM	3056	CA	ILE	426	34.043	28.493	12.137	1.00	0.00	3A4
ATOM	3057	CB	ILE	426	34.648	29.716	12.854	1.00	0.00	3A4
ATOM	3058	CG2	ILE	426	36.105	29.402	13.297	1.00	0.00	3A4
ATOM	3059	CG1	ILE	426	34.591	30.966	11.928	1.00	0.00	3A4
ATOM	3060	CD	ILE	426	35.100	32.260	12.569	1.00	0.00	3A4
ATOM	3061	C	ILE	426	33.870	27.289	13.047	1.00	0.00	3A4
ATOM	3062	O	ILE	426	34.107	26.155	12.633	1.00	0.00	3A4
ATOM	3063	N	ASP	427	33.447	27.532	14.315	1.00	0.00	3A4
ATOM	3064	CA	ASP	427	33.204	26.537	15.348	1.00	0.00	3A4
ATOM	3065	CB	ASP	427	34.320	26.450	16.444	1.00	0.00	3A4
ATOM	3066	CG	ASP	427	35.639	25.963	15.828	1.00	0.00	3A4
ATOM	3067	OD1	ASP	427	35.660	24.821	15.293	1.00	0.00	3A4
ATOM	3068	OD2	ASP	427	36.643	26.722	15.888	1.00	0.00	3A4
ATOM	3069	C	ASP	427	31.841	26.813	15.973	1.00	0.00	3A4
ATOM	3070	O	ASP	427	31.098	25.842	16.103	1.00	0.00	3A4
ATOM	3071	N	PRO	428	31.390	28.043	16.369	1.00	0.00	3A4
ATOM	3072	CA	PRO	428	29.983	28.361	16.637	1.00	0.00	3A4
ATOM	3073	CD	PRO	428	32.272	29.141	16.778	1.00	0.00	3A4
ATOM	3074	CB	PRO	428	30.041	29.613	17.539	1.00	0.00	3A4
ATOM	3075	CG	PRO	428	31.359	30.308	17.172	1.00	0.00	3A4
ATOM	3076	C	PRO	428	29.245	28.611	15.321	1.00	0.00	3A4
ATOM	3077	O	PRO	428	29.471	29.640	14.687	1.00	0.00	3A4
ATOM	3078	N	TYR	429	28.385	27.650	14.899	1.00	0.00	3A4
ATOM	3079	CA	TYR	429	27.755	27.649	13.596	1.00	0.00	3A4
ATOM	3080	CB	TYR	429	28.727	27.191	12.437	1.00	0.00	3A4
ATOM	3081	CG	TYR	429	29.325	25.786	12.428	1.00	0.00	3A4
ATOM	3082	CD1	TYR	429	29.871	25.334	11.208	1.00	0.00	3A4
ATOM	3083	CD2	TYR	429	29.371	24.901	13.532	1.00	0.00	3A4
ATOM	3084	CE1	TYR	429	30.418	24.050	11.078	1.00	0.00	3A4
ATOM	3085	CE2	TYR	429	29.917	23.615	13.410	1.00	0.00	3A4
ATOM	3086	CZ	TYR	429	30.437	23.186	12.181	1.00	0.00	3A4
ATOM	3087	OH	TYR	429	30.972	21.885	12.055	1.00	0.00	3A4
ATOM	3088	C	TYR	429	26.500	26.805	13.683	1.00	0.00	3A4
ATOM	3089	O	TYR	429	25.984	26.542	14.769	1.00	0.00	3A4
ATOM	3090	N	ILE	430	26.004	26.339	12.499	1.00	0.00	3A4
ATOM	3091	CA	ILE	430	24.912	25.392	12.301	1.00	0.00	3A4
ATOM	3092	CB	ILE	430	23.953	25.845	11.196	1.00	0.00	3A4
ATOM	3093	CG2	ILE	430	23.323	27.171	11.680	1.00	0.00	3A4
ATOM	3094	CG1	ILE	430	24.623	26.004	9.800	1.00	0.00	3A4
ATOM	3095	CD	ILE	430	23.667	26.472	8.700	1.00	0.00	3A4
ATOM	3096	C	ILE	430	25.562	24.051	12.005	1.00	0.00	3A4
ATOM	3097	O	ILE	430	26.789	23.977	12.016	1.00	0.00	3A4
ATOM	3098	N	TYR	431	24.773	22.951	11.760	1.00	0.00	3A4
ATOM	3099	CA	TYR	431	25.198	21.604	11.414	1.00	0.00	3A4
ATOM	3100	CB	TYR	431	26.437	21.470	10.410	1.00	0.00	3A4
ATOM	3101	CG	TYR	431	26.384	22.218	9.097	1.00	0.00	3A4
ATOM	3102	CD1	TYR	431	25.749	21.647	7.983	1.00	0.00	3A4
ATOM	3103	CD2	TYR	431	27.142	23.393	8.894	1.00	0.00	3A4
ATOM	3104	CE1	TYR	431	25.834	22.246	6.714	1.00	0.00	3A4
ATOM	3105	CE2	TYR	431	27.212	24.010	7.638	1.00	0.00	3A4
ATOM	3106	CZ	TYR	431	26.551	23.437	6.544	1.00	0.00	3A4
ATOM	3107	OH	TYR	431	26.632	24.036	5.267	1.00	0.00	3A4
ATOM	3108	C	TYR	431	25.647	20.889	12.688	1.00	0.00	3A4
ATOM	3109	O	TYR	431	26.635	21.285	13.303	1.00	0.00	3A4
ATOM	3110	N	THR	432	24.989	19.782	13.089	1.00	0.00	3A4
ATOM	3111	CA	THR	432	25.445	18.960	14.203	1.00	0.00	3A4
ATOM	3112	CB	THR	432	24.381	18.938	15.316	1.00	0.00	3A4
ATOM	3113	OG1	THR	432	23.070	18.659	14.826	1.00	0.00	3A4
ATOM	3114	CG2	THR	432	24.399	20.310	16.028	1.00	0.00	3A4
ATOM	3115	C	THR	432	25.810	17.558	13.781	1.00	0.00	3A4
ATOM	3116	O	THR	432	25.565	16.648	14.576	1.00	0.00	3A4
ATOM	3117	N	PRO	433	26.389	17.234	12.610	1.00	0.00	3A4
ATOM	3118	CA	PRO	433	26.601	15.849	12.240	1.00	0.00	3A4
ATOM	3119	CD	PRO	433	27.173	18.101	11.724	1.00	0.00	3A4
ATOM	3120	CB	PRO	433	26.947	15.918	10.740	1.00	0.00	3A4
ATOM	3121	CG	PRO	433	27.743	17.221	10.601	1.00	0.00	3A4
ATOM	3122	C	PRO	433	27.748	15.209	13.022	1.00	0.00	3A4
ATOM	3123	O	PRO	433	27.771	13.993	13.150	1.00	0.00	3A4
ATOM	3124	N	PHE	434	28.673	16.013	13.587	1.00	0.00	3A4
ATOM	3125	CA	PHE	434	29.782	15.548	14.382	1.00	0.00	3A4

ATOM	3126	CB	PHE	434	31.108	16.257	13.997	1.00	0.00	3A4
ATOM	3127	CG	PHE	434	31.591	15.810	12.639	1.00	0.00	3A4
ATOM	3128	CD1	PHE	434	31.353	16.451	11.514	1.00	0.00	3A4
ATOM	3129	CD2	PHE	434	32.354	14.754	12.363	1.00	0.00	3A4
ATOM	3130	CE1	PHE	434	31.813	16.203	10.200	1.00	0.00	3A4
ATOM	3131	CE2	PHE	434	32.860	14.287	11.129	1.00	0.00	3A4
ATOM	3132	CZ	PHE	434	32.592	15.066	10.009	1.00	0.00	3A4
ATOM	3133	C	PHE	434	29.528	15.802	15.833	1.00	0.00	3A4
ATOM	3134	O	PHE	434	30.427	15.663	16.655	1.00	0.00	3A4
ATOM	3135	N	GLY	435	28.291	16.210	16.191	1.00	0.00	3A4
ATOM	3136	CA	GLY	435	27.923	16.495	17.561	1.00	0.00	3A4
ATOM	3137	C	GLY	435	28.209	17.917	17.875	1.00	0.00	3A4
ATOM	3138	O	GLY	435	28.305	18.719	16.943	1.00	0.00	3A4
ATOM	3139	N	SER	436	28.348	18.248	19.183	1.00	0.00	3A4
ATOM	3140	CA	SER	436	28.384	19.623	19.578	1.00	0.00	3A4
ATOM	3141	CB	SER	436	26.947	20.258	19.543	1.00	0.00	3A4
ATOM	3142	OG	SER	436	26.948	21.683	19.489	1.00	0.00	3A4
ATOM	3143	C	SER	436	29.197	19.916	20.769	1.00	0.00	3A4
ATOM	3144	O	SER	436	30.134	20.642	20.647	1.00	0.00	3A4
ATOM	3145	N	GLY	437	28.951	19.486	21.973	1.00	0.00	3A4
ATOM	3146	CA	GLY	437	29.675	19.961	23.144	1.00	0.00	3A4
ATOM	3147	C	GLY	437	31.130	19.558	23.314	1.00	0.00	3A4
ATOM	3148	O	GLY	437	31.959	19.487	22.402	1.00	0.00	3A4
ATOM	3149	N	PRO	438	31.502	19.228	24.529	1.00	0.00	3A4
ATOM	3150	CA	PRO	438	32.875	18.727	24.776	1.00	0.00	3A4
ATOM	3151	CD	PRO	438	30.927	19.742	25.770	1.00	0.00	3A4
ATOM	3152	CB	PRO	438	33.100	18.880	26.266	1.00	0.00	3A4
ATOM	3153	CG	PRO	438	31.706	19.063	26.880	1.00	0.00	3A4
ATOM	3154	C	PRO	438	33.099	17.295	24.317	1.00	0.00	3A4
ATOM	3155	O	PRO	438	34.230	16.824	24.348	1.00	0.00	3A4
ATOM	3156	N	ARG	439	32.033	16.608	23.850	1.00	0.00	3A4
ATOM	3157	CA	ARG	439	32.068	15.264	23.366	1.00	0.00	3A4
ATOM	3158	CB	ARG	439	30.905	14.467	23.961	1.00	0.00	3A4
ATOM	3159	CG	ARG	439	30.793	14.766	25.461	1.00	0.00	3A4
ATOM	3160	CD	ARG	439	30.197	13.690	26.366	1.00	0.00	3A4
ATOM	3161	NE	ARG	439	30.391	14.136	27.786	1.00	0.00	3A4
ATOM	3162	CZ	ARG	439	30.091	13.354	28.866	1.00	0.00	3A4
ATOM	3163	NH1	ARG	439	30.342	13.836	30.116	1.00	0.00	3A4
ATOM	3164	NH2	ARG	439	29.553	12.109	28.713	1.00	0.00	3A4
ATOM	3165	C	ARG	439	31.980	15.221	21.890	1.00	0.00	3A4
ATOM	3166	O	ARG	439	31.776	14.165	21.309	1.00	0.00	3A4
ATOM	3167	N	ASN	440	32.201	16.364	21.200	1.00	0.00	3A4
ATOM	3168	CA	ASN	440	32.204	16.474	19.756	1.00	0.00	3A4
ATOM	3169	CB	ASN	440	32.625	17.886	19.354	1.00	0.00	3A4
ATOM	3170	CG	ASN	440	32.279	18.329	17.901	1.00	0.00	3A4
ATOM	3171	OD1	ASN	440	32.746	17.778	16.907	1.00	0.00	3A4
ATOM	3172	ND2	ASN	440	31.452	19.401	17.765	1.00	0.00	3A4
ATOM	3173	C	ASN	440	33.216	15.539	19.171	1.00	0.00	3A4
ATOM	3174	O	ASN	440	34.241	15.285	19.807	1.00	0.00	3A4
ATOM	3175	N	CYS	441	32.950	14.993	17.974	1.00	0.00	3A4
ATOM	3176	CA	CYS	441	33.782	14.009	17.328	1.00	0.00	3A4
ATOM	3177	CB	CYS	441	33.288	13.772	15.899	1.00	0.00	3A4
ATOM	3178	SG	CYS	441	34.028	12.338	15.029	1.00	0.00	3A4
ATOM	3179	C	CYS	441	35.241	14.414	17.264	1.00	0.00	3A4
ATOM	3180	O	CYS	441	35.564	15.528	16.866	1.00	0.00	3A4
ATOM	3181	N	ILE	442	-36.131	13.531	17.746	1.00	0.00	3A4
ATOM	3182	CA	ILE	442	37.556	13.799	17.790	1.00	0.00	3A4
ATOM	3183	CB	ILE	442	38.223	12.944	18.848	1.00	0.00	3A4
ATOM	3184	CG2	ILE	442	38.388	11.476	18.448	1.00	0.00	3A4
ATOM	3185	CG1	ILE	442	39.528	13.570	19.391	1.00	0.00	3A4
ATOM	3186	CD	ILE	442	39.336	14.819	20.250	1.00	0.00	3A4
ATOM	3187	C	ILE	442	38.181	13.605	16.408	1.00	0.00	3A4
ATOM	3188	O	ILE	442	39.180	14.220	16.048	1.00	0.00	3A4
ATOM	3189	N	GLY	443	37.524	12.758	15.590	1.00	0.00	3A4
ATOM	3190	CA	GLY	443	37.942	12.408	14.266	1.00	0.00	3A4
ATOM	3191	C	GLY	443	37.399	13.252	13.158	1.00	0.00	3A4
ATOM	3192	O	GLY	443	37.591	12.902	12.001	1.00	0.00	3A4
ATOM	3193	N	MET	444	36.732	14.396	13.456	1.00	0.00	3A4
ATOM	3194	CA	MET	444	36.082	15.266	12.493	1.00	0.00	3A4
ATOM	3195	CB	MET	444	35.408	16.458	13.192	1.00	0.00	3A4
ATOM	3196	CG	MET	444	36.294	17.310	14.126	1.00	0.00	3A4
ATOM	3197	SD	MET	444	35.375	18.583	15.041	1.00	0.00	3A4

ATOM	3198	CE	MET	444	36.695	18.911	16.244	1.00	0.00	3A4
ATOM	3199	C	MET	444	36.968	15.807	11.395	1.00	0.00	3A4
ATOM	3200	O	MET	444	36.570	15.844	10.236	1.00	0.00	3A4
ATOM	3201	N	ARG	445	38.230	16.170	11.727	1.00	0.00	3A4
ATOM	3202	CA	ARG	445	39.211	16.708	10.801	1.00	0.00	3A4
ATOM	3203	CB	ARG	445	40.435	17.321	11.549	1.00	0.00	3A4
ATOM	3204	CG	ARG	445	40.058	18.332	12.647	1.00	0.00	3A4
ATOM	3205	CD	ARG	445	39.223	19.529	12.155	1.00	0.00	3A4
ATOM	3206	NE	ARG	445	38.880	20.389	13.341	1.00	0.00	3A4
ATOM	3207	CZ	ARG	445	37.901	21.351	13.313	1.00	0.00	3A4
ATOM	3208	NH1	ARG	445	37.643	22.071	14.443	1.00	0.00	3A4
ATOM	3209	NH2	ARG	445	37.171	21.600	12.186	1.00	0.00	3A4
ATOM	3210	C	ARG	445	39.695	15.651	9.828	1.00	0.00	3A4
ATOM	3211	O	ARG	445	39.790	15.886	8.628	1.00	0.00	3A4
ATOM	3212	N	PHE	446	39.920	14.418	10.335	1.00	0.00	3A4
ATOM	3213	CA	PHE	446	40.293	13.256	9.549	1.00	0.00	3A4
ATOM	3214	CB	PHE	446	40.683	12.116	10.501	1.00	0.00	3A4
ATOM	3215	CG	PHE	446	41.549	11.008	9.982	1.00	0.00	3A4
ATOM	3216	CD1	PHE	446	42.800	11.292	9.403	1.00	0.00	3A4
ATOM	3217	CD2	PHE	446	41.248	9.684	10.350	1.00	0.00	3A4
ATOM	3218	CE1	PHE	446	43.749	10.278	9.241	1.00	0.00	3A4
ATOM	3219	CE2	PHE	446	42.210	8.678	10.222	1.00	0.00	3A4
ATOM	3220	CZ	PHE	446	43.469	8.983	9.689	1.00	0.00	3A4
ATOM	3221	C	PHE	446	39.172	12.804	8.647	1.00	0.00	3A4
ATOM	3222	O	PHE	446	39.384	12.508	7.480	1.00	0.00	3A4
ATOM	3223	N	ALA	447	37.921	12.812	9.148	1.00	0.00	3A4
ATOM	3224	CA	ALA	447	36.738	12.472	8.393	1.00	0.00	3A4
ATOM	3225	CB	ALA	447	35.499	12.464	9.272	1.00	0.00	3A4
ATOM	3226	C	ALA	447	36.489	13.392	7.228	1.00	0.00	3A4
ATOM	3227	O	ALA	447	36.216	12.950	6.120	1.00	0.00	3A4
ATOM	3228	N	LEU	448	36.656	14.715	7.427	1.00	0.00	3A4
ATOM	3229	CA	LEU	448	36.469	15.704	6.386	1.00	0.00	3A4
ATOM	3230	CB	LEU	448	36.399	17.124	6.962	1.00	0.00	3A4
ATOM	3231	CG	LEU	448	35.089	17.408	7.731	1.00	0.00	3A4
ATOM	3232	CD1	LEU	448	35.223	18.721	8.515	1.00	0.00	3A4
ATOM	3233	CD2	LEU	448	33.842	17.445	6.826	1.00	0.00	3A4
ATOM	3234	C	LEU	448	37.561	15.661	5.351	1.00	0.00	3A4
ATOM	3235	O	LEU	448	37.299	15.865	4.175	1.00	0.00	3A4
ATOM	3236	N	MET	449	38.806	15.319	5.746	1.00	0.00	3A4
ATOM	3237	CA	MET	449	39.935	15.178	4.853	1.00	0.00	3A4
ATOM	3238	CB	MET	449	41.269	15.033	5.617	1.00	0.00	3A4
ATOM	3239	CG	MET	449	41.841	16.358	6.130	1.00	0.00	3A4
ATOM	3240	SD	MET	449	43.382	16.135	7.075	1.00	0.00	3A4
ATOM	3241	CE	MET	449	43.701	17.904	7.332	1.00	0.00	3A4
ATOM	3242	C	MET	449	39.772	13.984	3.951	1.00	0.00	3A4
ATOM	3243	O	MET	449	39.956	14.095	2.746	1.00	0.00	3A4
ATOM	3244	N	ASN	450	39.332	12.829	4.502	1.00	0.00	3A4
ATOM	3245	CA	ASN	450	39.098	11.625	3.740	1.00	0.00	3A4
ATOM	3246	CB	ASN	450	38.915	10.385	4.623	1.00	0.00	3A4
ATOM	3247	CG	ASN	450	37.685	10.130	5.531	1.00	0.00	3A4
ATOM	3248	OD1	ASN	450	36.512	10.268	5.191	1.00	0.00	3A4
ATOM	3249	ND2	ASN	450	37.990	9.606	6.751	1.00	0.00	3A4
ATOM	3250	C	ASN	450	37.976	11.740	2.750	1.00	0.00	3A4
ATOM	3251	O	ASN	450	38.095	11.281	1.623	1.00	0.00	3A4
ATOM	3252	N	MET	451	36.874	12.422	3.129	1.00	0.00	3A4
ATOM	3253	CA	MET	451	35.744	12.687	2.267	1.00	0.00	3A4
ATOM	3254	CB	MET	451	34.596	13.445	3.021	1.00	0.00	3A4
ATOM	3255	CG	MET	451	33.788	12.610	4.010	1.00	0.00	3A4
ATOM	3256	SD	MET	451	32.502	13.565	4.863	1.00	0.00	3A4
ATOM	3257	CE	MET	451	33.061	13.383	6.570	1.00	0.00	3A4
ATOM	3258	C	MET	451	36.081	13.580	1.106	1.00	0.00	3A4
ATOM	3259	O	MET	451	35.746	13.314	-0.041	1.00	0.00	3A4
ATOM	3260	N	LYS	452	36.821	14.667	1.389	1.00	0.00	3A4
ATOM	3261	CA	LYS	452	37.237	15.652	0.424	1.00	0.00	3A4
ATOM	3262	CB	LYS	452	37.854	16.860	1.154	1.00	0.00	3A4
ATOM	3263	CG	LYS	452	37.750	18.227	0.470	1.00	0.00	3A4
ATOM	3264	CD	LYS	452	38.346	19.380	1.301	1.00	0.00	3A4
ATOM	3265	CE	LYS	452	38.006	19.391	2.808	1.00	0.00	3A4
ATOM	3266	NZ	LYS	452	36.543	19.337	3.053	1.00	0.00	3A4
ATOM	3267	C	LYS	452	38.228	15.110	-0.572	1.00	0.00	3A4
ATOM	3268	O	LYS	452	38.108	15.335	-1.769	1.00	0.00	3A4
ATOM	3269	N	LEU	453	39.207	14.309	-0.102	1.00	0.00	3A4

ATOM	3270	CA	LEU	453	40.212	13.676	-0.927	1.00	0.00	3A4
ATOM	3271	CB	LEU	453	41.342	13.071	-0.061	1.00	0.00	3A4
ATOM	3272	CG	LEU	453	42.298	14.219	0.403	1.00	0.00	3A4
ATOM	3273	CD1	LEU	453	43.187	13.854	1.595	1.00	0.00	3A4
ATOM	3274	CD2	LEU	453	43.191	14.764	-0.734	1.00	0.00	3A4
ATOM	3275	C	LEU	453	39.621	12.644	-1.845	1.00	0.00	3A4
ATOM	3276	O	LEU	453	39.939	12.613	-3.026	1.00	0.00	3A4
ATOM	3277	N	ALA	454	38.662	11.829	-1.353	1.00	0.00	3A4
ATOM	3278	CA	ALA	454	37.935	10.847	-2.131	1.00	0.00	3A4
ATOM	3279	CB	ALA	454	37.013	9.992	-1.240	1.00	0.00	3A4
ATOM	3280	C	ALA	454	37.093	11.464	-3.225	1.00	0.00	3A4
ATOM	3281	O	ALA	454	37.181	11.055	-4.371	1.00	0.00	3A4
ATOM	3282	N	LEU	455	36.307	12.514	-2.904	1.00	0.00	3A4
ATOM	3283	CA	LEU	455	35.457	13.201	-3.852	1.00	0.00	3A4
ATOM	3284	CB	LEU	455	34.480	14.157	-3.157	1.00	0.00	3A4
ATOM	3285	CG	LEU	455	33.366	13.559	-2.303	1.00	0.00	3A4
ATOM	3286	CD1	LEU	455	32.576	14.761	-1.760	1.00	0.00	3A4
ATOM	3287	CD2	LEU	455	32.474	12.556	-3.064	1.00	0.00	3A4
ATOM	3288	C	LEU	455	36.203	14.018	-4.886	1.00	0.00	3A4
ATOM	3289	O	LEU	455	35.736	14.147	-6.009	1.00	0.00	3A4
ATOM	3290	N	ILE	456	37.412	14.540	-4.555	1.00	0.00	3A4
ATOM	3291	CA	ILE	456	38.284	15.264	-5.474	1.00	0.00	3A4
ATOM	3292	CB	ILE	456	39.413	16.061	-4.749	1.00	0.00	3A4
ATOM	3293	CG2	ILE	456	40.832	16.074	-5.412	1.00	0.00	3A4
ATOM	3294	CG1	ILE	456	39.003	17.537	-4.565	1.00	0.00	3A4
ATOM	3295	CD	ILE	456	38.041	17.823	-3.423	1.00	0.00	3A4
ATOM	3296	C	ILE	456	38.894	14.318	-6.496	1.00	0.00	3A4
ATOM	3297	O	ILE	456	39.099	14.677	-7.647	1.00	0.00	3A4
ATOM	3298	N	ARG	457	39.181	13.066	-6.083	1.00	0.00	3A4
ATOM	3299	CA	ARG	457	39.859	12.081	-6.895	1.00	0.00	3A4
ATOM	3300	CB	ARG	457	40.758	11.186	-6.025	1.00	0.00	3A4
ATOM	3301	CG	ARG	457	41.905	12.005	-5.430	1.00	0.00	3A4
ATOM	3302	CD	ARG	457	42.735	11.300	-4.341	1.00	0.00	3A4
ATOM	3303	NE	ARG	457	43.559	12.343	-3.632	1.00	0.00	3A4
ATOM	3304	CZ	ARG	457	44.624	12.985	-4.211	1.00	0.00	3A4
ATOM	3305	NH1	ARG	457	45.148	14.087	-3.601	1.00	0.00	3A4
ATOM	3306	NH2	ARG	457	45.174	12.558	-5.385	1.00	0.00	3A4
ATOM	3307	C	ARG	457	38.924	11.235	-7.722	1.00	0.00	3A4
ATOM	3308	O	ARG	457	39.246	10.873	-8.848	1.00	0.00	3A4
ATOM	3309	N	VAL	458	37.713	10.918	-7.207	1.00	0.00	3A4
ATOM	3310	CA	VAL	458	36.711	10.092	-7.872	1.00	0.00	3A4
ATOM	3311	CB	VAL	458	35.631	9.662	-6.887	1.00	0.00	3A4
ATOM	3312	CG1	VAL	458	34.290	9.133	-7.471	1.00	0.00	3A4
ATOM	3313	CG2	VAL	458	36.253	8.556	-6.006	1.00	0.00	3A4
ATOM	3314	C	VAL	458	36.101	10.798	-9.063	1.00	0.00	3A4
ATOM	3315	O	VAL	458	36.040	10.236	-10.146	1.00	0.00	3A4
ATOM	3316	N	LEU	459	35.685	12.071	-8.900	1.00	0.00	3A4
ATOM	3317	CA	LEU	459	34.979	12.841	-9.906	1.00	0.00	3A4
ATOM	3318	CB	LEU	459	34.354	14.096	-9.255	1.00	0.00	3A4
ATOM	3319	CG	LEU	459	33.225	13.778	-8.265	1.00	0.00	3A4
ATOM	3320	CD1	LEU	459	32.786	15.037	-7.500	1.00	0.00	3A4
ATOM	3321	CD2	LEU	459	32.041	13.132	-8.991	1.00	0.00	3A4
ATOM	3322	C	LEU	459	35.826	13.309	-11.060	1.00	0.00	3A4
ATOM	3323	O	LEU	459	35.319	13.601	-12.136	1.00	0.00	3A4
ATOM	3324	N	GLN	460	37.158	13.371	-10.874	1.00	0.00	3A4
ATOM	3325	CA	GLN	460	38.070	13.748	-11.927	1.00	0.00	3A4
ATOM	3326	CB	GLN	460	39.373	14.365	-11.376	1.00	0.00	3A4
ATOM	3327	CG	GLN	460	39.106	15.740	-10.736	1.00	0.00	3A4
ATOM	3328	CD	GLN	460	40.408	16.286	-10.160	1.00	0.00	3A4
ATOM	3329	OE1	GLN	460	41.430	15.608	-10.237	1.00	0.00	3A4
ATOM	3330	NE2	GLN	460	40.380	17.515	-9.575	1.00	0.00	3A4
ATOM	3331	C	GLN	460	38.365	12.562	-12.815	1.00	0.00	3A4
ATOM	3332	O	GLN	460	38.683	12.730	-13.990	1.00	0.00	3A4
ATOM	3333	N	ASN	461	38.258	11.332	-12.266	1.00	0.00	3A4
ATOM	3334	CA	ASN	461	38.598	10.113	-12.957	1.00	0.00	3A4
ATOM	3335	CB	ASN	461	39.328	9.125	-12.018	1.00	0.00	3A4
ATOM	3336	CG	ASN	461	40.725	9.722	-11.730	1.00	0.00	3A4
ATOM	3337	OD1	ASN	461	41.364	10.283	-12.617	1.00	0.00	3A4
ATOM	3338	ND2	ASN	461	41.239	9.604	-10.482	1.00	0.00	3A4
ATOM	3339	C	ASN	461	37.402	9.427	-13.562	1.00	0.00	3A4
ATOM	3340	O	ASN	461	37.588	8.603	-14.451	1.00	0.00	3A4
ATOM	3341	N	PHE	462	36.167	9.725	-13.107	1.00	0.00	3A4

```
ATOM   3342  CA  PHE   462      34.983   8.975 -13.533  1.00  0.00          3A4
ATOM   3343  CB  PHE   462      34.346   8.159 -12.354  1.00  0.00          3A4
ATOM   3344  CG  PHE   462      35.274   7.073 -11.873  1.00  0.00          3A4
ATOM   3345  CD1 PHE   462      35.686   6.051 -12.745  1.00  0.00          3A4
ATOM   3346  CD2 PHE   462      35.718   7.025 -10.540  1.00  0.00          3A4
ATOM   3347  CE1 PHE   462      36.530   5.021 -12.307  1.00  0.00          3A4
ATOM   3348  CE2 PHE   462      36.561   6.001 -10.089  1.00  0.00          3A4
ATOM   3349  CZ  PHE   462      36.972   5.002 -10.978  1.00  0.00          3A4
ATOM   3350  C   PHE   462      33.836   9.848 -14.135  1.00  0.00          3A4
ATOM   3351  O   PHE   462      33.734  11.037 -13.828  1.00  0.00          3A4
ATOM   3352  N   SER   463      32.784   9.198 -15.007  1.00  0.00          3A4
ATOM   3353  CA  SER   463      31.446   9.622 -15.542  1.00  0.00          3A4
ATOM   3354  CB  SER   463      31.400   9.685 -17.094  1.00  0.00          3A4
ATOM   3355  OG  SER   463      32.293  10.684 -17.565  1.00  0.00          3A4
ATOM   3356  C   SER   463      30.513   8.581 -15.014  1.00  0.00          3A4
ATOM   3357  O   SER   463      30.243   7.578 -15.673  1.00  0.00          3A4
ATOM   3358  N   PHE   464      30.012   8.774 -13.767  1.00  0.00          3A4
ATOM   3359  CA  PHE   464      29.251   7.754 -13.078  1.00  0.00          3A4
ATOM   3360  CB  PHE   464      29.689   7.483 -11.603  1.00  0.00          3A4
ATOM   3361  CG  PHE   464      29.600   8.582 -10.565  1.00  0.00          3A4
ATOM   3362  CD1 PHE   464      30.780   9.102  -9.999  1.00  0.00          3A4
ATOM   3363  CD2 PHE   464      28.364   8.952  -9.990  1.00  0.00          3A4
ATOM   3364  CE1 PHE   464      30.727   9.958  -8.891  1.00  0.00          3A4
ATOM   3365  CE2 PHE   464      28.310   9.832  -8.899  1.00  0.00          3A4
ATOM   3366  CZ  PHE   464      29.493  10.333  -8.347  1.00  0.00          3A4
ATOM   3367  C   PHE   464      27.768   7.948 -13.199  1.00  0.00          3A4
ATOM   3368  O   PHE   464      27.238   9.056 -13.175  1.00  0.00          3A4
ATOM   3369  N   LYS   465      27.076   6.801 -13.331  1.00  0.00          3A4
ATOM   3370  CA  LYS   465      25.646   6.719 -13.439  1.00  0.00          3A4
ATOM   3371  CB  LYS   465      25.197   6.398 -14.891  1.00  0.00          3A4
ATOM   3372  CG  LYS   465      25.553   7.484 -15.915  1.00  0.00          3A4
ATOM   3373  CD  LYS   465      25.067   7.162 -17.333  1.00  0.00          3A4
ATOM   3374  CE  LYS   465      25.438   8.228 -18.374  1.00  0.00          3A4
ATOM   3375  NZ  LYS   465      26.910   8.360 -18.512  1.00  0.00          3A4
ATOM   3376  C   LYS   465      25.212   5.614 -12.507  1.00  0.00          3A4
ATOM   3377  O   LYS   465      25.982   4.688 -12.254  1.00  0.00          3A4
ATOM   3378  N   PRO   466      23.983   5.622 -11.985  1.00  0.00          3A4
ATOM   3379  CA  PRO   466      23.422   4.511 -11.249  1.00  0.00          3A4
ATOM   3380  CD  PRO   466      23.090   6.783 -11.993  1.00  0.00          3A4
ATOM   3381  CB  PRO   466      22.300   5.151 -10.405  1.00  0.00          3A4
ATOM   3382  CG  PRO   466      21.827   6.358 -11.228  1.00  0.00          3A4
ATOM   3383  C   PRO   466      22.906   3.470 -12.228  1.00  0.00          3A4
ATOM   3384  O   PRO   466      22.333   3.808 -13.264  1.00  0.00          3A4
ATOM   3385  N   CYS   467      23.088   2.179 -11.890  1.00  0.00          3A4
ATOM   3386  CA  CYS   467      22.624   1.049 -12.667  1.00  0.00          3A4
ATOM   3387  CB  CYS   467      23.617  -0.143 -12.501  1.00  0.00          3A4
ATOM   3388  SG  CYS   467      23.434  -1.534 -13.674  1.00  0.00          3A4
ATOM   3389  C   CYS   467      21.212   0.659 -12.220  1.00  0.00          3A4
ATOM   3390  O   CYS   467      20.555  -0.179 -12.834  1.00  0.00          3A4
ATOM   3391  N   LYS   468      20.726   1.325 -11.130  1.00  0.00          3A4
ATOM   3392  CA  LYS   468      19.389   1.282 -10.573  1.00  0.00          3A4
ATOM   3393  CB  LYS   468      19.406   1.410  -9.027  1.00  0.00          3A4
ATOM   3394  CG  LYS   468      20.290   0.367  -8.339  1.00  0.00          3A4
ATOM   3395  CD  LYS   468      20.136   0.413  -6.821  1.00  0.00          3A4
ATOM   3396  CE  LYS   468      21.077  -0.534  -6.078  1.00  0.00          3A4
ATOM   3397  NZ  LYS   468      20.807  -0.485  -4.626  1.00  0.00          3A4
ATOM   3398  C   LYS   468      18.586   2.429 -11.148  1.00  0.00          3A4
ATOM   3399  O   LYS   468      19.145   3.450 -11.548  1.00  0.00          3A4
ATOM   3400  N   GLU   469      17.238   2.263 -11.203  1.00  0.00          3A4
ATOM   3401  CA  GLU   469      16.301   3.177 -11.832  1.00  0.00          3A4
ATOM   3402  CB  GLU   469      15.428   2.446 -12.905  1.00  0.00          3A4
ATOM   3403  CG  GLU   469      16.234   1.719 -14.000  1.00  0.00          3A4
ATOM   3404  CD  GLU   469      17.104   2.712 -14.780  1.00  0.00          3A4
ATOM   3405  OE1 GLU   469      16.530   3.642 -15.407  1.00  0.00          3A4
ATOM   3406  OE2 GLU   469      18.355   2.551 -14.761  1.00  0.00          3A4
ATOM   3407  C   GLU   469      15.433   3.792 -10.753  1.00  0.00          3A4
ATOM   3408  O   GLU   469      15.841   3.909  -9.598  1.00  0.00          3A4
ATOM   3409  N   THR   470      14.183   4.182 -11.133  1.00  0.00          3A4
ATOM   3410  CA  THR   470      13.125   4.722 -10.289  1.00  0.00          3A4
ATOM   3411  CB  THR   470      12.400   5.877 -10.998  1.00  0.00          3A4
ATOM   3412  OG1 THR   470      11.519   6.597 -10.138  1.00  0.00          3A4
ATOM   3413  CG2 THR   470      11.657   5.427 -12.286  1.00  0.00          3A4
```

ATOM	3414	C	THR	470	12.198	3.578	-9.882	1.00	0.00	3A4
ATOM	3415	O	THR	470	11.456	3.677	-8.906	1.00	0.00	3A4
ATOM	3416	N	GLN	471	12.279	2.447	-10.640	1.00	0.00	3A4
ATOM	3417	CA	GLN	471	11.670	1.158	-10.385	1.00	0.00	3A4
ATOM	3418	CB	GLN	471	10.997	0.559	-11.656	1.00	0.00	3A4
ATOM	3419	CG	GLN	471	11.811	0.665	-12.967	1.00	0.00	3A4
ATOM	3420	CD	GLN	471	10.976	0.103	-14.119	1.00	0.00	3A4
ATOM	3421	OE1	GLN	471	10.763	-1.106	-14.193	1.00	0.00	3A4
ATOM	3422	NE2	GLN	471	10.489	0.985	-15.035	1.00	0.00	3A4
ATOM	3423	C	GLN	471	12.773	0.276	-9.839	1.00	0.00	3A4
ATOM	3424	O	GLN	471	13.605	-0.249	-10.577	1.00	0.00	3A4
ATOM	3425	N	ILE	472	12.809	0.178	-8.475	1.00	0.00	3A4
ATOM	3426	CA	ILE	472	13.847	-0.369	-7.600	1.00	0.00	3A4
ATOM	3427	CB	ILE	472	14.451	-1.737	-7.993	1.00	0.00	3A4
ATOM	3428	CG2	ILE	472	15.447	-2.232	-6.907	1.00	0.00	3A4
ATOM	3429	CG1	ILE	472	13.359	-2.820	-8.240	1.00	0.00	3A4
ATOM	3430	CD	ILE	472	12.440	-3.129	-7.050	1.00	0.00	3A4
ATOM	3431	C	ILE	472	14.926	0.710	-7.400	1.00	0.00	3A4
ATOM	3432	O	ILE	472	15.870	0.760	-8.188	1.00	0.00	3A4
ATOM	3433	N	PRO	473	14.837	1.594	-6.373	1.00	0.00	3A4
ATOM	3434	CA	PRO	473	15.865	2.553	-5.978	1.00	0.00	3A4
ATOM	3435	CD	PRO	473	13.607	1.778	-5.600	1.00	0.00	3A4
ATOM	3436	CB	PRO	473	15.047	3.657	-5.263	1.00	0.00	3A4
ATOM	3437	CG	PRO	473	13.885	2.910	-4.607	1.00	0.00	3A4
ATOM	3438	C	PRO	473	16.926	1.936	-5.117	1.00	0.00	3A4
ATOM	3439	O	PRO	473	17.147	0.726	-5.098	1.00	0.00	3A4
ATOM	3440	N	LEU	474	17.606	2.821	-4.384	1.00	0.00	3A4
ATOM	3441	CA	LEU	474	18.692	2.518	-3.506	1.00	0.00	3A4
ATOM	3442	CB	LEU	474	19.658	3.718	-3.467	1.00	0.00	3A4
ATOM	3443	CG	LEU	474	20.935	3.548	-2.623	1.00	0.00	3A4
ATOM	3444	CD1	LEU	474	22.187	3.637	-3.503	1.00	0.00	3A4
ATOM	3445	CD2	LEU	474	20.962	4.569	-1.472	1.00	0.00	3A4
ATOM	3446	C	LEU	474	18.157	2.198	-2.136	1.00	0.00	3A4
ATOM	3447	O	LEU	474	17.397	2.966	-1.547	1.00	0.00	3A4
ATOM	3448	N	LYS	475	18.561	1.016	-1.612	1.00	0.00	3A4
ATOM	3449	CA	LYS	475	18.133	0.502	-0.330	1.00	0.00	3A4
ATOM	3450	CB	LYS	475	18.199	-1.049	-0.249	1.00	0.00	3A4
ATOM	3451	CG	LYS	475	17.520	-1.656	0.999	1.00	0.00	3A4
ATOM	3452	CD	LYS	475	17.579	-3.189	1.074	1.00	0.00	3A4
ATOM	3453	CE	LYS	475	18.981	-3.776	1.311	1.00	0.00	3A4
ATOM	3454	NZ	LYS	475	19.572	-3.282	2.580	1.00	0.00	3A4
ATOM	3455	C	LYS	475	18.961	1.086	0.775	1.00	0.00	3A4
ATOM	3456	O	LYS	475	20.173	0.909	0.825	1.00	0.00	3A4
ATOM	3457	N	LEU	476	18.276	1.798	1.695	1.00	0.00	3A4
ATOM	3458	CA	LEU	476	18.860	2.419	2.855	1.00	0.00	3A4
ATOM	3459	CB	LEU	476	18.422	3.903	3.070	1.00	0.00	3A4
ATOM	3460	CG	LEU	476	16.930	4.243	3.360	1.00	0.00	3A4
ATOM	3461	CD1	LEU	476	16.813	5.725	3.764	1.00	0.00	3A4
ATOM	3462	CD2	LEU	476	15.956	3.930	2.201	1.00	0.00	3A4
ATOM	3463	C	LEU	476	18.580	1.579	4.038	1.00	0.00	3A4
ATOM	3464	O	LEU	476	17.524	0.970	4.149	1.00	0.00	3A4
ATOM	3465	N	SER	477	19.543	1.495	4.973	1.00	0.00	3A4
ATOM	3466	CA	SER	477	19.480	0.545	6.040	1.00	0.00	3A4
ATOM	3467	CB	SER	477	20.807	-0.220	6.343	1.00	0.00	3A4
ATOM	3468	OG	SER	477	20.584	-1.554	6.795	1.00	0.00	3A4
ATOM	3469	C	SER	477	18.826	1.150	7.228	1.00	0.00	3A4
ATOM	3470	O	SER	477	18.936	2.334	7.525	1.00	0.00	3A4
ATOM	3471	N	LEU	478	18.068	0.282	7.917	1.00	0.00	3A4
ATOM	3472	CA	LEU	478	17.386	0.588	9.132	1.00	0.00	3A4
ATOM	3473	CB	LEU	478	16.072	-0.245	9.288	1.00	0.00	3A4
ATOM	3474	CG	LEU	478	15.314	-0.208	10.653	1.00	0.00	3A4
ATOM	3475	CD1	LEU	478	14.954	1.206	11.152	1.00	0.00	3A4
ATOM	3476	CD2	LEU	478	14.057	-1.098	10.607	1.00	0.00	3A4
ATOM	3477	C	LEU	478	18.338	0.280	10.281	1.00	0.00	3A4
ATOM	3478	O	LEU	478	18.566	-0.855	10.665	1.00	0.00	3A4
ATOM	3479	N	GLY	479	18.982	1.308	10.841	1.00	0.00	3A4
ATOM	3480	CA	GLY	479	19.983	1.119	11.875	1.00	0.00	3A4
ATOM	3481	C	GLY	479	19.558	1.665	13.192	1.00	0.00	3A4
ATOM	3482	O	GLY	479	19.405	0.936	14.154	1.00	0.00	3A4
ATOM	3483	N	GLY	480	19.416	2.996	13.329	1.00	0.00	3A4
ATOM	3484	CA	GLY	480	19.205	3.607	14.623	1.00	0.00	3A4
ATOM	3485	C	GLY	480	20.442	4.355	14.943	1.00	0.00	3A4

ATOM	3486	O	GLY	480	20.430	5.574	14.961	1.00	0.00	3A4
ATOM	3487	N	LEU	481	21.566	3.643	15.196	1.00	0.00	3A4
ATOM	3488	CA	LEU	481	22.833	4.218	15.597	1.00	0.00	3A4
ATOM	3489	CB	LEU	481	23.634	3.303	16.586	1.00	0.00	3A4
ATOM	3490	CG	LEU	481	23.971	1.830	16.194	1.00	0.00	3A4
ATOM	3491	CD1	LEU	481	25.057	1.273	17.135	1.00	0.00	3A4
ATOM	3492	CD2	LEU	481	22.767	0.861	16.168	1.00	0.00	3A4
ATOM	3493	C	LEU	481	23.664	4.637	14.398	1.00	0.00	3A4
ATOM	3494	O	LEU	481	24.121	5.774	14.349	1.00	0.00	3A4
ATOM	3495	N	LEU	482	23.838	3.733	13.398	1.00	0.00	3A4
ATOM	3496	CA	LEU	482	24.486	3.984	12.124	1.00	0.00	3A4
ATOM	3497	CB	LEU	482	25.613	2.951	11.765	1.00	0.00	3A4
ATOM	3498	CG	LEU	482	26.965	3.067	12.517	1.00	0.00	3A4
ATOM	3499	CD1	LEU	482	27.722	4.365	12.213	1.00	0.00	3A4
ATOM	3500	CD2	LEU	482	26.897	2.808	14.028	1.00	0.00	3A4
ATOM	3501	C	LEU	482	23.378	3.835	11.115	1.00	0.00	3A4
ATOM	3502	O	LEU	482	22.784	2.766	11.044	1.00	0.00	3A4
ATOM	3503	N	GLN	483	23.090	4.887	10.291	1.00	0.00	3A4
ATOM	3504	CA	GLN	483	22.131	4.849	9.194	1.00	0.00	3A4
ATOM	3505	CB	GLN	483	21.199	6.105	9.194	1.00	0.00	3A4
ATOM	3506	CG	GLN	483	20.316	6.274	10.449	1.00	0.00	3A4
ATOM	3507	CD	GLN	483	19.134	5.295	10.458	1.00	0.00	3A4
ATOM	3508	OE1	GLN	483	18.982	4.423	9.605	1.00	0.00	3A4
ATOM	3509	NE2	GLN	483	18.236	5.459	11.467	1.00	0.00	3A4
ATOM	3510	C	GLN	483	22.916	4.815	7.900	1.00	0.00	3A4
ATOM	3511	O	GLN	483	23.541	5.820	7.606	1.00	0.00	3A4
ATOM	3512	N	PRO	484	22.951	3.748	7.093	1.00	0.00	3A4
ATOM	3513	CA	PRO	484	23.817	3.721	5.925	1.00	0.00	3A4
ATOM	3514	CD	PRO	484	22.874	2.409	7.687	1.00	0.00	3A4
ATOM	3515	CB	PRO	484	24.769	2.558	6.262	1.00	0.00	3A4
ATOM	3516	CG	PRO	484	23.861	1.520	6.915	1.00	0.00	3A4
ATOM	3517	C	PRO	484	23.035	3.412	4.673	1.00	0.00	3A4
ATOM	3518	O	PRO	484	21.816	3.307	4.680	1.00	0.00	3A4
ATOM	3519	N	GLU	485	23.773	3.212	3.562	1.00	0.00	3A4
ATOM	3520	CA	GLU	485	23.248	2.558	2.383	1.00	0.00	3A4
ATOM	3521	CB	GLU	485	23.098	3.493	1.177	1.00	0.00	3A4
ATOM	3522	CG	GLU	485	24.327	4.316	0.781	1.00	0.00	3A4
ATOM	3523	CD	GLU	485	24.829	3.771	-0.540	1.00	0.00	3A4
ATOM	3524	OE1	GLU	485	24.837	4.541	-1.536	1.00	0.00	3A4
ATOM	3525	OE2	GLU	485	25.209	2.571	-0.567	1.00	0.00	3A4
ATOM	3526	C	GLU	485	24.043	1.288	2.206	1.00	0.00	3A4
ATOM	3527	O	GLU	485	25.260	1.289	2.296	1.00	0.00	3A4
ATOM	3528	N	LYS	486	23.368	0.126	2.027	1.00	0.00	3A4
ATOM	3529	CA	LYS	486	24.038	-1.172	1.973	1.00	0.00	3A4
ATOM	3530	CB	LYS	486	23.286	-2.272	2.791	1.00	0.00	3A4
ATOM	3531	CG	LYS	486	24.070	-3.558	3.141	1.00	0.00	3A4
ATOM	3532	CD	LYS	486	24.136	-4.672	2.074	1.00	0.00	3A4
ATOM	3533	CE	LYS	486	22.782	-5.249	1.626	1.00	0.00	3A4
ATOM	3534	NZ	LYS	486	22.037	-5.839	2.765	1.00	0.00	3A4
ATOM	3535	C	LYS	486	24.427	-1.507	0.545	1.00	0.00	3A4
ATOM	3536	O	LYS	486	25.595	-1.841	0.334	1.00	0.00	3A4
ATOM	3537	N	PRO	487	23.564	-1.396	-0.475	1.00	0.00	3A4
ATOM	3538	CA	PRO	487	23.980	-1.646	-1.846	1.00	0.00	3A4
ATOM	3539	CD	PRO	487	22.127	-1.666	-0.334	1.00	0.00	3A4
ATOM	3540	CB	PRO	487	22.967	-2.687	-2.354	1.00	0.00	3A4
ATOM	3541	CG	PRO	487	21.658	-2.329	-1.638	1.00	0.00	3A4
ATOM	3542	C	PRO	487	23.927	-0.353	-2.647	1.00	0.00	3A4
ATOM	3543	O	PRO	487	22.999	0.443	-2.510	1.00	0.00	3A4
ATOM	3544	N	VAL	488	24.915	-0.147	-3.541	1.00	0.00	3A4
ATOM	3545	CA	VAL	488	24.946	1.001	-4.417	1.00	0.00	3A4
ATOM	3546	CB	VAL	488	25.614	2.234	-3.794	1.00	0.00	3A4
ATOM	3547	CG1	VAL	488	26.927	1.920	-3.030	1.00	0.00	3A4
ATOM	3548	CG2	VAL	488	25.731	3.431	-4.776	1.00	0.00	3A4
ATOM	3549	C	VAL	488	25.663	0.556	-5.657	1.00	0.00	3A4
ATOM	3550	O	VAL	488	26.886	0.485	-5.692	1.00	0.00	3A4
ATOM	3551	N	VAL	489	24.905	0.264	-6.743	1.00	0.00	3A4
ATOM	3552	CA	VAL	489	25.452	-0.202	-8.007	1.00	0.00	3A4
ATOM	3553	CB	VAL	489	24.587	-1.266	-8.687	1.00	0.00	3A4
ATOM	3554	CG1	VAL	489	25.369	-1.938	-9.848	1.00	0.00	3A4
ATOM	3555	CG2	VAL	489	24.212	-2.339	-7.638	1.00	0.00	3A4
ATOM	3556	C	VAL	489	25.702	0.999	-8.916	1.00	0.00	3A4
ATOM	3557	O	VAL	489	24.854	1.864	-9.093	1.00	0.00	3A4

ATOM	3558	N	LEU	490	26.915	1.064	-9.499	1.00	0.00	3A4
ATOM	3559	CA	LEU	490	27.387	2.104	-10.386	1.00	0.00	3A4
ATOM	3560	CB	LEU	490	28.695	2.765	-9.828	1.00	0.00	3A4
ATOM	3561	CG	LEU	490	29.556	3.732	-10.717	1.00	0.00	3A4
ATOM	3562	CD1	LEU	490	30.364	4.675	-9.816	1.00	0.00	3A4
ATOM	3563	CD2	LEU	490	30.579	3.092	-11.694	1.00	0.00	3A4
ATOM	3564	C	LEU	490	27.689	1.443	-11.710	1.00	0.00	3A4
ATOM	3565	O	LEU	490	28.311	0.382	-11.714	1.00	0.00	3A4
ATOM	3566	N	LYS	491	27.223	2.080	-12.824	1.00	0.00	3A4
ATOM	3567	CA	LYS	491	27.177	1.589	-14.188	1.00	0.00	3A4
ATOM	3568	CB	LYS	491	25.982	2.230	-14.965	1.00	0.00	3A4
ATOM	3569	CG	LYS	491	25.687	1.704	-16.388	1.00	0.00	3A4
ATOM	3570	CD	LYS	491	25.319	0.219	-16.460	1.00	0.00	3A4
ATOM	3571	CE	LYS	491	25.043	-0.263	-17.889	1.00	0.00	3A4
ATOM	3572	NZ	LYS	491	24.678	-1.699	-17.899	1.00	0.00	3A4
ATOM	3573	C	LYS	491	28.494	1.812	-14.912	1.00	0.00	3A4
ATOM	3574	O	LYS	491	29.380	0.964	-14.854	1.00	0.00	3A4
ATOM	3575	N	VAL	492	28.641	2.966	-15.620	1.00	0.00	3A4
ATOM	3576	CA	VAL	492	29.700	3.255	-16.574	1.00	0.00	3A4
ATOM	3577	CB	VAL	492	29.112	3.889	-17.838	1.00	0.00	3A4
ATOM	3578	CG1	VAL	492	28.415	5.242	-17.560	1.00	0.00	3A4
ATOM	3579	CG2	VAL	492	30.130	3.946	-19.001	1.00	0.00	3A4
ATOM	3580	C	VAL	492	30.777	4.082	-15.898	1.00	0.00	3A4
ATOM	3581	O	VAL	492	30.519	4.769	-14.911	1.00	0.00	3A4
ATOM	3582	N	GLU	493	32.030	3.983	-16.415	1.00	0.00	3A4
ATOM	3583	CA	GLU	493	33.215	4.574	-15.836	1.00	0.00	3A4
ATOM	3584	CB	GLU	493	33.962	3.566	-14.901	1.00	0.00	3A4
ATOM	3585	CG	GLU	493	34.397	2.206	-15.502	1.00	0.00	3A4
ATOM	3586	CD	GLU	493	35.792	2.272	-16.141	1.00	0.00	3A4
ATOM	3587	OE1	GLU	493	36.769	2.568	-15.402	1.00	0.00	3A4
ATOM	3588	OE2	GLU	493	35.901	2.024	-17.372	1.00	0.00	3A4
ATOM	3589	C	GLU	493	34.100	5.031	-16.967	1.00	0.00	3A4
ATOM	3590	O	GLU	493	33.928	4.629	-18.117	1.00	0.00	3A4
ATOM	3591	N	SER	494	35.109	5.874	-16.624	1.00	0.00	3A4
ATOM	3592	CA	SER	494	36.209	6.283	-17.480	1.00	0.00	3A4
ATOM	3593	CB	SER	494	36.076	7.748	-18.010	1.00	0.00	3A4
ATOM	3594	OG	SER	494	35.765	8.692	-16.990	1.00	0.00	3A4
ATOM	3595	C	SER	494	37.455	6.059	-16.647	1.00	0.00	3A4
ATOM	3596	O	SER	494	37.360	5.784	-15.452	1.00	0.00	3A4
ATOM	3597	N	ARG	495	38.664	6.138	-17.262	1.00	0.00	3A4
ATOM	3598	CA	ARG	495	39.886	5.740	-16.587	1.00	0.00	3A4
ATOM	3599	CB	ARG	495	40.090	4.192	-16.590	1.00	0.00	3A4
ATOM	3600	CG	ARG	495	39.845	3.452	-17.916	1.00	0.00	3A4
ATOM	3601	CD	ARG	495	39.764	1.935	-17.697	1.00	0.00	3A4
ATOM	3602	NE	ARG	495	39.301	1.272	-18.966	1.00	0.00	3A4
ATOM	3603	CZ	ARG	495	38.710	0.032	-18.992	1.00	0.00	3A4
ATOM	3604	NH1	ARG	495	38.289	-0.478	-20.185	1.00	0.00	3A4
ATOM	3605	NH2	ARG	495	38.527	-0.702	-17.853	1.00	0.00	3A4
ATOM	3606	C	ARG	495	41.073	6.436	-17.202	1.00	0.00	3A4
ATOM	3607	O	ARG	495	41.144	6.643	-18.413	1.00	0.00	3A4
ATOM	3608	N	ASP	496	42.044	6.804	-16.320	1.00	0.00	3A4
ATOM	3609	CA	ASP	496	43.290	7.471	-16.647	1.00	0.00	3A4
ATOM	3610	CB	ASP	496	43.159	9.025	-16.860	1.00	0.00	3A4
ATOM	3611	CG	ASP	496	42.410	9.788	-15.743	1.00	0.00	3A4
ATOM	3612	OD1	ASP	496	43.070	10.614	-15.056	1.00	0.00	3A4
ATOM	3613	OD2	ASP	496	41.179	9.574	-15.577	1.00	0.00	3A4
ATOM	3614	C	ASP	496	44.272	7.071	-15.553	1.00	0.00	3A4
ATOM	3615	O	ASP	496	44.432	5.882	-15.283	1.00	0.00	3A4
ATOM	3616	N	GLY	497	44.958	8.050	-14.898	1.00	0.00	3A4
ATOM	3617	CA	GLY	497	45.950	7.790	-13.872	1.00	0.00	3A4
ATOM	3618	C	GLY	497	46.123	9.024	-13.031	1.00	0.00	3A4
ATOM	3619	O	GLY	497	46.262	10.127	-13.557	1.00	0.00	3A4
ATOM	3620	N	THR	498	46.127	8.846	-11.677	1.00	0.00	3A4
ATOM	3621	CA	THR	498	46.355	9.879	-10.674	1.00	0.00	3A4
ATOM	3622	CB	THR	498	45.075	10.401	-9.995	1.00	0.00	3A4
ATOM	3623	OG1	THR	498	44.194	9.349	-9.600	1.00	0.00	3A4
ATOM	3624	CG2	THR	498	44.332	11.355	-10.957	1.00	0.00	3A4
ATOM	3625	C	THR	498	47.290	9.274	-9.640	1.00	0.00	3A4
ATOM	3626	O	THR	498	47.189	8.089	-9.326	1.00	0.00	3A4
ATOM	3627	N	VAL	499	48.205	10.109	-9.074	1.00	0.00	3A4
ATOM	3628	CA	VAL	499	49.121	9.727	-8.014	1.00	0.00	3A4
ATOM	3629	CB	VAL	499	50.272	8.816	-8.476	1.00	0.00	3A4

```
ATOM   3630  CG1 VAL   499      51.133   9.436  -9.607  1.00  0.00          3A4
ATOM   3631  CG2 VAL   499      51.110   8.313  -7.273  1.00  0.00          3A4
ATOM   3632  C   VAL   499      49.614  11.021  -7.391  1.00  0.00          3A4
ATOM   3633  O   VAL   499      49.977  11.961  -8.097  1.00  0.00          3A4
ATOM   3634  N   SER   500      49.647  11.075  -6.030  1.00  0.00          3A4
ATOM   3635  CA  SER   500      50.251  12.152  -5.269  1.00  0.00          3A4
ATOM   3636  CB  SER   500      49.434  13.486  -5.230  1.00  0.00          3A4
ATOM   3637  OG  SER   500      48.086  13.306  -4.816  1.00  0.00          3A4
ATOM   3638  C   SER   500      50.524  11.618  -3.882  1.00  0.00          3A4
ATOM   3639  O   SER   500      49.694  10.933  -3.286  1.00  0.00          3A4
ATOM   3640  N   GLY   501      51.736  11.945  -3.355  1.00  0.00          3A4
ATOM   3641  CA  GLY   501      52.249  11.543  -2.061  1.00  0.00          3A4
ATOM   3642  C   GLY   501      53.489  10.727  -2.291  1.00  0.00          3A4
ATOM   3643  O   GLY   501      54.576  11.087  -1.841  1.00  0.00          3A4
ATOM   3644  N   ALA   502      53.331   9.596  -3.020  1.00  0.00          3A4
ATOM   3645  CA  ALA   502      54.406   8.722  -3.424  1.00  0.00          3A4
ATOM   3646  CB  ALA   502      54.772   7.642  -2.379  1.00  0.00          3A4
ATOM   3647  C   ALA   502      53.912   8.031  -4.704  1.00  0.00          3A4
ATOM   3648  OT1 ALA   502      54.439   8.364  -5.800  1.00  0.00          3A4
ATOM   3649  OT2 ALA   502      52.987   7.178  -4.607  1.00  0.00          3A4
TER    3650       ALA   502
HETATM 3651  FE  HEM   600      33.118  10.391  15.288  1.00  0.00          HEM
HETATM 3652  NA  HEM   600      31.497  11.115  16.171  1.00  0.00          HEM
HETATM 3653  NB  HEM   600      32.274  10.658  13.514  1.00  0.00          HEM
HETATM 3654  NC  HEM   600      34.752   9.684  14.430  1.00  0.00          HEM
HETATM 3655  ND  HEM   600      33.949  10.106  17.065  1.00  0.00          HEM
HETATM 3656  C1A HEM   600      31.254  11.251  17.515  1.00  0.00          HEM
HETATM 3657  C2A HEM   600      29.887  11.659  17.752  1.00  0.00          HEM
HETATM 3658  C3A HEM   600      29.316  11.871  16.542  1.00  0.00          HEM
HETATM 3659  C4A HEM   600      30.322  11.523  15.568  1.00  0.00          HEM
HETATM 3660  C1B HEM   600      31.012  11.136  13.233  1.00  0.00          HEM
HETATM 3661  C2B HEM   600      30.761  11.218  11.804  1.00  0.00          HEM
HETATM 3662  C3B HEM   600      31.901  10.761  11.185  1.00  0.00          HEM
HETATM 3663  C4B HEM   600      32.828  10.426  12.273  1.00  0.00          HEM
HETATM 3664  C1C HEM   600      35.044   9.645  13.089  1.00  0.00          HEM
HETATM 3665  C2C HEM   600      36.395   9.168  12.838  1.00  0.00          HEM
HETATM 3666  C3C HEM   600      36.920   8.833  14.067  1.00  0.00          HEM
HETATM 3667  C4C HEM   600      35.879   9.167  15.033  1.00  0.00          HEM
HETATM 3668  C1D HEM   600      35.150   9.494  17.358  1.00  0.00          HEM
HETATM 3669  C2D HEM   600      35.382   9.408  18.787  1.00  0.00          HEM
HETATM 3670  C3D HEM   600      34.329  10.035  19.375  1.00  0.00          HEM
HETATM 3671  C4D HEM   600      33.438  10.439  18.306  1.00  0.00          HEM
HETATM 3672  CHA HEM   600      32.186  10.978  18.500  1.00  0.00          HEM
HETATM 3673  CHB HEM   600      30.115  11.530  14.204  1.00  0.00          HEM
HETATM 3674  CHC HEM   600      34.131   9.963  12.102  1.00  0.00          HEM
HETATM 3675  CHD HEM   600      36.032   9.062  16.407  1.00  0.00          HEM
HETATM 3676  CMA HEM   600      27.911  12.344  16.281  1.00  0.00          HEM
HETATM 3677  CAA HEM   600      29.208  11.695  19.088  1.00  0.00          HEM
HETATM 3678  CBA HEM   600      29,154  13.045  19.638  1.00  0.00          HEM
HETATM 3679  CGA HEM   600      28.459  13.237  20.946  1.00  0.00          HEM
HETATM 3680  O1A HEM   600      28.097  12.278  21.566  1.00  0.00          HEM
HETATM 3681  O2A HEM   600      28.217  14.323  21.438  1.00  0.00          HEM
HETATM 3682  CMB HEM   600      29.483  11.742  11.185  1.00  0.00          HEM
HETATM 3683  CAB HEM   600      32.219  10.602   9.818  1.00  0.00          HEM
HETATM 3684  CBB HEM   600      31.527  10.978   8.735  1.00  0.00          HEM
HETATM 3685  CMC HEM   600      37.047   9.116  11.471  1.00  0.00          HEM
HETATM 3686  CAC HEM   600      38.159   8.288  14.465  1.00  0.00          HEM
HETATM 3687  CBC HEM   600      39.265   8.069  13.758  1.00  0.00          HEM
HETATM 3688  CMD HEM   600      36.499   8.680  19.483  1.00  0.00          HEM
HETATM 3689  CAD HEM   600      34.101  10.253  20.849  1.00  0.00          HEM
HETATM 3690  CBD HEM   600      34.689  11.583  21.366  1.00  0.00          HEM
HETATM 3691  CGD HEM   600      34.355  11.863  22.843  1.00  0.00          HEM
HETATM 3692  O1D HEM   600      35.050  12.735  23.424  1.00  0.00          HEM
HETATM 3693  O2D HEM   600      33.381  11.284  23.380  1.00  0.00          HEM
END
```

Table 4 : Providing the coordinates of the CYP3A model

```
HEADER     CYP3A7
TITLE      MODEL OF HUMAN CYTOCHROME P450 CYP3A7
AUTHOR     N. LOISEAU,F.ANDRE,M.DELAFORGE,M.COTTEVIEILLE
SEQRES    1     459  PRO PHE LEU GLY ASN ALA LEU SER PHE ARG LYS GLY TYR
SEQRES    2     459  TRP THR PHE ASP MET GLU CYS TYR LYS LYS TYR ARG LYS
SEQRES    3     459  VAL TRP GLY ILE TYR ASP CYS GLN GLN PRO MET LEU ALA
SEQRES    4     459  ILE THR ASP PRO ASP MET ILE LYS THR VAL LEU VAL LYS
SEQRES    5     459  GLU CYS TYR SER VAL PHE THR ASN ARG ARG PRO PHE GLY
SEQRES    6     459  PRO VAL GLY PHE MET LYS ASN ALA ILE SER ILE ALA GLU
SEQRES    7     459  ASP GLU GLU TRP LYS ARG ILE ARG SER LEU LEU SER PRO
SEQRES    8     459  THR PHE THR SER GLY LYS LEU LYS GLU MET VAL PRO ILE
SEQRES    9     459  ILE ALA GLN TYR GLY ASP VAL LEU VAL ARG ASN LEU ARG
SEQRES   10     459  ARG GLU ALA GLU THR GLY LYS PRO VAL THR LEU LYS HIS
SEQRES   11     459  VAL PHE GLY ALA TYR SER MET ASP VAL ILE THR SER THR
SEQRES   12     459  SER PHE GLY VAL SER ILE ASP SER LEU ASN ASN PRO GLN
SEQRES   13     459  ASP PRO PHE VAL GLU ASN THR LYS LYS LEU LEU ARG PHE
SEQRES   14     459  ASN PRO LEU ASP PRO PHE VAL LEU SER ILE LYS VAL PHE
SEQRES   15     459  PRO PHE LEU THR PRO ILE LEU GLU ALA LEU ASN ILE THR
SEQRES   16     459  VAL PHE PRO ARG LYS VAL ILE SER PHE LEU THR LYS SER
SEQRES   17     459  VAL LYS GLN ILE LYS GLU GLY ARG LEU LYS GLU THR GLN
SEQRES   18     459  LYS HIS ARG VAL ASP PHE LEU GLN LEU MET ILE ASP SER
SEQRES   19     459  GLN ASN SER LYS ASP SER GLU THR HIS LYS ALA LEU SER
SEQRES   20     459  ASP LEU GLU LEU MET ALA GLN SER ILE ILE PHE ILE PHE
SEQRES   21     459  ALA GLY TYR GLU THR THR SER SER VAL LEU SER PHE ILE
SEQRES   22     459  ILE TYR GLU LEU ALA THR HIS PRO ASP VAL GLN GLN LYS
SEQRES   23     459  VAL GLN LYS GLU ILE ASP THR VAL LEU PRO ASN LYS ALA
SEQRES   24     459  PRO PRO THR TYR ASP THR VAL LEU GLN LEU GLU TYR LEU
SEQRES   25     459  ASP MET VAL VAL ASN GLU THR LEU ARG LEU PHE PRO VAL
SEQRES   26     459  ALA MET ARG LEU GLU ARG VAL CYS LYS LYS ASP VAL GLU
SEQRES   27     459  ILE ASN GLY MET PHE ILE PRO LYS GLY VAL VAL VAL MET
SEQRES   28     459  ILE PRO SER TYR VAL LEU HIS HIS ASP PRO LYS TYR TRP
SEQRES   29     459  THR GLU PRO GLU LYS PHE LEU PRO GLU ARG PHE SER LYS
SEQRES   30     459  LYS ASN LYS ASP ASN ILE ASP PRO TYR ILE TYR THR PRO
SEQRES   31     459  PHE GLY SER GLY PRO ARG ASN CYS ILE GLY MET ARG PHE
SEQRES   32     459  ALA LEU VAL ASN MET LYS LEU ALA LEU VAL ARG VAL LEU
SEQRES   33     459  GLN ASN PHE SER PHE LYS PRO CYS LYS GLU THR GLN ILE
SEQRES   34     459  PRO LEU LYS LEU ARG PHE GLY GLY LEU LEU LEU THR GLU
SEQRES   35     459  LYS PRO ILE VAL LEU LYS ALA GLU SER ARG ASP GLU THR
SEQRES   36     459  VAL SER GLY ALA
HET     HEM     600
HETNAM HEM     HEME
HETSYN HEM     3,7,12,17-TETRAMETHYL-8,13-DIVINYL-2,18-PORPHINEDIPROPIONIC ACID
FORMUL HEM     C34 H34 N4 O4 FE1
ATOM       1  N   PRO    45      24.768   6.244  -5.895  1.00  0.00          3A7
ATOM       2  CD  PRO    45      25.053   5.448  -4.648  1.00  0.00          3A7
ATOM       3  CA  PRO    45      24.705   5.319  -7.064  1.00  0.00          3A7
ATOM       4  CB  PRO    45      24.467   3.950  -6.422  1.00  0.00          3A7
ATOM       5  CG  PRO    45      25.292   4.018  -5.139  1.00  0.00          3A7
ATOM       6  C   PRO    45      23.594   5.801  -7.950  1.00  0.00          3A7
ATOM       7  O   PRO    45      23.387   7.010  -8.057  1.00  0.00          3A7
ATOM       8  N   PHE    46      22.870   4.857  -8.600  1.00  0.00          3A7
ATOM       9  CA  PHE    46      21.751   5.140  -9.472  1.00  0.00          3A7
ATOM      10  CB  PHE    46      21.853   4.416 -10.835  1.00  0.00          3A7
ATOM      11  CG  PHE    46      23.083   4.887 -11.553  1.00  0.00          3A7
ATOM      12  CD1 PHE    46      24.173   4.033 -11.730  1.00  0.00          3A7
ATOM      13  CD2 PHE    46      23.155   6.189 -12.049  1.00  0.00          3A7
ATOM      14  CE1 PHE    46      25.317   4.474 -12.390  1.00  0.00          3A7
ATOM      15  CE2 PHE    46      24.297   6.633 -12.709  1.00  0.00          3A7
ATOM      16  CZ  PHE    46      25.380   5.775 -12.879  1.00  0.00          3A7
ATOM      17  C   PHE    46      20.491   4.691  -8.782  1.00  0.00          3A7
ATOM      18  O   PHE    46      19.400   5.166  -9.096  1.00  0.00          3A7
ATOM      19  N   LEU    47      20.629   3.749  -7.814  1.00  0.00          3A7
ATOM      20  CA  LEU    47      19.541   3.204  -7.035  1.00  0.00          3A7
ATOM      21  CB  LEU    47      19.661   1.667  -6.874  1.00  0.00          3A7
ATOM      22  CG  LEU    47      18.490   0.978  -6.129  1.00  0.00          3A7
ATOM      23  CD1 LEU    47      17.133   1.202  -6.826  1.00  0.00          3A7
ATOM      24  CD2 LEU    47      18.768  -0.526  -5.942  1.00  0.00          3A7
ATOM      25  C   LEU    47      19.573   3.860  -5.681  1.00  0.00          3A7
ATOM      26  O   LEU    47      20.619   3.930  -5.036  1.00  0.00          3A7
ATOM      27  N   GLY    48      18.396   4.349  -5.225  1.00  0.00          3A7
ATOM      28  CA  GLY    48      18.240   4.966  -3.933  1.00  0.00          3A7
```

ATOM	29	C	GLY	48	16.930	4.491	-3.395	1.00	0.00	3A7
ATOM	30	O	GLY	48	15.938	5.218	-3.414	1.00	0.00	3A7
ATOM	31	N	ASN	49	16.911	3.229	-2.898	1.00	0.00	3A7
ATOM	32	CA	ASN	49	15.741	2.585	-2.348	1.00	0.00	3A7
ATOM	33	CB	ASN	49	15.445	1.235	-3.059	1.00	0.00	3A7
ATOM	34	CG	ASN	49	14.046	0.705	-2.706	1.00	0.00	3A7
ATOM	35	OD1	ASN	49	13.035	1.349	-3.011	1.00	0.00	3A7
ATOM	36	ND2	ASN	49	14.005	-0.494	-2.051	1.00	0.00	3A7
ATOM	37	C	ASN	49	16.016	2.375	-0.880	1.00	0.00	3A7
ATOM	38	O	ASN	49	17.169	2.278	-0.463	1.00	0.00	3A7
ATOM	39	N	ALA	50	14.933	2.293	-0.065	1.00	0.00	3A7
ATOM	40	CA	ALA	50	14.998	2.111	1.369	1.00	0.00	3A7
ATOM	41	CB	ALA	50	13.847	2.834	2.098	1.00	0.00	3A7
ATOM	42	C	ALA	50	14.941	0.641	1.697	1.00	0.00	3A7
ATOM	43	O	ALA	50	13.866	0.049	1.787	1.00	0.00	3A7
ATOM	44	N	LEU	51	16.133	0.032	1.885	1.00	0.00	3A7
ATOM	45	CA	LEU	51	16.271	-1.360	2.232	1.00	0.00	3A7
ATOM	46	CB	LEU	51	16.271	-2.314	1.001	1.00	0.00	3A7
ATOM	47	CG	LEU	51	17.055	-1.862	-0.262	1.00	0.00	3A7
ATOM	48	CD1	LEU	51	18.587	-1.811	-0.098	1.00	0.00	3A7
ATOM	49	CD2	LEU	51	16.690	-2.765	-1.456	1.00	0.00	3A7
ATOM	50	C	LEU	51	17.550	-1.468	3.012	1.00	0.00	3A7
ATOM	51	O	LEU	51	18.327	-0.517	3.085	1.00	0.00	3A7
ATOM	52	N	SER	52	17.794	-2.657	3.613	1.00	0.00	3A7
ATOM	53	CA	SER	52	19.005	-2.956	4.343	1.00	0.00	3A7
ATOM	54	CB	SER	52	18.741	-3.361	5.821	1.00	0.00	3A7
ATOM	55	OG	SER	52	17.737	-4.363	5.945	1.00	0.00	3A7
ATOM	56	C	SER	52	19.734	-4.023	3.562	1.00	0.00	3A7
ATOM	57	O	SER	52	20.164	-3.782	2.435	1.00	0.00	3A7
ATOM	58	N	PHE	53	19.898	-5.231	4.155	1.00	0.00	3A7
ATOM	59	CA	PHE	53	20.599	-6.341	3.550	1.00	0.00	3A7
ATOM	60	CB	PHE	53	21.908	-6.703	4.297	1.00	0.00	3A7
ATOM	61	CG	PHE	53	22.730	-5.456	4.439	1.00	0.00	3A7
ATOM	62	CD1	PHE	53	22.819	-4.809	5.673	1.00	0.00	3A7
ATOM	63	CD2	PHE	53	23.346	-4.880	3.327	1.00	0.00	3A7
ATOM	64	CE1	PHE	53	23.491	-3.598	5.793	1.00	0.00	3A7
ATOM	65	CE2	PHE	53	24.018	-3.667	3.446	1.00	0.00	3A7
ATOM	66	CZ	PHE	53	24.085	-3.022	4.675	1.00	0.00	3A7
ATOM	67	C	PHE	53	19.639	-7.494	3.594	1.00	0.00	3A7
ATOM	68	O	PHE	53	19.885	-8.495	4.264	1.00	0.00	3A7
ATOM	69	N	ARG	54	18.491	-7.330	2.875	1.00	0.00	3A7
ATOM	70	CA	ARG	54	17.327	-8.205	2.828	1.00	0.00	3A7
ATOM	71	CB	ARG	54	17.629	-9.719	2.641	1.00	0.00	3A7
ATOM	72	CG	ARG	54	18.536	-10.045	1.437	1.00	0.00	3A7
ATOM	73	CD	ARG	54	17.996	-9.573	0.079	1.00	0.00	3A7
ATOM	74	NE	ARG	54	19.049	-9.836	-0.962	1.00	0.00	3A7
ATOM	75	CZ	ARG	54	19.036	-10.925	-1.791	1.00	0.00	3A7
ATOM	76	NH1	ARG	54	20.065	-11.113	-2.669	1.00	0.00	3A7
ATOM	77	NH2	ARG	54	18.013	-11.826	-1.753	1.00	0.00	3A7
ATOM	78	C	ARG	54	16.514	-7.983	4.087	1.00	0.00	3A7
ATOM	79	O	ARG	54	16.760	-8.611	5.116	1.00	0.00	3A7
ATOM	80	N	LYS	55	15.545	-7.030	4.028	1.00	0.00	3A7
ATOM	81	CA	LYS	55	14.927	-6.447	5.205	1.00	0.00	3A7
ATOM	82	CB	LYS	55	14.520	-4.971	5.023	1.00	0.00	3A7
ATOM	83	CG	LYS	55	13.327	-4.656	4.092	1.00	0.00	3A7
ATOM	84	CD	LYS	55	13.574	-4.842	2.582	1.00	0.00	3A7
ATOM	85	CE	LYS	55	13.074	-6.171	1.993	1.00	0.00	3A7
ATOM	86	NZ	LYS	55	11.612	-6.322	2.178	1.00	0.00	3A7
ATOM	87	C	LYS	55	13.767	-7.241	5.777	1.00	0.00	3A7
ATOM	88	O	LYS	55	13.403	-7.067	6.938	1.00	0.00	3A7
ATOM	89	N	GLY	56	13.158	-8.146	4.991	1.00	0.00	3A7
ATOM	90	CA	GLY	56	12.066	-8.950	5.491	1.00	0.00	3A7
ATOM	91	C	GLY	56	11.995	-10.146	4.604	1.00	0.00	3A7
ATOM	92	O	GLY	56	11.061	-10.334	3.823	1.00	0.00	3A7
ATOM	93	N	TYR	57	13.009	-11.031	4.730	1.00	0.00	3A7
ATOM	94	CA	TYR	57	13.171	-12.222	3.922	1.00	0.00	3A7
ATOM	95	CB	TYR	57	14.496	-12.913	4.319	1.00	0.00	3A7
ATOM	96	CG	TYR	57	15.183	-13.558	3.146	1.00	0.00	3A7
ATOM	97	CD1	TYR	57	15.496	-12.832	1.995	1.00	0.00	3A7
ATOM	98	CD2	TYR	57	15.566	-14.898	3.223	1.00	0.00	3A7
ATOM	99	CE1	TYR	57	16.160	-13.440	0.934	1.00	0.00	3A7
ATOM	100	CE2	TYR	57	16.240	-15.506	2.168	1.00	0.00	3A7

ATOM	101	CZ	TYR	57	16.538	-14.777	1.021	1.00	0.00	3A7
ATOM	102	OH	TYR	57	17.229	-15.392	-0.043	1.00	0.00	3A7
ATOM	103	C	TYR	57	12.013	-13.191	4.022	1.00	0.00	3A7
ATOM	104	O	TYR	57	11.631	-13.781	3.021	1.00	0.00	3A7
ATOM	105	N	TRP	58	11.379	-13.353	5.211	1.00	0.00	3A7
ATOM	106	CA	TRP	58	10.261	-14.269	5.359	1.00	0.00	3A7
ATOM	107	CB	TRP	58	9.872	-14.515	6.832	1.00	0.00	3A7
ATOM	108	CG	TRP	58	9.333	-13.318	7.606	1.00	0.00	3A7
ATOM	109	CD2	TRP	58	8.006	-13.247	8.157	1.00	0.00	3A7
ATOM	110	CD1	TRP	58	9.925	-12.115	7.871	1.00	0.00	3A7
ATOM	111	NE1	TRP	58	9.051	-11.297	8.548	1.00	0.00	3A7
ATOM	112	CE2	TRP	58	7.869	-11.978	8.741	1.00	0.00	3A7
ATOM	113	CE3	TRP	58	6.969	-14.158	8.175	1.00	0.00	3A7
ATOM	114	CZ2	TRP	58	6.694	-11.604	9.360	1.00	0.00	3A7
ATOM	115	CZ3	TRP	58	5.782	-13.780	8.796	1.00	0.00	3A7
ATOM	116	CH2	TRP	58	5.647	-12.522	9.382	1.00	0.00	3A7
ATOM	117	C	TRP	58	9.036	-13.824	4.612	1.00	0.00	3A7
ATOM	118	O	TRP	58	8.302	-14.664	4.106	1.00	0.00	3A7
ATOM	119	N	THR	59	8.780	-12.490	4.502	1.00	0.00	3A7
ATOM	120	CA	THR	59	7.645	-11.989	3.737	1.00	0.00	3A7
ATOM	121	CB	THR	59	7.213	-10.582	4.136	1.00	0.00	3A7
ATOM	122	OG1	THR	59	8.282	-9.643	4.073	1.00	0.00	3A7
ATOM	123	CG2	THR	59	6.673	-10.634	5.579	1.00	0.00	3A7
ATOM	124	C	THR	59	7.925	-12.067	2.267	1.00	0.00	3A7
ATOM	125	O	THR	59	7.011	-12.232	1.471	1.00	0.00	3A7
ATOM	126	N	PHE	60	9.218	-12.018	1.884	1.00	0.00	3A7
ATOM	127	CA	PHE	60	9.659	-12.244	0.530	1.00	0.00	3A7
ATOM	128	CB	PHE	60	11.132	-11.803	0.330	1.00	0.00	3A7
ATOM	129	CG	PHE	60	11.512	-11.735	-1.126	1.00	0.00	3A7
ATOM	130	CD1	PHE	60	10.889	-10.822	-1.978	1.00	0.00	3A7
ATOM	131	CD2	PHE	60	12.481	-12.595	-1.647	1.00	0.00	3A7
ATOM	132	CE1	PHE	60	11.222	-10.772	-3.328	1.00	0.00	3A7
ATOM	133	CE2	PHE	60	12.816	-12.548	-2.997	1.00	0.00	3A7
ATOM	134	CZ	PHE	60	12.186	-11.636	-3.839	1.00	0.00	3A7
ATOM	135	C	PHE	60	9.505	-13.695	0.122	1.00	0.00	3A7
ATOM	136	O	PHE	60	8.967	-14.011	-0.936	1.00	0.00	3A7
ATOM	137	N	ASP	61	9.940	-14.632	0.991	1.00	0.00	3A7
ATOM	138	CA	ASP	61	9.855	-16.051	0.737	1.00	0.00	3A7
ATOM	139	CB	ASP	61	10.621	-16.892	1.774	1.00	0.00	3A7
ATOM	140	CG	ASP	61	12.134	-16.729	1.612	1.00	0.00	3A7
ATOM	141	OD1	ASP	61	12.612	-16.736	0.447	1.00	0.00	3A7
ATOM	142	OD2	ASP	61	12.818	-16.555	2.655	1.00	0.00	3A7
ATOM	143	C	ASP	61	8.415	-16.503	0.698	1.00	0.00	3A7
ATOM	144	O	ASP	61	8.070	-17.371	-0.085	1.00	0.00	3A7
ATOM	145	N	MET	62	7.521	-15.870	1.491	1.00	0.00	3A7
ATOM	146	CA	MET	62	6.098	-16.134	1.452	1.00	0.00	3A7
ATOM	147	CB	MET	62	5.374	-15.468	2.623	1.00	0.00	3A7
ATOM	148	CG	MET	62	5.596	-16.224	3.947	1.00	0.00	3A7
ATOM	149	SD	MET	62	4.969	-15.359	5.422	1.00	0.00	3A7
ATOM	150	CE	MET	62	3.199	-15.481	5.031	1.00	0.00	3A7
ATOM	151	C	MET	62	5.450	-15.672	0.168	1.00	0.00	3A7
ATOM	152	O	MET	62	4.555	-16.335	-0.342	1.00	0.00	3A7
ATOM	153	N	GLU	63	5.922	-14.555	-0.430	1.00	0.00	3A7
ATOM	154	CA	GLU	63	5.457	-14.094	-1.722	1.00	0.00	3A7
ATOM	155	CB	GLU	63	5.987	-12.683	-2.039	1.00	0.00	3A7
ATOM	156	CG	GLU	63	5.290	-11.593	-1.206	1.00	0.00	3A7
ATOM	157	CD	GLU	63	5.961	-10.239	-1.427	1.00	0.00	3A7
ATOM	158	OE1	GLU	63	6.943	-10.169	-2.214	1.00	0.00	3A7
ATOM	159	OE2	GLU	63	5.495	-9.249	-0.802	1.00	0.00	3A7
ATOM	160	C	GLU	63	5.865	-15.044	-2.831	1.00	0.00	3A7
ATOM	161	O	GLU	63	5.087	-15.339	-3.734	1.00	0.00	3A7
ATOM	162	N	CYS	64	7.093	-15.606	-2.747	1.00	0.00	3A7
ATOM	163	CA	CYS	64	7.601	-16.598	-3.674	1.00	0.00	3A7
ATOM	164	CB	CYS	64	9.045	-16.969	-3.362	1.00	0.00	3A7
ATOM	165	SG	CYS	64	9.973	-15.524	-3.736	1.00	0.00	3A7
ATOM	166	C	CYS	64	6.805	-17.853	-3.631	1.00	0.00	3A7
ATOM	167	O	CYS	64	6.413	-18.402	-4.655	1.00	0.00	3A7
ATOM	168	N	TYR	65	6.477	-18.323	-2.413	1.00	0.00	3A7
ATOM	169	CA	TYR	65	5.695	-19.526	-2.251	1.00	0.00	3A7
ATOM	170	CB	TYR	65	5.638	-19.993	-0.802	1.00	0.00	3A7
ATOM	171	CG	TYR	65	7.043	-20.246	-0.379	1.00	0.00	3A7
ATOM	172	CD1	TYR	65	7.458	-19.725	0.834	1.00	0.00	3A7

ATOM	173	CD2	TYR	65	7.985	-20.850	-1.222	1.00	0.00	3A7
ATOM	174	CE1	TYR	65	8.800	-19.750	1.182	1.00	0.00	3A7
ATOM	175	CE2	TYR	65	9.336	-20.816	-0.901	1.00	0.00	3A7
ATOM	176	CZ	TYR	65	9.743	-20.216	0.283	1.00	0.00	3A7
ATOM	177	OH	TYR	65	11.101	-20.003	0.572	1.00	0.00	3A7
ATOM	178	C	TYR	65	4.275	-19.373	-2.701	1.00	0.00	3A7
ATOM	179	O	TYR	65	3.706	-20.319	-3.228	1.00	0.00	3A7
ATOM	180	N	LYS	66	3.656	-18.174	-2.556	1.00	0.00	3A7
ATOM	181	CA	LYS	66	2.313	-17.922	-3.043	1.00	0.00	3A7
ATOM	182	CB	LYS	66	1.810	-16.564	-2.544	1.00	0.00	3A7
ATOM	183	CG	LYS	66	1.450	-16.579	-1.049	1.00	0.00	3A7
ATOM	184	CD	LYS	66	1.162	-15.185	-0.470	1.00	0.00	3A7
ATOM	185	CE	LYS	66	-0.063	-14.502	-1.089	1.00	0.00	3A7
ATOM	186	NZ	LYS	66	-0.299	-13.182	-0.461	1.00	0.00	3A7
ATOM	187	C	LYS	66	2.244	-17.957	-4.556	1.00	0.00	3A7
ATOM	188	O	LYS	66	1.227	-18.326	-5.129	1.00	0.00	3A7
ATOM	189	N	LYS	67	3.349	-17.595	-5.243	1.00	0.00	3A7
ATOM	190	CA	LYS	67	3.417	-17.539	-6.682	1.00	0.00	3A7
ATOM	191	CB	LYS	67	4.377	-16.414	-7.137	1.00	0.00	3A7
ATOM	192	CG	LYS	67	4.368	-16.145	-8.651	1.00	0.00	3A7
ATOM	193	CD	LYS	67	5.148	-14.878	-9.034	1.00	0.00	3A7
ATOM	194	CE	LYS	67	5.201	-14.629	-10.547	1.00	0.00	3A7
ATOM	195	NZ	LYS	67	3.843	-14.424	-11.100	1.00	0.00	3A7
ATOM	196	C	LYS	67	3.853	-18.855	-7.284	1.00	0.00	3A7
ATOM	197	O	LYS	67	3.254	-19.336	-8.244	1.00	0.00	3A7
ATOM	198	N	TYR	68	4.942	-19.451	-6.748	1.00	0.00	3A7
ATOM	199	CA	TYR	68	5.626	-20.573	-7.355	1.00	0.00	3A7
ATOM	200	CB	TYR	68	7.148	-20.402	-7.314	1.00	0.00	3A7
ATOM	201	CG	TYR	68	7.522	-19.259	-8.216	1.00	0.00	3A7
ATOM	202	CD1	TYR	68	7.789	-17.989	-7.702	1.00	0.00	3A7
ATOM	203	CD2	TYR	68	7.593	-19.457	-9.595	1.00	0.00	3A7
ATOM	204	CE1	TYR	68	8.122	-16.937	-8.550	1.00	0.00	3A7
ATOM	205	CE2	TYR	68	7.927	-18.408	-10.447	1.00	0.00	3A7
ATOM	206	CZ	TYR	68	8.193	-17.146	-9.924	1.00	0.00	3A7
ATOM	207	OH	TYR	68	8.537	-16.080	-10.784	1.00	0.00	3A7
ATOM	208	C	TYR	68	5.236	-21.899	-6.770	1.00	0.00	3A7
ATOM	209	O	TYR	68	5.299	-22.918	-7.453	1.00	0.00	3A7
ATOM	210	N	ARG	69	4.785	-21.912	-5.500	1.00	0.00	3A7
ATOM	211	CA	ARG	69	4.142	-23.040	-4.856	1.00	0.00	3A7
ATOM	212	CB	ARG	69	3.046	-23.733	-5.717	1.00	0.00	3A7
ATOM	213	CG	ARG	69	1.942	-22.762	-6.180	1.00	0.00	3A7
ATOM	214	CD	ARG	69	0.844	-23.441	-7.009	1.00	0.00	3A7
ATOM	215	NE	ARG	69	1.454	-23.933	-8.287	1.00	0.00	3A7
ATOM	216	CZ	ARG	69	0.741	-24.664	-9.197	1.00	0.00	3A7
ATOM	217	NH1	ARG	69	1.345	-25.083	-10.347	1.00	0.00	3A7
ATOM	218	NH2	ARG	69	-0.565	-24.981	-8.963	1.00	0.00	3A7
ATOM	219	C	ARG	69	5.132	-23.968	-4.257	1.00	0.00	3A7
ATOM	220	O	ARG	69	6.140	-23.556	-3.663	1.00	0.00	3A7
ATOM	221	N	LYS	70	4.815	-25.251	-4.585	1.00	0.00	3A7
ATOM	222	CA	LYS	70	5.551	-26.459	-4.410	1.00	0.00	3A7
ATOM	223	CB	LYS	70	4.828	-27.726	-4.955	1.00	0.00	3A7
ATOM	224	CG	LYS	70	3.527	-28.142	-4.233	1.00	0.00	3A7
ATOM	225	CD	LYS	70	2.245	-27.345	-4.536	1.00	0.00	3A7
ATOM	226	CE	LYS	70	1.635	-27.577	-5.929	1.00	0.00	3A7
ATOM	227	NZ	LYS	70	2.449	-26.976	-7.009	1.00	0.00	3A7
ATOM	228	C	LYS	70	6.866	-26.352	-5.122	1.00	0.00	3A7
ATOM	229	O	LYS	70	7.015	-26.860	-6.233	1.00	0.00	3A7
ATOM	230	N	VAL	71	7.834	-25.662	-4.449	1.00	0.00	3A7
ATOM	231	CA	VAL	71	9.235	-25.641	-4.770	1.00	0.00	3A7
ATOM	232	CB	VAL	71	9.760	-26.967	-5.362	1.00	0.00	3A7
ATOM	233	CG1	VAL	71	11.270	-26.882	-5.635	1.00	0.00	3A7
ATOM	234	CG2	VAL	71	9.523	-28.158	-4.411	1.00	0.00	3A7
ATOM	235	C	VAL	71	9.454	-24.472	-5.708	1.00	0.00	3A7
ATOM	236	O	VAL	71	8.810	-24.376	-6.751	1.00	0.00	3A7
ATOM	237	N	TRP	72	10.373	-23.545	-5.337	1.00	0.00	3A7
ATOM	238	CA	TRP	72	10.743	-22.433	-6.182	1.00	0.00	3A7
ATOM	239	CB	TRP	72	10.009	-21.089	-5.839	1.00	0.00	3A7
ATOM	240	CG	TRP	72	10.772	-19.873	-5.306	1.00	0.00	3A7
ATOM	241	CD2	TRP	72	11.148	-18.737	-6.108	1.00	0.00	3A7
ATOM	242	CD1	TRP	72	11.256	-19.633	-4.054	1.00	0.00	3A7
ATOM	243	NE1	TRP	72	11.935	-18.438	-4.024	1.00	0.00	3A7
ATOM	244	CE2	TRP	72	11.871	-17.866	-5.277	1.00	0.00	3A7

ATOM	245	CE3	TRP	72	10.923	-18.434	-7.436	1.00	0.00	3A7
ATOM	246	CZ2	TRP	72	12.368	-16.672	-5.760	1.00	0.00	3A7
ATOM	247	CZ3	TRP	72	11.414	-17.223	-7.920	1.00	0.00	3A7
ATOM	248	CH2	TRP	72	12.124	-16.354	-7.094	1.00	0.00	3A7
ATOM	249	C	TRP	72	12.229	-22.293	-6.064	1.00	0.00	3A7
ATOM	250	O	TRP	72	12.824	-22.782	-5.112	1.00	0.00	3A7
ATOM	251	N	GLY	73	12.861	-21.582	-7.022	1.00	0.00	3A7
ATOM	252	CA	GLY	73	14.278	-21.323	-6.985	1.00	0.00	3A7
ATOM	253	C	GLY	73	14.511	-19.850	-6.821	1.00	0.00	3A7
ATOM	254	O	GLY	73	13.812	-19.031	-7.409	1.00	0.00	3A7
ATOM	255	N	ILE	74	15.530	-19.484	-6.009	1.00	0.00	3A7
ATOM	256	CA	ILE	74	15.929	-18.120	-5.754	1.00	0.00	3A7
ATOM	257	CB	ILE	74	15.600	-17.676	-4.328	1.00	0.00	3A7
ATOM	258	CG2	ILE	74	16.301	-18.543	-3.258	1.00	0.00	3A7
ATOM	259	CG1	ILE	74	15.835	-16.159	-4.124	1.00	0.00	3A7
ATOM	260	CD	ILE	74	15.205	-15.621	-2.836	1.00	0.00	3A7
ATOM	261	C	ILE	74	17.407	-18.077	-6.023	1.00	0.00	3A7
ATOM	262	O	ILE	74	18.100	-19.082	-5.904	1.00	0.00	3A7
ATOM	263	N	TYR	75	17.928	-16.900	-6.425	1.00	0.00	3A7
ATOM	264	CA	TYR	75	19.303	-16.765	-6.827	1.00	0.00	3A7
ATOM	265	CB	TYR	75	19.424	-16.348	-8.308	1.00	0.00	3A7
ATOM	266	CG	TYR	75	18.811	-17.400	-9.184	1.00	0.00	3A7
ATOM	267	CD1	TYR	75	17.487	-17.281	-9.613	1.00	0.00	3A7
ATOM	268	CD2	TYR	75	19.554	-18.513	-9.582	1.00	0.00	3A7
ATOM	269	CE1	TYR	75	16.911	-18.261	-10.415	1.00	0.00	3A7
ATOM	270	CE2	TYR	75	18.983	-19.489	-10.394	1.00	0.00	3A7
ATOM	271	CZ	TYR	75	17.660	-19.367	-10.807	1.00	0.00	3A7
ATOM	272	OH	TYR	75	17.079	-20.361	-11.624	1.00	0.00	3A7
ATOM	273	C	TYR	75	19.927	-15.716	-5.954	1.00	0.00	3A7
ATOM	274	O	TYR	75	19.589	-14.543	-6.059	1.00	0.00	3A7
ATOM	275	N	ASP	76	20.867	-16.106	-5.059	1.00	0.00	3A7
ATOM	276	CA	ASP	76	21.559	-15.171	-4.194	1.00	0.00	3A7
ATOM	277	CB	ASP	76	21.470	-15.513	-2.685	1.00	0.00	3A7
ATOM	278	CG	ASP	76	20.053	-15.259	-2.172	1.00	0.00	3A7
ATOM	279	OD1	ASP	76	19.105	-15.935	-2.652	1.00	0.00	3A7
ATOM	280	OD2	ASP	76	19.905	-14.382	-1.279	1.00	0.00	3A7
ATOM	281	C	ASP	76	23.004	-15.175	-4.597	1.00	0.00	3A7
ATOM	282	O	ASP	76	23.790	-16.000	-4.149	1.00	0.00	3A7
ATOM	283	N	CYS	77	23.393	-14.210	-5.459	1.00	0.00	3A7
ATOM	284	CA	CYS	77	24.738	-13.896	-5.902	1.00	0.00	3A7
ATOM	285	CB	CYS	77	25.569	-13.074	-4.858	1.00	0.00	3A7
ATOM	286	SG	CYS	77	25.906	-13.854	-3.237	1.00	0.00	3A7
ATOM	287	C	CYS	77	25.544	-15.056	-6.442	1.00	0.00	3A7
ATOM	288	O	CYS	77	26.561	-15.442	-5.879	1.00	0.00	3A7
ATOM	289	N	GLN	78	25.091	-15.613	-7.583	1.00	0.00	3A7
ATOM	290	CA	GLN	78	25.770	-16.622	-8.369	1.00	0.00	3A7
ATOM	291	CB	GLN	78	27.325	-16.549	-8.440	1.00	0.00	3A7
ATOM	292	CG	GLN	78	27.848	-15.222	-9.017	1.00	0.00	3A7
ATOM	293	CD	GLN	78	29.378	-15.274	-9.063	1.00	0.00	3A7
ATOM	294	OE1	GLN	78	29.961	-16.057	-9.823	1.00	0.00	3A7
ATOM	295	NE2	GLN	78	30.031	-14.415	-8.222	1.00	0.00	3A7
ATOM	296	C	GLN	78	25.375	-18.037	-8.023	1.00	0.00	3A7
ATOM	297	O	GLN	78	25.715	-18.949	-8.771	1.00	0.00	3A7
ATOM	298	N	GLN	79	24.653	-18.277	-6.903	1.00	0.00	3A7
ATOM	299	CA	GLN	79	24.270	-19.620	-6.516	1.00	0.00	3A7
ATOM	300	CB	GLN	79	24.718	-19.978	-5.085	1.00	0.00	3A7
ATOM	301	CG	GLN	79	26.242	-19.895	-4.897	1.00	0.00	3A7
ATOM	302	CD	GLN	79	26.582	-20.276	-3.453	1.00	0.00	3A7
ATOM	303	OE1	GLN	79	26.176	-19.589	-2.508	1.00	0.00	3A7
ATOM	304	NE2	GLN	79	27.346	-21.399	-3.294	1.00	0.00	3A7
ATOM	305	C	GLN	79	22.765	-19.774	-6.615	1.00	0.00	3A7
ATOM	306	O	GLN	79	22.037	-18.847	-6.260	1.00	0.00	3A7
ATOM	307	N	PRO	80	22.241	-20.926	-7.069	1.00	0.00	3A7
ATOM	308	CA	PRO	80	20.824	-21.225	-7.042	1.00	0.00	3A7
ATOM	309	CD	PRO	80	22.976	-21.867	-7.907	1.00	0.00	3A7
ATOM	310	CB	PRO	80	20.605	-22.191	-8.214	1.00	0.00	3A7
ATOM	311	CG	PRO	80	21.950	-22.915	-8.360	1.00	0.00	3A7
ATOM	312	C	PRO	80	20.502	-21.899	-5.737	1.00	0.00	3A7
ATOM	313	O	PRO	80	21.269	-22.746	-5.277	1.00	0.00	3A7
ATOM	314	N	MET	81	19.342	-21.571	-5.140	1.00	0.00	3A7
ATOM	315	CA	MET	81	18.883	-22.233	-3.952	1.00	0.00	3A7
ATOM	316	CB	MET	81	19.098	-21.392	-2.669	1.00	0.00	3A7

```
ATOM    317  CG  MET    81      20.582 -21.043  -2.428  1.00  0.00          3A7
ATOM    318  SD  MET    81      20.947 -20.209  -0.854  1.00  0.00          3A7
ATOM    319  CE  MET    81      20.120 -18.650  -1.276  1.00  0.00          3A7
ATOM    320  C   MET    81      17.447 -22.487  -4.177  1.00  0.00          3A7
ATOM    321  O   MET    81      16.677 -21.572  -4.447  1.00  0.00          3A7
ATOM    322  N   LEU    82      17.035 -23.763  -4.052  1.00  0.00          3A7
ATOM    323  CA  LEU    82      15.657 -24.130  -4.201  1.00  0.00          3A7
ATOM    324  CB  LEU    82      15.468 -25.434  -4.990  1.00  0.00          3A7
ATOM    325  CG  LEU    82      15.574 -25.122  -6.509  1.00  0.00          3A7
ATOM    326  CD1 LEU    82      16.903 -25.569  -7.137  1.00  0.00          3A7
ATOM    327  CD2 LEU    82      14.352 -25.622  -7.300  1.00  0.00          3A7
ATOM    328  C   LEU    82      15.022 -24.179  -2.843  1.00  0.00          3A7
ATOM    329  O   LEU    82      15.439 -24.903  -1.947  1.00  0.00          3A7
ATOM    330  N   ALA    83      13.975 -23.351  -2.673  1.00  0.00          3A7
ATOM    331  CA  ALA    83      13.243 -23.210  -1.443  1.00  0.00          3A7
ATOM    332  CB  ALA    83      12.731 -21.792  -1.267  1.00  0.00          3A7
ATOM    333  C   ALA    83      12.040 -24.096  -1.430  1.00  0.00          3A7
ATOM    334  O   ALA    83      11.193 -24.025  -2.320  1.00  0.00          3A7
ATOM    335  N   ILE    84      11.963 -24.967  -0.399  1.00  0.00          3A7
ATOM    336  CA  ILE    84      10.949 -25.985  -0.290  1.00  0.00          3A7
ATOM    337  CB  ILE    84      11.517 -27.364   0.009  1.00  0.00          3A7
ATOM    338  CG2 ILE    84      10.376 -28.307   0.374  1.00  0.00          3A7
ATOM    339  CG1 ILE    84      12.173 -28.016  -1.243  1.00  0.00          3A7
ATOM    340  CD  ILE    84      13.207 -27.201  -2.013  1.00  0.00          3A7
ATOM    341  C   ILE    84      10.004 -25.576   0.802  1.00  0.00          3A7
ATOM    342  O   ILE    84      10.404 -25.289   1.921  1.00  0.00          3A7
ATOM    343  N   THR    85       8.689 -25.597   0.509  1.00  0.00          3A7
ATOM    344  CA  THR    85       7.672 -25.139   1.413  1.00  0.00          3A7
ATOM    345  CB  THR    85       7.073 -23.819   0.999  1.00  0.00          3A7
ATOM    346  OG1 THR    85       7.093 -23.627  -0.412  1.00  0.00          3A7
ATOM    347  CG2 THR    85       7.922 -22.782   1.725  1.00  0.00          3A7
ATOM    348  C   THR    85       6.562 -26.125   1.486  1.00  0.00          3A7
ATOM    349  O   THR    85       6.050 -26.730   0.619  1.00  0.00          3A7
ATOM    350  N   ASP    86       5.995 -26.396   2.502  1.00  0.00          3A7
ATOM    351  CA  ASP    86       4.810 -27.263   2.510  1.00  0.00          3A7
ATOM    352  CB  ASP    86       3.722 -27.421   1.361  1.00  0.00          3A7
ATOM    353  CG  ASP    86       3.168 -26.055   0.952  1.00  0.00          3A7
ATOM    354  OD1 ASP    86       2.591 -25.362   1.833  1.00  0.00          3A7
ATOM    355  OD2 ASP    86       3.312 -25.692  -0.246  1.00  0.00          3A7
ATOM    356  C   ASP    86       5.268 -28.602   3.011  1.00  0.00          3A7
ATOM    357  O   ASP    86       6.399 -28.994   2.738  1.00  0.00          3A7
ATOM    358  N   PRO    87       4.433 -29.324   3.756  1.00  0.00          3A7
ATOM    359  CA  PRO    87       4.827 -30.519   4.472  1.00  0.00          3A7
ATOM    360  CD  PRO    87       3.262 -28.734   4.388  1.00  0.00          3A7
ATOM    361  CB  PRO    87       3.599 -30.942   5.276  1.00  0.00          3A7
ATOM    362  CG  PRO    87       2.505 -29.914   4.977  1.00  0.00          3A7
ATOM    363  C   PRO    87       5.202 -31.641   3.571  1.00  0.00          3A7
ATOM    364  O   PRO    87       6.112 -32.375   3.920  1.00  0.00          3A7
ATOM    365  N   ASP    88       4.533 -31.800   2.413  1.00  0.00          3A7
ATOM    366  CA  ASP    88       4.791 -32.846   1.455  1.00  0.00          3A7
ATOM    367  CB  ASP    88       3.829 -32.701   0.270  1.00  0.00          3A7
ATOM    368  CG  ASP    88       2.381 -32.826   0.749  1.00  0.00          3A7
ATOM    369  OD1 ASP    88       2.122 -33.640   1.676  1.00  0.00          3A7
ATOM    370  OD2 ASP    88       1.516 -32.094   0.198  1.00  0.00          3A7
ATOM    371  C   ASP    88       6.196 -32.787   0.909  1.00  0.00          3A7
ATOM    372  O   ASP    88       6.874 -33.798   0.830  1.00  0.00          3A7
ATOM    373  N   MET    89       6.691 -31.588   0.554  1.00  0.00          3A7
ATOM    374  CA  MET    89       8.014 -31.388   0.009  1.00  0.00          3A7
ATOM    375  CB  MET    89       8.081 -30.073  -0.773  1.00  0.00          3A7
ATOM    376  CG  MET    89       7.065 -30.035  -1.918  1.00  0.00          3A7
ATOM    377  SD  MET    89       5.914 -28.663  -1.731  1.00  0.00          3A7
ATOM    378  CE  MET    89       7.247 -27.425  -1.755  1.00  0.00          3A7
ATOM    379  C   MET    89       9.069 -31.390   1.081  1.00  0.00          3A7
ATOM    380  O   MET    89      10.152 -31.936   0.893  1.00  0.00          3A7
ATOM    381  N   ILE    90       8.754 -30.824   2.267  1.00  0.00          3A7
ATOM    382  CA  ILE    90       9.657 -30.812   3.398  1.00  0.00          3A7
ATOM    383  CB  ILE    90       9.126 -29.908   4.501  1.00  0.00          3A7
ATOM    384  CG2 ILE    90       9.952 -30.036   5.807  1.00  0.00          3A7
ATOM    385  CG1 ILE    90       9.060 -28.467   3.973  1.00  0.00          3A7
ATOM    386  CD  ILE    90      10.436 -27.853   3.815  1.00  0.00          3A7
ATOM    387  C   ILE    90       9.898 -32.218   3.920  1.00  0.00          3A7
ATOM    388  O   ILE    90      11.016 -32.588   4.248  1.00  0.00          3A7
```

ATOM	389	N	LYS	91	8.877	-33.100	3.925	1.00	0.00	3A7
ATOM	390	CA	LYS	91	9.058	-34.479	4.328	1.00	0.00	3A7
ATOM	391	CB	LYS	91	7.722	-35.240	4.361	1.00	0.00	3A7
ATOM	392	CG	LYS	91	7.790	-36.619	5.036	1.00	0.00	3A7
ATOM	393	CD	LYS	91	6.407	-37.269	5.192	1.00	0.00	3A7
ATOM	394	CE	LYS	91	6.465	-38.628	5.898	1.00	0.00	3A7
ATOM	395	NZ	LYS	91	5.108	-39.206	6.031	1.00	0.00	3A7
ATOM	396	C	LYS	91	10.010	-35.209	3.414	1.00	0.00	3A7
ATOM	397	O	LYS	91	10.824	-36.021	3.838	1.00	0.00	3A7
ATOM	398	N	THR	92	9.969	-34.861	2.113	1.00	0.00	3A7
ATOM	399	CA	THR	92	10.864	-35.382	1.113	1.00	0.00	3A7
ATOM	400	CB	THR	92	10.441	-34.980	-0.272	1.00	0.00	3A7
ATOM	401	OG1	THR	92	9.047	-35.206	-0.430	1.00	0.00	3A7
ATOM	402	CG2	THR	92	11.180	-35.836	-1.323	1.00	0.00	3A7
ATOM	403	C	THR	92	12.263	-34.904	1.326	1.00	0.00	3A7
ATOM	404	O	THR	92	13.222	-35.657	1.196	1.00	0.00	3A7
ATOM	405	N	VAL	93	12.395	-33.620	1.730	1.00	0.00	3A7
ATOM	406	CA	VAL	93	13.674	-33.006	1.938	1.00	0.00	3A7
ATOM	407	CB	VAL	93	13.628	-31.500	2.127	1.00	0.00	3A7
ATOM	408	CG1	VAL	93	12.833	-30.752	1.061	1.00	0.00	3A7
ATOM	409	CG2	VAL	93	13.354	-31.074	3.585	1.00	0.00	3A7
ATOM	410	C	VAL	93	14.483	-33.705	3.034	1.00	0.00	3A7
ATOM	411	O	VAL	93	15.703	-33.627	3.002	1.00	0.00	3A7
ATOM	412	N	LEU	94	13.861	-34.522	3.946	1.00	0.00	3A7
ATOM	413	CA	LEU	94	14.509	-35.450	4.889	1.00	0.00	3A7
ATOM	414	CB	LEU	94	13.538	-36.540	5.429	1.00	0.00	3A7
ATOM	415	CG	LEU	94	12.454	-36.028	6.397	1.00	0.00	3A7
ATOM	416	CD1	LEU	94	11.435	-37.136	6.726	1.00	0.00	3A7
ATOM	417	CD2	LEU	94	13.079	-35.489	7.687	1.00	0.00	3A7
ATOM	418	C	LEU	94	15.673	-36.253	4.325	1.00	0.00	3A7
ATOM	419	O	LEU	94	16.786	-36.171	4.842	1.00	0.00	3A7
ATOM	420	N	VAL	95	15.389	-37.041	3.249	1.00	0.00	3A7
ATOM	421	CA	VAL	95	16.254	-37.904	2.446	1.00	0.00	3A7
ATOM	422	CB	VAL	95	17.146	-37.147	1.449	1.00	0.00	3A7
ATOM	423	CG1	VAL	95	18.293	-36.331	2.088	1.00	0.00	3A7
ATOM	424	CG2	VAL	95	17.667	-38.131	0.379	1.00	0.00	3A7
ATOM	425	C	VAL	95	17.019	-38.932	3.269	1.00	0.00	3A7
ATOM	426	O	VAL	95	17.910	-38.606	4.052	1.00	0.00	3A7
ATOM	427	N	LYS	96	16.651	-40.226	3.099	1.00	0.00	3A7
ATOM	428	CA	LYS	96	17.216	-41.310	3.864	1.00	0.00	3A7
ATOM	429	CB	LYS	96	16.284	-41.757	5.021	1.00	0.00	3A7
ATOM	430	CG	LYS	96	16.863	-42.863	5.922	1.00	0.00	3A7
ATOM	431	CD	LYS	96	15.917	-43.296	7.055	1.00	0.00	3A7
ATOM	432	CE	LYS	96	15.646	-42.211	8.105	1.00	0.00	3A7
ATOM	433	NZ	LYS	96	16.899	-41.808	8.783	1.00	0.00	3A7
ATOM	434	C	LYS	96	17.438	-42.463	2.917	1.00	0.00	3A7
ATOM	435	O	LYS	96	16.460	-42.998	2.397	1.00	0.00	3A7
ATOM	436	N	GLU	97	18.697	-42.930	2.649	1.00	0.00	3A7
ATOM	437	CA	GLU	97	20.025	-42.451	3.016	1.00	0.00	3A7
ATOM	438	CB	GLU	97	20.351	-41.024	2.498	1.00	0.00	3A7
ATOM	439	CG	GLU	97	20.271	-40.894	0.966	1.00	0.00	3A7
ATOM	440	CD	GLU	97	21.342	-41.763	0.314	1.00	0.00	3A7
ATOM	441	OE1	GLU	97	20.968	-42.695	-0.447	1.00	0.00	3A7
ATOM	442	OE2	GLU	97	22.549	-41.504	0.567	1.00	0.00	3A7
ATOM	443	C	GLU	97	20.318	-42.531	4.499	1.00	0.00	3A7
ATOM	444	O	GLU	97	20.158	-41.560	5.238	1.00	0.00	3A7
ATOM	445	N	CYS	98	20.813	-43.711	4.956	1.00	0.00	3A7
ATOM	446	CA	CYS	98	21.223	-43.956	6.327	1.00	0.00	3A7
ATOM	447	CB	CYS	98	21.159	-45.456	6.703	1.00	0.00	3A7
ATOM	448	SG	CYS	98	19.470	-46.111	6.530	1.00	0.00	3A7
ATOM	449	C	CYS	98	22.633	-43.454	6.538	1.00	0.00	3A7
ATOM	450	O	CYS	98	23.032	-43.131	7.656	1.00	0.00	3A7
ATOM	451	N	TYR	99	23.399	-43.358	5.423	1.00	0.00	3A7
ATOM	452	CA	TYR	99	24.680	-42.699	5.352	1.00	0.00	3A7
ATOM	453	CB	TYR	99	25.794	-43.602	4.775	1.00	0.00	3A7
ATOM	454	CG	TYR	99	26.067	-44.708	5.749	1.00	0.00	3A7
ATOM	455	CD1	TYR	99	25.528	-45.981	5.553	1.00	0.00	3A7
ATOM	456	CD2	TYR	99	26.855	-44.471	6.875	1.00	0.00	3A7
ATOM	457	CE1	TYR	99	25.771	-47.000	6.470	1.00	0.00	3A7
ATOM	458	CE2	TYR	99	27.103	-45.488	7.791	1.00	0.00	3A7
ATOM	459	CZ	TYR	99	26.560	-46.754	7.591	1.00	0.00	3A7
ATOM	460	OH	TYR	99	26.807	-47.785	8.524	1.00	0.00	3A7

ATOM	461	C	TYR	99	24.459	-41.520	4.445	1.00	0.00	3A7
ATOM	462	O	TYR	99	24.717	-41.584	3.244	1.00	0.00	3A7
ATOM	463	N	SER	100	23.943	-40.407	5.029	1.00	0.00	3A7
ATOM	464	CA	SER	100	23.548	-39.211	4.317	1.00	0.00	3A7
ATOM	465	CB	SER	100	22.340	-38.501	4.990	1.00	0.00	3A7
ATOM	466	OG	SER	100	22.547	-38.275	6.381	1.00	0.00	3A7
ATOM	467	C	SER	100	24.721	-38.267	4.207	1.00	0.00	3A7
ATOM	468	O	SER	100	25.295	-37.848	5.211	1.00	0.00	3A7
ATOM	469	N	VAL	101	25.093	-37.923	2.947	1.00	0.00	3A7
ATOM	470	CA	VAL	101	26.233	-37.096	2.616	1.00	0.00	3A7
ATOM	471	CB	VAL	101	26.925	-37.529	1.327	1.00	0.00	3A7
ATOM	472	CG1	VAL	101	28.244	-36.746	1.143	1.00	0.00	3A7
ATOM	473	CG2	VAL	101	27.188	-39.049	1.394	1.00	0.00	3A7
ATOM	474	C	VAL	101	25.777	-35.663	2.512	1.00	0.00	3A7
ATOM	475	O	VAL	101	25.384	-35.187	1.447	1.00	0.00	3A7
ATOM	476	N	PHE	102	25.851	-34.944	3.658	1.00	0.00	3A7
ATOM	477	CA	PHE	102	25.588	-33.531	3.774	1.00	0.00	3A7
ATOM	478	CB	PHE	102	24.757	-33.208	5.051	1.00	0.00	3A7
ATOM	479	CG	PHE	102	24.515	-31.734	5.284	1.00	0.00	3A7
ATOM	480	CD1	PHE	102	24.224	-30.854	4.236	1.00	0.00	3A7
ATOM	481	CD2	PHE	102	24.602	-31.227	6.582	1.00	0.00	3A7
ATOM	482	CE1	PHE	102	24.063	-29.493	4.481	1.00	0.00	3A7
ATOM	483	CE2	PHE	102	24.424	-29.870	6.830	1.00	0.00	3A7
ATOM	484	CZ	PHE	102	24.163	-29.000	5.777	1.00	0.00	3A7
ATOM	485	C	PHE	102	26.945	-32.887	3.838	1.00	0.00	3A7
ATOM	486	O	PHE	102	27.728	-33.174	4.741	1.00	0.00	3A7
ATOM	487	N	THR	103	27.238	-31.980	2.869	1.00	0.00	3A7
ATOM	488	CA	THR	103	28.502	-31.281	2.757	1.00	0.00	3A7
ATOM	489	CB	THR	103	28.814	-30.904	1.308	1.00	0.00	3A7
ATOM	490	OG1	THR	103	30.168	-30.496	1.135	1.00	0.00	3A7
ATOM	491	CG2	THR	103	27.858	-29.816	0.779	1.00	0.00	3A7
ATOM	492	C	THR	103	28.484	-30.083	3.685	1.00	0.00	3A7
ATOM	493	O	THR	103	27.430	-29.672	4.169	1.00	0.00	3A7
ATOM	494	N	ASN	104	29.682	-29.507	3.955	1.00	0.00	3A7
ATOM	495	CA	ASN	104	29.888	-28.430	4.899	1.00	0.00	3A7
ATOM	496	CB	ASN	104	31.378	-28.320	5.343	1.00	0.00	3A7
ATOM	497	CG	ASN	104	32.353	-28.168	4.161	1.00	0.00	3A7
ATOM	498	OD1	ASN	104	32.706	-27.047	3.775	1.00	0.00	3A7
ATOM	499	ND2	ASN	104	32.796	-29.333	3.597	1.00	0.00	3A7
ATOM	500	C	ASN	104	29.418	-27.105	4.342	1.00	0.00	3A7
ATOM	501	O	ASN	104	29.471	-26.868	3.135	1.00	0.00	3A7
ATOM	502	N	ARG	105	28.961	-26.205	5.250	1.00	0.00	3A7
ATOM	503	CA	ARG	105	28.538	-24.859	4.929	1.00	0.00	3A7
ATOM	504	CB	ARG	105	27.556	-24.275	5.967	1.00	0.00	3A7
ATOM	505	CG	ARG	105	26.214	-25.018	6.037	1.00	0.00	3A7
ATOM	506	CD	ARG	105	25.300	-24.418	7.111	1.00	0.00	3A7
ATOM	507	NE	ARG	105	24.029	-25.205	7.173	1.00	0.00	3A7
ATOM	508	CZ	ARG	105	23.007	-24.845	8.007	1.00	0.00	3A7
ATOM	509	NH1	ARG	105	21.860	-25.583	8.027	1.00	0.00	3A7
ATOM	510	NH2	ARG	105	23.124	-23.752	8.816	1.00	0.00	3A7
ATOM	511	C	ARG	105	29.756	-23.977	4.884	1.00	0.00	3A7
ATOM	512	O	ARG	105	30.703	-24.170	5.645	1.00	0.00	3A7
ATOM	513	N	ARG	106	29.750	-22.991	3.955	1.00	0.00	3A7
ATOM	514	CA	ARG	106	30.909	-22.177	3.639	1.00	0.00	3A7
ATOM	515	CB	ARG	106	30.852	-21.586	2.205	1.00	0.00	3A7
ATOM	516	CG	ARG	106	30.675	-22.664	1.121	1.00	0.00	3A7
ATOM	517	CD	ARG	106	30.504	-22.088	-0.292	1.00	0.00	3A7
ATOM	518	NE	ARG	106	31.739	-21.318	-0.652	1.00	0.00	3A7
ATOM	519	CZ	ARG	106	31.841	-20.619	-1.824	1.00	0.00	3A7
ATOM	520	NH1	ARG	106	32.985	-19.927	-2.100	1.00	0.00	3A7
ATOM	521	NH2	ARG	106	30.809	-20.607	-2.718	1.00	0.00	3A7
ATOM	522	C	ARG	106	31.190	-21.087	4.647	1.00	0.00	3A7
ATOM	523	O	ARG	106	32.357	-20.971	5.015	1.00	0.00	3A7
ATOM	524	N	PRO	107	30.250	-20.287	5.178	1.00	0.00	3A7
ATOM	525	CA	PRO	107	30.565	-19.212	6.105	1.00	0.00	3A7
ATOM	526	CD	PRO	107	28.890	-20.159	4.663	1.00	0.00	3A7
ATOM	527	CB	PRO	107	29.245	-18.456	6.287	1.00	0.00	3A7
ATOM	528	CG	PRO	107	28.480	-18.724	4.991	1.00	0.00	3A7
ATOM	529	C	PRO	107	31.061	-19.732	7.435	1.00	0.00	3A7
ATOM	530	O	PRO	107	31.834	-19.045	8.098	1.00	0.00	3A7
ATOM	531	N	PHE	108	30.645	-20.949	7.846	1.00	0.00	3A7
ATOM	532	CA	PHE	108	30.989	-21.534	9.116	1.00	0.00	3A7

ATOM	533	CB	PHE	108	29.984	-22.623	9.543	1.00	0.00	3A7
ATOM	534	CG	PHE	108	28.575	-22.099	9.639	1.00	0.00	3A7
ATOM	535	CD1	PHE	108	27.823	-21.852	8.488	1.00	0.00	3A7
ATOM	536	CD2	PHE	108	27.969	-21.924	10.885	1.00	0.00	3A7
ATOM	537	CE1	PHE	108	26.496	-21.446	8.575	1.00	0.00	3A7
ATOM	538	CE2	PHE	108	26.638	-21.528	10.976	1.00	0.00	3A7
ATOM	539	CZ	PHE	108	25.898	-21.298	9.821	1.00	0.00	3A7
ATOM	540	C	PHE	108	32.360	-22.153	9.070	1.00	0.00	3A7
ATOM	541	O	PHE	108	33.016	-22.269	10.095	1.00	0.00	3A7
ATOM	542	N	GLY	109	32.846	-22.555	7.875	1.00	0.00	3A7
ATOM	543	CA	GLY	109	34.159	-23.135	7.691	1.00	0.00	3A7
ATOM	544	C	GLY	109	35.333	-22.254	8.056	1.00	0.00	3A7
ATOM	545	O	GLY	109	36.321	-22.774	8.561	1.00	0.00	3A7
ATOM	546	N	PRO	110	35.267	-20.938	7.853	1.00	0.00	3A7
ATOM	547	CA	PRO	110	36.311	-20.023	8.270	1.00	0.00	3A7
ATOM	548	CD	PRO	110	34.680	-20.430	6.620	1.00	0.00	3A7
ATOM	549	CB	PRO	110	35.805	-18.682	7.743	1.00	0.00	3A7
ATOM	550	CG	PRO	110	35.292	-19.054	6.361	1.00	0.00	3A7
ATOM	551	C	PRO	110	36.590	-19.895	9.765	1.00	0.00	3A7
ATOM	552	O	PRO	110	37.717	-19.525	10.094	1.00	0.00	3A7
ATOM	553	N	VAL	111	35.620	-20.153	10.690	1.00	0.00	3A7
ATOM	554	CA	VAL	111	35.799	-19.847	12.107	1.00	0.00	3A7
ATOM	555	CB	VAL	111	34.495	-19.678	12.890	1.00	0.00	3A7
ATOM	556	CG1	VAL	111	33.623	-18.645	12.147	1.00	0.00	3A7
ATOM	557	CG2	VAL	111	33.745	-21.007	13.118	1.00	0.00	3A7
ATOM	558	C	VAL	111	36.707	-20.855	12.787	1.00	0.00	3A7
ATOM	559	O	VAL	111	36.539	-22.067	12.658	1.00	0.00	3A7
ATOM	560	N	GLY	112	37.725	-20.325	13.502	1.00	0.00	3A7
ATOM	561	CA	GLY	112	38.761	-21.102	14.130	1.00	0.00	3A7
ATOM	562	C	GLY	112	40.044	-20.384	13.863	1.00	0.00	3A7
ATOM	563	O	GLY	112	40.101	-19.155	13.891	1.00	0.00	3A7
ATOM	564	N	PHE	113	41.113	-21.162	13.582	1.00	0.00	3A7
ATOM	565	CA	PHE	113	42.395	-20.640	13.182	1.00	0.00	3A7
ATOM	566	CB	PHE	113	43.376	-20.476	14.380	1.00	0.00	3A7
ATOM	567	CG	PHE	113	44.692	-19.854	13.980	1.00	0.00	3A7
ATOM	568	CD1	PHE	113	45.891	-20.468	14.346	1.00	0.00	3A7
ATOM	569	CD2	PHE	113	44.738	-18.671	13.239	1.00	0.00	3A7
ATOM	570	CE1	PHE	113	47.113	-19.918	13.971	1.00	0.00	3A7
ATOM	571	CE2	PHE	113	45.959	-18.120	12.861	1.00	0.00	3A7
ATOM	572	CZ	PHE	113	47.148	-18.744	13.226	1.00	0.00	3A7
ATOM	573	C	PHE	113	42.890	-21.648	12.181	1.00	0.00	3A7
ATOM	574	O	PHE	113	43.853	-22.372	12.431	1.00	0.00	3A7
ATOM	575	N	MET	114	42.193	-21.708	11.011	1.00	0.00	3A7
ATOM	576	CA	MET	114	42.417	-22.600	9.882	1.00	0.00	3A7
ATOM	577	CB	MET	114	43.873	-22.624	9.331	1.00	0.00	3A7
ATOM	578	CG	MET	114	44.322	-21.313	8.647	1.00	0.00	3A7
ATOM	579	SD	MET	114	44.745	-19.936	9.761	1.00	0.00	3A7
ATOM	580	CE	MET	114	45.205	-18.779	8.440	1.00	0.00	3A7
ATOM	581	C	MET	114	41.966	-24.012	10.217	1.00	0.00	3A7
ATOM	582	O	MET	114	41.563	-24.294	11.346	1.00	0.00	3A7
ATOM	583	N	LYS	115	42.028	-24.924	9.208	1.00	0.00	3A7
ATOM	584	CA	LYS	115	41.701	-26.343	9.268	1.00	0.00	3A7
ATOM	585	CB	LYS	115	42.359	-27.158	10.423	1.00	0.00	3A7
ATOM	586	CG	LYS	115	43.868	-27.432	10.251	1.00	0.00	3A7
ATOM	587	CD	LYS	115	44.814	-26.252	10.533	1.00	0.00	3A7
ATOM	588	CE	LYS	115	44.796	-25.758	11.988	1.00	0.00	3A7
ATOM	589	NZ	LYS	115	45.206	-26.832	12.922	1.00	0.00	3A7
ATOM	590	C	LYS	115	40.202	-26.569	9.300	1.00	0.00	3A7
ATOM	591	O	LYS	115	39.622	-26.979	8.297	1.00	0.00	3A7
ATOM	592	N	ASN	116	39.579	-26.341	10.491	1.00	0.00	3A7
ATOM	593	CA	ASN	116	38.192	-26.560	10.889	1.00	0.00	3A7
ATOM	594	CB	ASN	116	37.101	-25.724	10.133	1.00	0.00	3A7
ATOM	595	CG	ASN	116	36.831	-26.079	8.657	1.00	0.00	3A7
ATOM	596	OD1	ASN	116	37.384	-25.453	7.745	1.00	0.00	3A7
ATOM	597	ND2	ASN	116	35.919	-27.074	8.437	1.00	0.00	3A7
ATOM	598	C	ASN	116	37.862	-28.039	10.949	1.00	0.00	3A7
ATOM	599	O	ASN	116	38.029	-28.777	9.979	1.00	0.00	3A7
ATOM	600	N	ALA	117	37.387	-28.501	12.134	1.00	0.00	3A7
ATOM	601	CA	ALA	117	37.152	-29.900	12.415	1.00	0.00	3A7
ATOM	602	CB	ALA	117	37.393	-30.247	13.899	1.00	0.00	3A7
ATOM	603	C	ALA	117	35.750	-30.294	12.024	1.00	0.00	3A7
ATOM	604	O	ALA	117	35.542	-30.857	10.951	1.00	0.00	3A7

ATOM	605	N	ILE	118	34.758	-30.027	12.909	1.00	0.00	3A7
ATOM	606	CA	ILE	118	33.403	-30.498	12.732	1.00	0.00	3A7
ATOM	607	CB	ILE	118	33.060	-31.666	13.661	1.00	0.00	3A7
ATOM	608	CG2	ILE	118	33.620	-32.948	13.008	1.00	0.00	3A7
ATOM	609	CG1	ILE	118	33.625	-31.523	15.097	1.00	0.00	3A7
ATOM	610	CD	ILE	118	32.902	-30.511	15.983	1.00	0.00	3A7
ATOM	611	C	ILE	118	32.454	-29.333	12.894	1.00	0.00	3A7
ATOM	612	O	ILE	118	31.481	-29.399	13.643	1.00	0.00	3A7
ATOM	613	N	SER	119	32.700	-28.231	12.139	1.00	0.00	3A7
ATOM	614	CA	SER	119	31.852	-27.054	12.114	1.00	0.00	3A7
ATOM	615	CB	SER	119	32.666	-25.747	11.972	1.00	0.00	3A7
ATOM	616	OG	SER	119	33.544	-25.595	13.079	1.00	0.00	3A7
ATOM	617	C	SER	119	30.902	-27.178	10.949	1.00	0.00	3A7
ATOM	618	O	SER	119	31.063	-26.507	9.930	1.00	0.00	3A7
ATOM	619	N	ILE	120	29.898	-28.096	11.093	1.00	0.00	3A7
ATOM	620	CA	ILE	120	28.963	-28.576	10.086	1.00	0.00	3A7
ATOM	621	CB	ILE	120	28.220	-27.497	9.294	1.00	0.00	3A7
ATOM	622	CG2	ILE	120	27.196	-28.166	8.349	1.00	0.00	3A7
ATOM	623	CG1	ILE	120	27.521	-26.482	10.237	1.00	0.00	3A7
ATOM	624	CD	ILE	120	26.467	-27.096	11.166	1.00	0.00	3A7
ATOM	625	C	ILE	120	29.730	-29.507	9.171	1.00	0.00	3A7
ATOM	626	O	ILE	120	30.456	-29.081	8.276	1.00	0.00	3A7
ATOM	627	N	ALA	121	29.621	-30.825	9.421	1.00	0.00	3A7
ATOM	628	CA	ALA	121	30.540	-31.779	8.845	1.00	0.00	3A7
ATOM	629	CB	ALA	121	31.516	-32.322	9.891	1.00	0.00	3A7
ATOM	630	C	ALA	121	29.781	-32.895	8.190	1.00	0.00	3A7
ATOM	631	O	ALA	121	28.574	-33.051	8.369	1.00	0.00	3A7
ATOM	632	N	GLU	122	30.519	-33.699	7.384	1.00	0.00	3A7
ATOM	633	CA	GLU	122	30.006	-34.785	6.580	1.00	0.00	3A7
ATOM	634	CB	GLU	122	30.832	-34.988	5.292	1.00	0.00	3A7
ATOM	635	CG	GLU	122	31.075	-33.676	4.532	1.00	0.00	3A7
ATOM	636	CD	GLU	122	31.734	-33.979	3.190	1.00	0.00	3A7
ATOM	637	OE1	GLU	122	31.094	-34.679	2.360	1.00	0.00	3A7
ATOM	638	OE2	GLU	122	32.884	-33.510	2.975	1.00	0.00	3A7
ATOM	639	C	GLU	122	30.077	-36.057	7.368	1.00	0.00	3A7
ATOM	640	O	GLU	122	30.753	-36.091	8.393	1.00	0.00	3A7
ATOM	641	N	ASP	123	29.389	-37.130	6.889	1.00	0.00	3A7
ATOM	642	CA	ASP	123	29.236	-38.402	7.576	1.00	0.00	3A7
ATOM	643	CB	ASP	123	27.977	-39.195	7.107	1.00	0.00	3A7
ATOM	644	CG	ASP	123	28.012	-39.602	5.628	1.00	0.00	3A7
ATOM	645	OD1	ASP	123	28.196	-38.707	4.763	1.00	0.00	3A7
ATOM	646	OD2	ASP	123	27.861	-40.822	5.354	1.00	0.00	3A7
ATOM	647	C	ASP	123	30.485	-39.259	7.471	1.00	0.00	3A7
ATOM	648	O	ASP	123	30.724	-39.955	6.485	1.00	0.00	3A7
ATOM	649	N	GLU	124	31.302	-39.189	8.540	1.00	0.00	3A7
ATOM	650	CA	GLU	124	32.560	-39.870	8.683	1.00	0.00	3A7
ATOM	651	CB	GLU	124	33.626	-39.519	7.609	1.00	0.00	3A7
ATOM	652	CG	GLU	124	34.965	-40.257	7.793	1.00	0.00	3A7
ATOM	653	CD	GLU	124	35.918	-39.851	6.672	1.00	0.00	3A7
ATOM	654	OE1	GLU	124	36.993	-39.275	6.989	1.00	0.00	3A7
ATOM	655	OE2	GLU	124	35.585	-40.115	5.486	1.00	0.00	3A7
ATOM	656	C	GLU	124	33.018	-39.381	10.020	1.00	0.00	3A7
ATOM	657	O	GLU	124	33.474	-40.149	10.866	1.00	0.00	3A7
ATOM	658	N	GLU	125	32.873	-38.047	10.219	1.00	0.00	3A7
ATOM	659	CA	GLU	125	33.141	-37.358	11.455	1.00	0.00	3A7
ATOM	660	CB	GLU	125	33.984	-36.078	11.267	1.00	0.00	3A7
ATOM	661	CG	GLU	125	35.301	-36.303	10.505	1.00	0.00	3A7
ATOM	662	CD	GLU	125	36.159	-37.314	11.254	1.00	0.00	3A7
ATOM	663	OE1	GLU	125	36.439	-38.392	10.667	1.00	0.00	3A7
ATOM	664	OE2	GLU	125	36.546	-37.024	12.418	1.00	0.00	3A7
ATOM	665	C	GLU	125	31.844	-36.969	12.096	1.00	0.00	3A7
ATOM	666	O	GLU	125	31.785	-36.775	13.306	1.00	0.00	3A7
ATOM	667	N	TRP	126	30.739	-36.843	11.315	1.00	0.00	3A7
ATOM	668	CA	TRP	126	29.448	-36.458	11.855	1.00	0.00	3A7
ATOM	669	CB	TRP	126	28.460	-36.001	10.762	1.00	0.00	3A7
ATOM	670	CG	TRP	126	27.427	-34.955	11.159	1.00	0.00	3A7
ATOM	671	CD2	TRP	126	27.726	-33.684	11.776	1.00	0.00	3A7
ATOM	672	CD1	TRP	126	26.092	-34.933	10.869	1.00	0.00	3A7
ATOM	673	NE1	TRP	126	25.536	-33.741	11.271	1.00	0.00	3A7
ATOM	674	CE2	TRP	126	26.527	-32.954	11.818	1.00	0.00	3A7
ATOM	675	CE3	TRP	126	28.905	-33.139	12.252	1.00	0.00	3A7
ATOM	676	CZ2	TRP	126	26.494	-31.670	12.329	1.00	0.00	3A7

ATOM	677	CZ3	TRP	126	28.868	-31.850	12.774	1.00	0.00	3A7
ATOM	678	CH2	TRP	126	27.680	-31.123	12.810	1.00	0.00	3A7
ATOM	679	C	TRP	126	28.874	-37.602	12.636	1.00	0.00	3A7
ATOM	680	O	TRP	126	28.393	-37.423	13.750	1.00	0.00	3A7
ATOM	681	N	LYS	127	28.962	-38.842	12.090	1.00	0.00	3A7
ATOM	682	CA	LYS	127	28.511	-40.060	12.743	1.00	0.00	3A7
ATOM	683	CB	LYS	127	28.749	-41.279	11.833	1.00	0.00	3A7
ATOM	684	CG	LYS	127	28.086	-42.581	12.315	1.00	0.00	3A7
ATOM	685	CD	LYS	127	28.264	-43.736	11.316	1.00	0.00	3A7
ATOM	686	CE	LYS	127	27.607	-45.046	11.770	1.00	0.00	3A7
ATOM	687	NZ	LYS	127	26.139	-44.893	11.883	1.00	0.00	3A7
ATOM	688	C	LYS	127	29.196	-40.320	14.072	1.00	0.00	3A7
ATOM	689	O	LYS	127	28.561	-40.651	15.070	1.00	0.00	3A7
ATOM	690	N	ARG	128	30.530	-40.112	14.123	1.00	0.00	3A7
ATOM	691	CA	ARG	128	31.301	-40.271	15.331	1.00	0.00	3A7
ATOM	692	CB	ARG	128	32.812	-40.274	15.061	1.00	0.00	3A7
ATOM	693	CG	ARG	128	33.252	-41.515	14.267	1.00	0.00	3A7
ATOM	694	CD	ARG	128	34.765	-41.777	14.317	1.00	0.00	3A7
ATOM	695	NE	ARG	128	35.198	-41.942	15.749	1.00	0.00	3A7
ATOM	696	CZ	ARG	128	34.997	-43.090	16.469	1.00	0.00	3A7
ATOM	697	NH1	ARG	128	35.389	-43.140	17.776	1.00	0.00	3A7
ATOM	698	NH2	ARG	128	34.422	-44.186	15.894	1.00	0.00	3A7
ATOM	699	C	ARG	128	30.991	-39.217	16.367	1.00	0.00	3A7
ATOM	700	O	ARG	128	30.847	-39.549	17.535	1.00	0.00	3A7
ATOM	701	N	ILE	129	30.823	-37.931	15.976	1.00	0.00	3A7
ATOM	702	CA	ILE	129	30.486	-36.852	16.897	1.00	0.00	3A7
ATOM	703	CB	ILE	129	30.651	-35.498	16.229	1.00	0.00	3A7
ATOM	704	CG2	ILE	129	29.684	-34.398	16.740	1.00	0.00	3A7
ATOM	705	CG1	ILE	129	32.104	-34.975	16.405	1.00	0.00	3A7
ATOM	706	CD	ILE	129	33.250	-35.944	16.093	1.00	0.00	3A7
ATOM	707	C	ILE	129	29.095	-37.028	17.444	1.00	0.00	3A7
ATOM	708	O	ILE	129	28.882	-36.896	18.640	1.00	0.00	3A7
ATOM	709	N	ARG	130	28.114	-37.398	16.595	1.00	0.00	3A7
ATOM	710	CA	ARG	130	26.759	-37.661	17.021	1.00	0.00	3A7
ATOM	711	CB	ARG	130	25.849	-37.943	15.811	1.00	0.00	3A7
ATOM	712	CG	ARG	130	25.540	-36.681	14.987	1.00	0.00	3A7
ATOM	713	CD	ARG	130	24.607	-36.942	13.796	1.00	0.00	3A7
ATOM	714	NE	ARG	130	25.280	-37.896	12.857	1.00	0.00	3A7
ATOM	715	CZ	ARG	130	24.691	-38.311	11.694	1.00	0.00	3A7
ATOM	716	NH1	ARG	130	25.358	-39.169	10.868	1.00	0.00	3A7
ATOM	717	NH2	ARG	130	23.446	-37.869	11.351	1.00	0.00	3A7
ATOM	718	C	ARG	130	26.695	-38.843	17.970	1.00	0.00	3A7
ATOM	719	O	ARG	130	26.037	-38.756	18.996	1.00	0.00	3A7
ATOM	720	N	SER	131	27.443	-39.943	17.701	1.00	0.00	3A7
ATOM	721	CA	SER	131	27.492	-41.105	18.571	1.00	0.00	3A7
ATOM	722	CB	SER	131	28.322	-42.268	17.985	1.00	0.00	3A7
ATOM	723	OG	SER	131	29.697	-41.986	17.760	1.00	0.00	3A7
ATOM	724	C	SER	131	28.053	-40.816	19.936	1.00	0.00	3A7
ATOM	725	O	SER	131	27.615	-41.352	20.947	1.00	0.00	3A7
ATOM	726	N	LEU	132	29.066	-39.936	19.998	1.00	0.00	3A7
ATOM	727	CA	LEU	132	29.705	-39.583	21.240	1.00	0.00	3A7
ATOM	728	CB	LEU	132	31.017	-38.838	20.968	1.00	0.00	3A7
ATOM	729	CG	LEU	132	32.105	-39.732	20.333	1.00	0.00	3A7
ATOM	730	CD1	LEU	132	33.135	-38.875	19.583	1.00	0.00	3A7
ATOM	731	CD2	LEU	132	32.782	-40.648	21.366	1.00	0.00	3A7
ATOM	732	C	LEU	132	28.808	-38.721	22.089	1.00	0.00	3A7
ATOM	733	O	LEU	132	28.688	-38.937	23.289	1.00	0.00	3A7
ATOM	734	N	LEU	133	28.116	-37.745	21.460	1.00	0.00	3A7
ATOM	735	CA	LEU	133	27.269	-36.794	22.145	1.00	0.00	3A7
ATOM	736	CB	LEU	133	26.997	-35.547	21.272	1.00	0.00	3A7
ATOM	737	CG	LEU	133	28.266	-34.787	20.869	1.00	0.00	3A7
ATOM	738	CD1	LEU	133	27.918	-33.493	20.117	1.00	0.00	3A7
ATOM	739	CD2	LEU	133	29.211	-34.589	22.052	1.00	0.00	3A7
ATOM	740	C	LEU	133	25.928	-37.334	22.547	1.00	0.00	3A7
ATOM	741	O	LEU	133	25.403	-36.955	23.590	1.00	0.00	3A7
ATOM	742	N	SER	134	25.333	-38.237	21.738	1.00	0.00	3A7
ATOM	743	CA	SER	134	24.003	-38.748	21.970	1.00	0.00	3A7
ATOM	744	CB	SER	134	23.511	-39.662	20.844	1.00	0.00	3A7
ATOM	745	OG	SER	134	24.394	-40.706	20.461	1.00	0.00	3A7
ATOM	746	C	SER	134	23.800	-39.430	23.296	1.00	0.00	3A7
ATOM	747	O	SER	134	22.725	-39.226	23.854	1.00	0.00	3A7
ATOM	748	N	PRO	135	24.715	-40.198	23.891	1.00	0.00	3A7

ATOM	749	CA	PRO	135	24.491	-40.773	25.190	1.00	0.00	3A7
ATOM	750	CD	PRO	135	25.854	-40.834	23.260	1.00	0.00	3A7
ATOM	751	CB	PRO	135	25.551	-41.871	25.355	1.00	0.00	3A7
ATOM	752	CG	PRO	135	25.961	-42.203	23.924	1.00	0.00	3A7
ATOM	753	C	PRO	135	24.618	-39.783	26.310	1.00	0.00	3A7
ATOM	754	O	PRO	135	23.867	-39.912	27.273	1.00	0.00	3A7
ATOM	755	N	THR	136	25.553	-38.805	26.231	1.00	0.00	3A7
ATOM	756	CA	THR	136	25.770	-37.840	27.291	1.00	0.00	3A7
ATOM	757	CB	THR	136	27.148	-37.210	27.207	1.00	0.00	3A7
ATOM	758	OG1	THR	136	27.386	-36.654	25.918	1.00	0.00	3A7
ATOM	759	CG2	THR	136	28.182	-38.319	27.492	1.00	0.00	3A7
ATOM	760	C	THR	136	24.693	-36.769	27.320	1.00	0.00	3A7
ATOM	761	O	THR	136	24.369	-36.212	28.360	1.00	0.00	3A7
ATOM	762	N	PHE	137	24.066	-36.471	26.165	1.00	0.00	3A7
ATOM	763	CA	PHE	137	23.044	-35.454	26.069	1.00	0.00	3A7
ATOM	764	CB	PHE	137	23.219	-34.665	24.778	1.00	0.00	3A7
ATOM	765	CG	PHE	137	24.305	-33.645	25.018	1.00	0.00	3A7
ATOM	766	CD1	PHE	137	25.578	-33.792	24.468	1.00	0.00	3A7
ATOM	767	CD2	PHE	137	24.057	-32.535	25.831	1.00	0.00	3A7
ATOM	768	CE1	PHE	137	26.580	-32.863	24.725	1.00	0.00	3A7
ATOM	769	CE2	PHE	137	25.050	-31.590	26.070	1.00	0.00	3A7
ATOM	770	CZ	PHE	137	26.316	-31.757	25.524	1.00	0.00	3A7
ATOM	771	C	PHE	137	21.711	-36.153	26.100	1.00	0.00	3A7
ATOM	772	O	PHE	137	20.779	-35.799	25.406	1.00	0.00	3A7
ATOM	773	N	THR	138	21.542	-37.179	26.952	1.00	0.00	3A7
ATOM	774	CA	THR	138	20.246	-37.782	27.179	1.00	0.00	3A7
ATOM	775	CB	THR	138	20.313	-39.259	27.505	1.00	0.00	3A7
ATOM	776	OG1	THR	138	21.270	-39.549	28.518	1.00	0.00	3A7
ATOM	777	CG2	THR	138	20.673	-40.035	26.226	1.00	0.00	3A7
ATOM	778	C	THR	138	19.588	-37.063	28.326	1.00	0.00	3A7
ATOM	779	O	THR	138	20.234	-36.412	29.149	1.00	0.00	3A7
ATOM	780	N	SER	139	18.250	-37.211	28.416	1.00	0.00	3A7
ATOM	781	CA	SER	139	17.433	-36.585	29.427	1.00	0.00	3A7
ATOM	782	CB	SER	139	15.917	-36.809	29.183	1.00	0.00	3A7
ATOM	783	OG	SER	139	15.590	-38.188	29.037	1.00	0.00	3A7
ATOM	784	C	SER	139	17.797	-37.053	30.810	1.00	0.00	3A7
ATOM	785	O	SER	139	17.738	-36.290	31.765	1.00	0.00	3A7
ATOM	786	N	GLY	140	18.263	-38.318	30.922	1.00	0.00	3A7
ATOM	787	CA	GLY	140	18.713	-38.898	32.158	1.00	0.00	3A7
ATOM	788	C	GLY	140	20.032	-38.362	32.618	1.00	0.00	3A7
ATOM	789	O	GLY	140	20.273	-38.260	33.820	1.00	0.00	3A7
ATOM	790	N	LYS	141	20.933	-38.021	31.673	1.00	0.00	3A7
ATOM	791	CA	LYS	141	22.309	-37.803	32.064	1.00	0.00	3A7
ATOM	792	CB	LYS	141	23.285	-38.611	31.169	1.00	0.00	3A7
ATOM	793	CG	LYS	141	23.070	-40.129	31.293	1.00	0.00	3A7
ATOM	794	CD	LYS	141	24.150	-40.944	30.571	1.00	0.00	3A7
ATOM	795	CE	LYS	141	23.916	-42.456	30.655	1.00	0.00	3A7
ATOM	796	NZ	LYS	141	24.978	-43.189	29.928	1.00	0.00	3A7
ATOM	797	C	LYS	141	22.832	-36.386	32.232	1.00	0.00	3A7
ATOM	798	O	LYS	141	22.859	-35.680	33.265	1.00	0.00	3A7
ATOM	799	N	LEU	142	23.635	-36.031	31.185	1.00	0.00	3A7
ATOM	800	CA	LEU	142	24.644	-34.970	31.099	1.00	0.00	3A7
ATOM	801	CB	LEU	142	23.972	-33.593	30.894	1.00	0.00	3A7
ATOM	802	CG	LEU	142	24.455	-32.799	29.656	1.00	0.00	3A7
ATOM	803	CD1	LEU	142	23.560	-31.564	29.439	1.00	0.00	3A7
ATOM	804	CD2	LEU	142	25.943	-32.407	29.718	1.00	0.00	3A7
ATOM	805	C	LEU	142	25.663	-34.903	32.241	1.00	0.00	3A7
ATOM	806	O	LEU	142	26.359	-33.901	32.398	1.00	0.00	3A7
ATOM	807	N	LYS	143	25.729	-35.975	33.085	1.00	0.00	3A7
ATOM	808	CA	LYS	143	26.391	-36.077	34.381	1.00	0.00	3A7
ATOM	809	CB	LYS	143	27.931	-35.966	34.315	1.00	0.00	3A7
ATOM	810	CG	LYS	143	28.567	-37.003	33.373	1.00	0.00	3A7
ATOM	811	CD	LYS	143	28.188	-38.480	33.614	1.00	0.00	3A7
ATOM	812	CE	LYS	143	28.784	-39.129	34.873	1.00	0.00	3A7
ATOM	813	NZ	LYS	143	28.177	-38.601	36.117	1.00	0.00	3A7
ATOM	814	C	LYS	143	25.831	-35.060	35.351	1.00	0.00	3A7
ATOM	815	O	LYS	143	26.561	-34.248	35.919	1.00	0.00	3A7
ATOM	816	N	GLU	144	24.476	-35.097	35.479	1.00	0.00	3A7
ATOM	817	CA	GLU	144	23.593	-34.122	36.090	1.00	0.00	3A7
ATOM	818	CB	GLU	144	24.058	-33.575	37.466	1.00	0.00	3A7
ATOM	819	CG	GLU	144	24.205	-34.669	38.535	1.00	0.00	3A7
ATOM	820	CD	GLU	144	24.730	-34.037	39.820	1.00	0.00	3A7

ATOM	821	OE1	GLU	144	25.849	-34.422	40.255	1.00	0.00	3A7
ATOM	822	OE2	GLU	144	24.022	-33.161	40.384	1.00	0.00	3A7
ATOM	823	C	GLU	144	23.380	-32.972	35.123	1.00	0.00	3A7
ATOM	824	O	GLU	144	24.284	-32.166	34.907	1.00	0.00	3A7
ATOM	825	N	MET	145	22.163	-32.867	34.523	1.00	0.00	3A7
ATOM	826	CA	MET	145	21.768	-31.691	33.757	1.00	0.00	3A7
ATOM	827	CB	MET	145	21.203	-31.937	32.347	1.00	0.00	3A7
ATOM	828	CG	MET	145	20.243	-33.140	32.238	1.00	0.00	3A7
ATOM	829	SD	MET	145	19.496	-33.350	30.593	1.00	0.00	3A7
ATOM	830	CE	MET	145	18.314	-31.978	30.743	1.00	0.00	3A7
ATOM	831	C	MET	145	20.736	-30.926	34.510	1.00	0.00	3A7
ATOM	832	O	MET	145	20.810	-29.704	34.599	1.00	0.00	3A7
ATOM	833	N	VAL	146	19.718	-31.609	35.082	1.00	0.00	3A7
ATOM	834	CA	VAL	146	18.618	-30.943	35.756	1.00	0.00	3A7
ATOM	835	CB	VAL	146	17.494	-31.869	36.146	1.00	0.00	3A7
ATOM	836	CG1	VAL	146	16.290	-30.982	36.556	1.00	0.00	3A7
ATOM	837	CG2	VAL	146	17.145	-32.759	34.935	1.00	0.00	3A7
ATOM	838	C	VAL	146	19.066	-30.148	36.957	1.00	0.00	3A7
ATOM	839	O	VAL	146	18.633	-29.004	37.094	1.00	0.00	3A7
ATOM	840	N	PRO	147	19.976	-30.644	37.801	1.00	0.00	3A7
ATOM	841	CA	PRO	147	20.491	-29.872	38.908	1.00	0.00	3A7
ATOM	842	CD	PRO	147	20.305	-32.060	37.960	1.00	0.00	3A7
ATOM	843	CB	PRO	147	21.360	-30.856	39.708	1.00	0.00	3A7
ATOM	844	CG	PRO	147	20.726	-32.213	39.420	1.00	0.00	3A7
ATOM	845	C	PRO	147	21.286	-28.672	38.470	1.00	0.00	3A7
ATOM	846	O	PRO	147	21.286	-27.680	39.190	1.00	0.00	3A7
ATOM	847	N	ILE	148	21.943	-28.722	37.294	1.00	0.00	3A7
ATOM	848	CA	ILE	148	22.723	-27.631	36.762	1.00	0.00	3A7
ATOM	849	CB	ILE	148	23.664	-28.114	35.675	1.00	0.00	3A7
ATOM	850	CG2	ILE	148	24.341	-26.923	34.952	1.00	0.00	3A7
ATOM	851	CG1	ILE	148	24.796	-29.020	36.211	1.00	0.00	3A7
ATOM	852	CD	ILE	148	24.460	-30.116	37.225	1.00	0.00	3A7
ATOM	853	C	ILE	148	21.813	-26.558	36.204	1.00	0.00	3A7
ATOM	854	O	ILE	148	22.073	-25.361	36.322	1.00	0.00	3A7
ATOM	855	N	ILE	149	20.672	-26.968	35.607	1.00	0.00	3A7
ATOM	856	CA	ILE	149	19.682	-26.045	35.098	1.00	0.00	3A7
ATOM	857	CB	ILE	149	18.645	-26.744	34.263	1.00	0.00	3A7
ATOM	858	CG2	ILE	149	17.595	-25.733	33.743	1.00	0.00	3A7
ATOM	859	CG1	ILE	149	19.377	-27.390	33.058	1.00	0.00	3A7
ATOM	860	CD	ILE	149	18.552	-28.444	32.319	1.00	0.00	3A7
ATOM	861	C	ILE	149	19.032	-25.338	36.240	1.00	0.00	3A7
ATOM	862	O	ILE	149	18.779	-24.137	36.179	1.00	0.00	3A7
ATOM	863	N	ALA	150	18.793	-26.059	37.357	1.00	0.00	3A7
ATOM	864	CA	ALA	150	18.229	-25.493	38.558	1.00	0.00	3A7
ATOM	865	CB	ALA	150	17.894	-26.586	39.578	1.00	0.00	3A7
ATOM	866	C	ALA	150	19.160	-24.490	39.195	1.00	0.00	3A7
ATOM	867	O	ALA	150	18.723	-23.461	39.693	1.00	0.00	3A7
ATOM	868	N	GLN	151	20.488	-24.737	39.144	1.00	0.00	3A7
ATOM	869	CA	GLN	151	21.492	-23.836	39.661	1.00	0.00	3A7
ATOM	870	CB	GLN	151	22.910	-24.428	39.555	1.00	0.00	3A7
ATOM	871	CG	GLN	151	23.192	-25.483	40.637	1.00	0.00	3A7
ATOM	872	CD	GLN	151	24.551	-26.129	40.357	1.00	0.00	3A7
ATOM	873	OE1	GLN	151	25.580	-25.444	40.306	1.00	0.00	3A7
ATOM	874	NE2	GLN	151	24.541	-27.485	40.172	1.00	0.00	3A7
ATOM	875	C	GLN	151	21.475	-22.493	38.989	1.00	0.00	3A7
ATOM	876	O	GLN	151	21.418	-21.447	39.634	1.00	0.00	3A7
ATOM	877	N	TYR	152	21.474	-22.502	37.644	1.00	0.00	3A7
ATOM	878	CA	TYR	152	21.438	-21.288	36.872	1.00	0.00	3A7
ATOM	879	CB	TYR	152	21.651	-21.508	35.367	1.00	0.00	3A7
ATOM	880	CG	TYR	152	22.236	-20.216	34.776	1.00	0.00	3A7
ATOM	881	CD1	TYR	152	23.578	-19.994	35.099	1.00	0.00	3A7
ATOM	882	CD2	TYR	152	21.411	-19.109	34.632	1.00	0.00	3A7
ATOM	883	CE1	TYR	152	24.053	-18.705	35.335	1.00	0.00	3A7
ATOM	884	CE2	TYR	152	21.870	-17.822	34.898	1.00	0.00	3A7
ATOM	885	CZ	TYR	152	23.208	-17.612	35.201	1.00	0.00	3A7
ATOM	886	OH	TYR	152	23.690	-16.302	35.411	1.00	0.00	3A7
ATOM	887	C	TYR	152	20.140	-20.556	37.038	1.00	0.00	3A7
ATOM	888	O	TYR	152	20.108	-19.335	37.134	1.00	0.00	3A7
ATOM	889	N	GLY	153	19.025	-21.301	37.117	1.00	0.00	3A7
ATOM	890	CA	GLY	153	17.715	-20.733	37.311	1.00	0.00	3A7
ATOM	891	C	GLY	153	17.596	-19.972	38.591	1.00	0.00	3A7
ATOM	892	O	GLY	153	16.977	-18.915	38.657	1.00	0.00	3A7

ATOM	893	N	ASP	154	18.270	-20.457	39.650	1.00	0.00	3A7
ATOM	894	CA	ASP	154	18.353	-19.782	40.919	1.00	0.00	3A7
ATOM	895	CB	ASP	154	19.017	-20.685	41.976	1.00	0.00	3A7
ATOM	896	CG	ASP	154	18.142	-21.901	42.299	1.00	0.00	3A7
ATOM	897	OD1	ASP	154	16.975	-21.960	41.830	1.00	0.00	3A7
ATOM	898	OD2	ASP	154	18.643	-22.790	43.039	1.00	0.00	3A7
ATOM	899	C	ASP	154	19.130	-18.483	40.808	1.00	0.00	3A7
ATOM	900	O	ASP	154	18.726	-17.469	41.361	1.00	0.00	3A7
ATOM	901	N	VAL	155	20.243	-18.474	40.041	1.00	0.00	3A7
ATOM	902	CA	VAL	155	21.039	-17.293	39.761	1.00	0.00	3A7
ATOM	903	CB	VAL	155	22.308	-17.637	38.989	1.00	0.00	3A7
ATOM	904	CG1	VAL	155	23.103	-16.370	38.590	1.00	0.00	3A7
ATOM	905	CG2	VAL	155	23.251	-18.537	39.870	1.00	0.00	3A7
ATOM	906	C	VAL	155	20.273	-16.247	39.005	1.00	0.00	3A7
ATOM	907	O	VAL	155	20.407	-15.062	39.286	1.00	0.00	3A7
ATOM	908	N	LEU	156	19.427	-16.653	38.035	1.00	0.00	3A7
ATOM	909	CA	LEU	156	18.566	-15.759	37.295	1.00	0.00	3A7
ATOM	910	CB	LEU	156	17.791	-16.496	36.208	1.00	0.00	3A7
ATOM	911	CG	LEU	156	17.040	-15.502	35.295	1.00	0.00	3A7
ATOM	912	CD1	LEU	156	17.539	-15.527	33.841	1.00	0.00	3A7
ATOM	913	CD2	LEU	156	15.520	-15.740	35.345	1.00	0.00	3A7
ATOM	914	C	LEU	156	17.570	-15.040	38.134	1.00	0.00	3A7
ATOM	915	O	LEU	156	17.442	-13.817	38.081	1.00	0.00	3A7
ATOM	916	N	VAL	157	16.840	-15.805	38.969	1.00	0.00	3A7
ATOM	917	CA	VAL	157	15.830	-15.290	39.861	1.00	0.00	3A7
ATOM	918	CB	VAL	157	15.164	-16.419	40.629	1.00	0.00	3A7
ATOM	919	CG1	VAL	157	14.204	-15.903	41.728	1.00	0.00	3A7
ATOM	920	CG2	VAL	157	14.373	-17.263	39.609	1.00	0.00	3A7
ATOM	921	C	VAL	157	16.437	-14.314	40.832	1.00	0.00	3A7
ATOM	922	O	VAL	157	15.906	-13.236	41.069	1.00	0.00	3A7
ATOM	923	N	ARG	158	17.626	-14.668	41.358	1.00	0.00	3A7
ATOM	924	CA	ARG	158	18.365	-13.822	42.251	1.00	0.00	3A7
ATOM	925	CB	ARG	158	19.590	-14.557	42.789	1.00	0.00	3A7
ATOM	926	CG	ARG	158	20.308	-13.863	43.961	1.00	0.00	3A7
ATOM	927	CD	ARG	158	21.475	-14.689	44.519	1.00	0.00	3A7
ATOM	928	NE	ARG	158	20.932	-15.988	45.038	1.00	0.00	3A7
ATOM	929	CZ	ARG	158	21.742	-17.042	45.358	1.00	0.00	3A7
ATOM	930	NH1	ARG	158	21.187	-18.206	45.808	1.00	0.00	3A7
ATOM	931	NH2	ARG	158	23.097	-16.943	45.230	1.00	0.00	3A7
ATOM	932	C	ARG	158	18.810	-12.537	41.638	1.00	0.00	3A7
ATOM	933	O	ARG	158	18.732	-11.498	42.274	1.00	0.00	3A7
ATOM	934	N	ASN	159	19.237	-12.550	40.359	1.00	0.00	3A7
ATOM	935	CA	ASN	159	19.621	-11.357	39.637	1.00	0.00	3A7
ATOM	936	CB	ASN	159	20.171	-11.697	38.250	1.00	0.00	3A7
ATOM	937	CG	ASN	159	21.490	-12.475	38.358	1.00	0.00	3A7
ATOM	938	OD1	ASN	159	22.072	-12.627	39.439	1.00	0.00	3A7
ATOM	939	ND2	ASN	159	21.964	-12.980	37.177	1.00	0.00	3A7
ATOM	940	C	ASN	159	18.466	-10.408	39.454	1.00	0.00	3A7
ATOM	941	O	ASN	159	18.606	-9.195	39.568	1.00	0.00	3A7
ATOM	942	N	LEU	160	17.267	-10.966	39.205	1.00	0.00	3A7
ATOM	943	CA	LEU	160	16.066	-10.198	39.031	1.00	0.00	3A7
ATOM	944	CB	LEU	160	14.972	-11.061	38.383	1.00	0.00	3A7
ATOM	945	CG	LEU	160	15.234	-11.457	36.902	1.00	0.00	3A7
ATOM	946	CD1	LEU	160	14.149	-12.430	36.402	1.00	0.00	3A7
ATOM	947	CD2	LEU	160	15.359	-10.246	35.959	1.00	0.00	3A7
ATOM	948	C	LEU	160	15.557	-9.655	40.349	1.00	0.00	3A7
ATOM	949	O	LEU	160	14.965	-8.580	40.420	1.00	0.00	3A7
ATOM	950	N	ARG	161	15.836	-10.377	41.455	1.00	0.00	3A7
ATOM	951	CA	ARG	161	15.487	-9.958	42.787	1.00	0.00	3A7
ATOM	952	CB	ARG	161	15.773	-11.052	43.830	1.00	0.00	3A7
ATOM	953	CG	ARG	161	14.640	-12.097	43.887	1.00	0.00	3A7
ATOM	954	CD	ARG	161	14.752	-13.097	45.047	1.00	0.00	3A7
ATOM	955	NE	ARG	161	15.964	-13.954	44.841	1.00	0.00	3A7
ATOM	956	CZ	ARG	161	16.221	-15.051	45.617	1.00	0.00	3A7
ATOM	957	NH1	ARG	161	17.333	-15.804	45.374	1.00	0.00	3A7
ATOM	958	NH2	ARG	161	15.375	-15.400	46.629	1.00	0.00	3A7
ATOM	959	C	ARG	161	16.228	-8.712	43.210	1.00	0.00	3A7
ATOM	960	O	ARG	161	15.673	-7.843	43.879	1.00	0.00	3A7
ATOM	961	N	ARG	162	17.510	-8.597	42.792	1.00	0.00	3A7
ATOM	962	CA	ARG	162	18.380	-7.499	43.134	1.00	0.00	3A7
ATOM	963	CB	ARG	162	19.851	-7.869	42.894	1.00	0.00	3A7
ATOM	964	CG	ARG	162	20.346	-8.986	43.829	1.00	0.00	3A7

ATOM	965	CD	ARG	162	21.838	-9.302	43.666	1.00	0.00	3A7
ATOM	966	NE	ARG	162	22.095	-9.696	42.242	1.00	0.00	3A7
ATOM	967	CZ	ARG	162	23.363	-9.855	41.755	1.00	0.00	3A7
ATOM	968	NH1	ARG	162	23.548	-10.141	40.433	1.00	0.00	3A7
ATOM	969	NH2	ARG	162	24.444	-9.724	42.577	1.00	0.00	3A7
ATOM	970	C	ARG	162	18.080	-6.236	42.355	1.00	0.00	3A7
ATOM	971	O	ARG	162	18.755	-5.220	42.500	1.00	0.00	3A7
ATOM	972	N	GLU	163	17.014	-6.247	41.519	1.00	0.00	3A7
ATOM	973	CA	GLU	163	16.615	-5.103	40.744	1.00	0.00	3A7
ATOM	974	CB	GLU	163	15.965	-5.504	39.413	1.00	0.00	3A7
ATOM	975	CG	GLU	163	16.981	-6.330	38.605	1.00	0.00	3A7
ATOM	976	CD	GLU	163	16.426	-6.716	37.246	1.00	0.00	3A7
ATOM	977	OE1	GLU	163	17.080	-6.372	36.227	1.00	0.00	3A7
ATOM	978	OE2	GLU	163	15.354	-7.376	37.210	1.00	0.00	3A7
ATOM	979	C	GLU	163	15.784	-4.183	41.582	1.00	0.00	3A7
ATOM	980	O	GLU	163	15.662	-2.998	41.288	1.00	0.00	3A7
ATOM	981	N	ALA	164	15.230	-4.708	42.699	1.00	0.00	3A7
ATOM	982	CA	ALA	164	14.728	-3.939	43.812	1.00	0.00	3A7
ATOM	983	CB	ALA	164	15.779	-2.963	44.394	1.00	0.00	3A7
ATOM	984	C	ALA	164	13.480	-3.200	43.529	1.00	0.00	3A7
ATOM	985	O	ALA	164	13.505	-1.993	43.644	1.00	0.00	3A7
ATOM	986	N	GLU	165	12.363	-3.878	43.176	1.00	0.00	3A7
ATOM	987	CA	GLU	165	10.993	-3.400	43.222	1.00	0.00	3A7
ATOM	988	CB	GLU	165	10.561	-2.688	44.540	1.00	0.00	3A7
ATOM	989	CG	GLU	165	10.851	-3.510	45.809	1.00	0.00	3A7
ATOM	990	CD	GLU	165	10.308	-2.803	47.050	1.00	0.00	3A7
ATOM	991	OE1	GLU	165	9.757	-1.678	46.915	1.00	0.00	3A7
ATOM	992	OE2	GLU	165	10.441	-3.390	48.158	1.00	0.00	3A7
ATOM	993	C	GLU	165	10.541	-2.574	42.031	1.00	0.00	3A7
ATOM	994	O	GLU	165	9.403	-2.728	41.595	1.00	0.00	3A7
ATOM	995	N	THR	166	11.382	-1.661	41.488	1.00	0.00	3A7
ATOM	996	CA	THR	166	10.979	-0.758	40.425	1.00	0.00	3A7
ATOM	997	CB	THR	166	10.351	0.509	40.932	1.00	0.00	3A7
ATOM	998	OG1	THR	166	9.175	0.217	41.676	1.00	0.00	3A7
ATOM	999	CG2	THR	166	9.944	1.442	39.767	1.00	0.00	3A7
ATOM	1000	C	THR	166	12.235	-0.374	39.728	1.00	0.00	3A7
ATOM	1001	O	THR	166	12.410	-0.652	38.547	1.00	0.00	3A7
ATOM	1002	N	GLY	167	13.141	0.230	40.560	1.00	0.00	3A7
ATOM	1003	CA	GLY	167	14.556	0.524	40.415	1.00	0.00	3A7
ATOM	1004	C	GLY	167	14.980	0.965	39.058	1.00	0.00	3A7
ATOM	1005	O	GLY	167	15.037	2.155	38.750	1.00	0.00	3A7
ATOM	1006	N	LYS	168	15.246	-0.048	38.208	1.00	0.00	3A7
ATOM	1007	CA	LYS	168	15.423	0.121	36.801	1.00	0.00	3A7
ATOM	1008	CB	LYS	168	16.887	-0.172	36.380	1.00	0.00	3A7
ATOM	1009	CG	LYS	168	17.309	0.475	35.050	1.00	0.00	3A7
ATOM	1010	CD	LYS	168	18.803	0.294	34.725	1.00	0.00	3A7
ATOM	1011	CE	LYS	168	19.236	-1.160	34.483	1.00	0.00	3A7
ATOM	1012	NZ	LYS	168	18.558	-1.731	33.297	1.00	0.00	3A7
ATOM	1013	C	LYS	168	14.438	-0.857	36.181	1.00	0.00	3A7
ATOM	1014	O	LYS	168	14.315	-1.969	36.694	1.00	0.00	3A7
ATOM	1015	N	PRO	169	13.751	-0.544	35.061	1.00	0.00	3A7
ATOM	1016	CA	PRO	169	13.228	-1.488	34.077	1.00	0.00	3A7
ATOM	1017	CD	PRO	169	13.706	0.834	34.565	1.00	0.00	3A7
ATOM	1018	CB	PRO	169	12.639	-0.568	33.005	1.00	0.00	3A7
ATOM	1019	CG	PRO	169	13.438	0.725	33.072	1.00	0.00	3A7
ATOM	1020	C	PRO	169	14.386	-2.289	33.508	1.00	0.00	3A7
ATOM	1021	O	PRO	169	15.533	-1.866	33.608	1.00	0.00	3A7
ATOM	1022	N	VAL	170	14.110	-3.480	32.963	1.00	0.00	3A7
ATOM	1023	CA	VAL	170	15.120	-4.462	32.688	1.00	0.00	3A7
ATOM	1024	CB	VAL	170	14.791	-5.773	33.379	1.00	0.00	3A7
ATOM	1025	CG1	VAL	170	15.992	-6.742	33.323	1.00	0.00	3A7
ATOM	1026	CG2	VAL	170	14.350	-5.485	34.825	1.00	0.00	3A7
ATOM	1027	C	VAL	170	15.190	-4.659	31.200	1.00	0.00	3A7
ATOM	1028	O	VAL	170	14.185	-4.556	30.501	1.00	0.00	3A7
ATOM	1029	N	THR	171	16.400	-4.984	30.690	1.00	0.00	3A7
ATOM	1030	CA	THR	171	16.616	-5.364	29.321	1.00	0.00	3A7
ATOM	1031	CB	THR	171	17.889	-4.784	28.730	1.00	0.00	3A7
ATOM	1032	OG1	THR	171	17.858	-3.368	28.857	1.00	0.00	3A7
ATOM	1033	CG2	THR	171	18.018	-5.145	27.233	1.00	0.00	3A7
ATOM	1034	C	THR	171	16.717	-6.854	29.319	1.00	0.00	3A7
ATOM	1035	O	THR	171	17.667	-7.434	29.839	1.00	0.00	3A7
ATOM	1036	N	LEU	172	15.716	-7.527	28.719	1.00	0.00	3A7

```
ATOM   1037  CA  LEU   172      15.566  -8.955  28.820  1.00  0.00          3A7
ATOM   1038  CB  LEU   172      14.147  -9.409  28.421  1.00  0.00          3A7
ATOM   1039  CG  LEU   172      12.958  -8.735  29.139  1.00  0.00          3A7
ATOM   1040  CD1 LEU   172      13.118  -8.664  30.670  1.00  0.00          3A7
ATOM   1041  CD2 LEU   172      12.633  -7.378  28.501  1.00  0.00          3A7
ATOM   1042  C   LEU   172      16.574  -9.705  27.991  1.00  0.00          3A7
ATOM   1043  O   LEU   172      17.033 -10.771  28.384  1.00  0.00          3A7
ATOM   1044  N   LYS   173      16.994  -9.161  26.826  1.00  0.00          3A7
ATOM   1045  CA  LYS   173      17.961  -9.803  25.952  1.00  0.00          3A7
ATOM   1046  CB  LYS   173      18.202  -8.967  24.685  1.00  0.00          3A7
ATOM   1047  CG  LYS   173      19.033  -9.687  23.605  1.00  0.00          3A7
ATOM   1048  CD  LYS   173      19.257  -8.825  22.357  1.00  0.00          3A7
ATOM   1049  CE  LYS   173      19.931  -9.589  21.211  1.00  0.00          3A7
ATOM   1050  NZ  LYS   173      20.065  -8.725  20.017  1.00  0.00          3A7
ATOM   1051  C   LYS   173      19.296 -10.057  26.620  1.00  0.00          3A7
ATOM   1052  O   LYS   173      19.912 -11.106  26.445  1.00  0.00          3A7
ATOM   1053  N   HIS   174      19.729  -9.103  27.472  1.00  0.00          3A7
ATOM   1054  CA  HIS   174      20.962  -9.190  28.204  1.00  0.00          3A7
ATOM   1055  ND1 HIS   174      23.840  -7.893  28.844  1.00  0.00          3A7
ATOM   1056  CG  HIS   174      22.644  -7.783  29.521  1.00  0.00          3A7
ATOM   1057  CB  HIS   174      21.288  -7.846  28.865  1.00  0.00          3A7
ATOM   1058  NE2 HIS   174      24.347  -7.664  30.996  1.00  0.00          3A7
ATOM   1059  CD2 HIS   174      22.973  -7.645  30.834  1.00  0.00          3A7
ATOM   1060  CE1 HIS   174      24.824  -7.814  29.775  1.00  0.00          3A7
ATOM   1061  C   HIS   174      20.970 -10.255  29.275  1.00  0.00          3A7
ATOM   1062  O   HIS   174      21.877 -11.082  29.317  1.00  0.00          3A7
ATOM   1063  N   VAL   175      19.954 -10.272  30.170  1.00  0.00          3A7
ATOM   1064  CA  VAL   175      19.876 -11.181  31.303  1.00  0.00          3A7
ATOM   1065  CB  VAL   175      18.832 -10.715  32.291  1.00  0.00          3A7
ATOM   1066  CG1 VAL   175      18.836 -11.586  33.568  1.00  0.00          3A7
ATOM   1067  CG2 VAL   175      19.117  -9.239  32.645  1.00  0.00          3A7
ATOM   1068  C   VAL   175      19.575 -12.603  30.872  1.00  0.00          3A7
ATOM   1069  O   VAL   175      20.055 -13.576  31.455  1.00  0.00          3A7
ATOM   1070  N   PHE   176      18.769 -12.751  29.799  1.00  0.00          3A7
ATOM   1071  CA  PHE   176      18.383 -14.047  29.302  1.00  0.00          3A7
ATOM   1072  CB  PHE   176      17.044 -13.978  28.573  1.00  0.00          3A7
ATOM   1073  CG  PHE   176      15.984 -14.019  29.651  1.00  0.00          3A7
ATOM   1074  CD1 PHE   176      15.271 -12.887  30.048  1.00  0.00          3A7
ATOM   1075  CD2 PHE   176      15.760 -15.216  30.337  1.00  0.00          3A7
ATOM   1076  CE1 PHE   176      14.380 -12.941  31.117  1.00  0.00          3A7
ATOM   1077  CE2 PHE   176      14.857 -15.282  31.394  1.00  0.00          3A7
ATOM   1078  CZ  PHE   176      14.171 -14.139  31.790  1.00  0.00          3A7
ATOM   1079  C   PHE   176      19.411 -14.648  28.382  1.00  0.00          3A7
ATOM   1080  O   PHE   176      19.429 -15.860  28.180  1.00  0.00          3A7
ATOM   1081  N   GLY   177      20.328 -13.824  27.829  1.00  0.00          3A7
ATOM   1082  CA  GLY   177      21.447 -14.314  27.061  1.00  0.00          3A7
ATOM   1083  C   GLY   177      22.530 -14.791  27.997  1.00  0.00          3A7
ATOM   1084  O   GLY   177      23.231 -15.756  27.714  1.00  0.00          3A7
ATOM   1085  N   ALA   178      22.657 -14.142  29.180  1.00  0.00          3A7
ATOM   1086  CA  ALA   178      23.616 -14.483  30.214  1.00  0.00          3A7
ATOM   1087  CB  ALA   178      23.639 -13.426  31.327  1.00  0.00          3A7
ATOM   1088  C   ALA   178      23.303 -15.805  30.855  1.00  0.00          3A7
ATOM   1089  O   ALA   178      24.178 -16.635  31.070  1.00  0.00          3A7
ATOM   1090  N   TYR   179      22.004 -16.063  31.127  1.00  0.00          3A7
ATOM   1091  CA  TYR   179      21.522 -17.288  31.732  1.00  0.00          3A7
ATOM   1092  CB  TYR   179      19.979 -17.174  31.929  1.00  0.00          3A7
ATOM   1093  CG  TYR   179      19.104 -18.432  31.952  1.00  0.00          3A7
ATOM   1094  CD1 TYR   179      18.538 -18.892  33.140  1.00  0.00          3A7
ATOM   1095  CD2 TYR   179      18.795 -19.133  30.778  1.00  0.00          3A7
ATOM   1096  CE1 TYR   179      17.873 -20.112  33.200  1.00  0.00          3A7
ATOM   1097  CE2 TYR   179      18.128 -20.354  30.824  1.00  0.00          3A7
ATOM   1098  CZ  TYR   179      17.709 -20.868  32.046  1.00  0.00          3A7
ATOM   1099  OH  TYR   179      17.108 -22.143  32.117  1.00  0.00          3A7
ATOM   1100  C   TYR   179      21.881 -18.504  30.914  1.00  0.00          3A7
ATOM   1101  O   TYR   179      22.420 -19.487  31.413  1.00  0.00          3A7
ATOM   1102  N   SER   180      21.607 -18.432  29.602  1.00  0.00          3A7
ATOM   1103  CA  SER   180      21.758 -19.553  28.719  1.00  0.00          3A7
ATOM   1104  CB  SER   180      20.943 -19.328  27.464  1.00  0.00          3A7
ATOM   1105  OG  SER   180      21.331 -18.109  26.860  1.00  0.00          3A7
ATOM   1106  C   SER   180      23.198 -19.852  28.402  1.00  0.00          3A7
ATOM   1107  O   SER   180      23.565 -21.010  28.278  1.00  0.00          3A7
ATOM   1108  N   MET   181      24.084 -18.834  28.319  1.00  0.00          3A7
```

```
ATOM   1109  CA  MET   181      25.507 -19.052  28.132  1.00  0.00          3A7
ATOM   1110  CB  MET   181      26.246 -17.722  27.978  1.00  0.00          3A7
ATOM   1111  CG  MET   181      25.986 -17.169  26.568  1.00  0.00          3A7
ATOM   1112  SD  MET   181      26.894 -15.667  26.130  1.00  0.00          3A7
ATOM   1113  CE  MET   181      25.919 -14.578  27.203  1.00  0.00          3A7
ATOM   1114  C   MET   181      26.127 -19.780  29.282  1.00  0.00          3A7
ATOM   1115  O   MET   181      26.923 -20.700  29.117  1.00  0.00          3A7
ATOM   1116  N   ASP   182      25.695 -19.407  30.493  1.00  0.00          3A7
ATOM   1117  CA  ASP   182      26.174 -20.008  31.695  1.00  0.00          3A7
ATOM   1118  CB  ASP   182      25.809 -19.160  32.908  1.00  0.00          3A7
ATOM   1119  CG  ASP   182      26.545 -17.813  32.877  1.00  0.00          3A7
ATOM   1120  OD1 ASP   182      27.380 -17.590  31.961  1.00  0.00          3A7
ATOM   1121  OD2 ASP   182      26.276 -16.986  33.788  1.00  0.00          3A7
ATOM   1122  C   ASP   182      25.645 -21.408  31.886  1.00  0.00          3A7
ATOM   1123  O   ASP   182      26.371 -22.258  32.382  1.00  0.00          3A7
ATOM   1124  N   VAL   183      24.401 -21.724  31.448  1.00  0.00          3A7
ATOM   1125  CA  VAL   183      23.887 -23.084  31.514  1.00  0.00          3A7
ATOM   1126  CB  VAL   183      22.419 -23.173  31.124  1.00  0.00          3A7
ATOM   1127  CG1 VAL   183      21.919 -24.632  30.984  1.00  0.00          3A7
ATOM   1128  CG2 VAL   183      21.578 -22.468  32.200  1.00  0.00          3A7
ATOM   1129  C   VAL   183      24.678 -24.016  30.610  1.00  0.00          3A7
ATOM   1130  O   VAL   183      25.065 -25.103  31.027  1.00  0.00          3A7
ATOM   1131  N   ILE   184      24.999 -23.597  29.353  1.00  0.00          3A7
ATOM   1132  CA  ILE   184      25.762 -24.395  28.439  1.00  0.00          3A7
ATOM   1133  CB  ILE   184      25.800 -23.816  27.039  1.00  0.00          3A7
ATOM   1134  CG2 ILE   184      26.594 -24.750  26.093  1.00  0.00          3A7
ATOM   1135  CG1 ILE   184      24.365 -23.617  26.489  1.00  0.00          3A7
ATOM   1136  CD  ILE   184      23.531 -24.898  26.404  1.00  0.00          3A7
ATOM   1137  C   ILE   184      27.167 -24.561  28.928  1.00  0.00          3A7
ATOM   1138  O   ILE   184      27.720 -25.652  28.859  1.00  0.00          3A7
ATOM   1139  N   THR   185      27.774 -23.489  29.486  1.00  0.00          3A7
ATOM   1140  CA  THR   185      29.125 -23.511  30.002  1.00  0.00          3A7
ATOM   1141  CB  THR   185      29.617 -22.111  30.359  1.00  0.00          3A7
ATOM   1142  OG1 THR   185      29.625 -21.307  29.187  1.00  0.00          3A7
ATOM   1143  CG2 THR   185      31.047 -22.108  30.943  1.00  0.00          3A7
ATOM   1144  C   THR   185      29.259 -24.418  31.192  1.00  0.00          3A7
ATOM   1145  O   THR   185      30.220 -25.166  31.343  1.00  0.00          3A7
ATOM   1146  N   SER   186      28.242 -24.404  32.066  1.00  0.00          3A7
ATOM   1147  CA  SER   186      28.262 -25.188  33.262  1.00  0.00          3A7
ATOM   1148  CB  SER   186      27.223 -24.719  34.259  1.00  0.00          3A7
ATOM   1149  OG  SER   186      27.539 -23.412  34.719  1.00  0.00          3A7
ATOM   1150  C   SER   186      28.037 -26.655  33.000  1.00  0.00          3A7
ATOM   1151  O   SER   186      28.693 -27.500  33.598  1.00  0.00          3A7
ATOM   1152  N   THR   187      27.128 -27.006  32.060  1.00  0.00          3A7
ATOM   1153  CA  THR   187      26.865 -28.386  31.711  1.00  0.00          3A7
ATOM   1154  CB  THR   187      25.561 -28.580  30.943  1.00  0.00          3A7
ATOM   1155  OG1 THR   187      25.480 -27.748  29.789  1.00  0.00          3A7
ATOM   1156  CG2 THR   187      24.359 -28.285  31.861  1.00  0.00          3A7
ATOM   1157  C   THR   187      27.994 -28.983  30.897  1.00  0.00          3A7
ATOM   1158  O   THR   187      28.202 -30.195  30.899  1.00  0.00          3A7
ATOM   1159  N   SER   188      28.739 -28.115  30.176  1.00  0.00          3A7
ATOM   1160  CA  SER   188      29.767 -28.556  29.280  1.00  0.00          3A7
ATOM   1161  CB  SER   188      29.905 -27.697  27.991  1.00  0.00          3A7
ATOM   1162  OG  SER   188      30.272 -26.347  28.250  1.00  0.00          3A7
ATOM   1163  C   SER   188      31.105 -28.690  29.970  1.00  0.00          3A7
ATOM   1164  O   SER   188      31.803 -29.681  29.768  1.00  0.00          3A7
ATOM   1165  N   PHE   189      31.513 -27.672  30.766  1.00  0.00          3A7
ATOM   1166  CA  PHE   189      32.870 -27.581  31.256  1.00  0.00          3A7
ATOM   1167  CB  PHE   189      33.653 -26.363  30.732  1.00  0.00          3A7
ATOM   1168  CG  PHE   189      33.446 -26.027  29.300  1.00  0.00          3A7
ATOM   1169  CD1 PHE   189      33.204 -24.694  28.976  1.00  0.00          3A7
ATOM   1170  CD2 PHE   189      33.468 -26.986  28.292  1.00  0.00          3A7
ATOM   1171  CE1 PHE   189      32.971 -24.317  27.665  1.00  0.00          3A7
ATOM   1172  CE2 PHE   189      33.182 -26.618  26.984  1.00  0.00          3A7
ATOM   1173  CZ  PHE   189      32.933 -25.284  26.668  1.00  0.00          3A7
ATOM   1174  C   PHE   189      32.919 -27.463  32.762  1.00  0.00          3A7
ATOM   1175  O   PHE   189      33.993 -27.441  33.361  1.00  0.00          3A7
ATOM   1176  N   GLY   190      31.743 -27.378  33.435  1.00  0.00          3A7
ATOM   1177  CA  GLY   190      31.654 -27.345  34.883  1.00  0.00          3A7
ATOM   1178  C   GLY   190      31.869 -25.956  35.418  1.00  0.00          3A7
ATOM   1179  O   GLY   190      31.005 -25.095  35.280  1.00  0.00          3A7
ATOM   1180  N   VAL   191      33.057 -25.744  36.044  1.00  0.00          3A7
```

ATOM	1181	CA	VAL	191	33.597	-24.510	36.596	1.00	0.00	3A7
ATOM	1182	CB	VAL	191	33.426	-23.250	35.727	1.00	0.00	3A7
ATOM	1183	CG1	VAL	191	32.199	-22.372	36.078	1.00	0.00	3A7
ATOM	1184	CG2	VAL	191	34.729	-22.424	35.812	1.00	0.00	3A7
ATOM	1185	C	VAL	191	33.100	-24.310	38.012	1.00	0.00	3A7
ATOM	1186	O	VAL	191	31.935	-24.551	38.325	1.00	0.00	3A7
ATOM	1187	N	SER	192	34.012	-23.844	38.900	1.00	0.00	3A7
ATOM	1188	CA	SER	192	33.727	-23.531	40.281	1.00	0.00	3A7
ATOM	1189	CB	SER	192	34.779	-24.116	41.252	1.00	0.00	3A7
ATOM	1190	OG	SER	192	34.799	-25.534	41.156	1.00	0.00	3A7
ATOM	1191	C	SER	192	33.716	-22.032	40.410	1.00	0.00	3A7
ATOM	1192	O	SER	192	34.136	-21.317	39.501	1.00	0.00	3A7
ATOM	1193	N	ILE	193	33.230	-21.524	41.572	1.00	0.00	3A7
ATOM	1194	CA	ILE	193	33.138	-20.109	41.867	1.00	0.00	3A7
ATOM	1195	CB	ILE	193	31.890	-19.756	42.671	1.00	0.00	3A7
ATOM	1196	CG2	ILE	193	31.794	-18.225	42.861	1.00	0.00	3A7
ATOM	1197	CG1	ILE	193	30.615	-20.322	41.992	1.00	0.00	3A7
ATOM	1198	CD	ILE	193	30.351	-19.784	40.581	1.00	0.00	3A7
ATOM	1199	C	ILE	193	34.389	-19.720	42.618	1.00	0.00	3A7
ATOM	1200	O	ILE	193	34.518	-19.967	43.816	1.00	0.00	3A7
ATOM	1201	N	ASP	194	35.344	-19.102	41.887	1.00	0.00	3A7
ATOM	1202	CA	ASP	194	36.617	-18.685	42.420	1.00	0.00	3A7
ATOM	1203	CB	ASP	194	37.706	-19.786	42.267	1.00	0.00	3A7
ATOM	1204	CG	ASP	194	38.984	-19.433	43.034	1.00	0.00	3A7
ATOM	1205	OD1	ASP	194	38.899	-19.270	44.280	1.00	0.00	3A7
ATOM	1206	OD2	ASP	194	40.056	-19.326	42.381	1.00	0.00	3A7
ATOM	1207	C	ASP	194	36.993	-17.442	41.654	1.00	0.00	3A7
ATOM	1208	O	ASP	194	37.756	-16.608	42.141	1.00	0.00	3A7
ATOM	1209	N	SER	195	36.443	-17.299	40.420	1.00	0.00	3A7
ATOM	1210	CA	SER	195	36.648	-16.163	39.548	1.00	0.00	3A7
ATOM	1211	CB	SER	195	36.679	-16.561	38.055	1.00	0.00	3A7
ATOM	1212	OG	SER	195	37.748	-17.464	37.811	1.00	0.00	3A7
ATOM	1213	C	SER	195	35.523	-15.185	39.763	1.00	0.00	3A7
ATOM	1214	O	SER	195	34.456	-15.547	40.256	1.00	0.00	3A7
ATOM	1215	N	LEU	196	35.759	-13.902	39.386	1.00	0.00	3A7
ATOM	1216	CA	LEU	196	34.826	-12.813	39.580	1.00	0.00	3A7
ATOM	1217	CB	LEU	196	35.494	-11.523	40.138	1.00	0.00	3A7
ATOM	1218	CG	LEU	196	36.127	-11.639	41.551	1.00	0.00	3A7
ATOM	1219	CD1	LEU	196	35.140	-12.190	42.599	1.00	0.00	3A7
ATOM	1220	CD2	LEU	196	37.469	-12.399	41.574	1.00	0.00	3A7
ATOM	1221	C	LEU	196	34.175	-12.481	38.258	1.00	0.00	3A7
ATOM	1222	O	LEU	196	33.796	-11.334	38.022	1.00	0.00	3A7
ATOM	1223	N	ASN	197	34.036	-13.503	37.366	1.00	0.00	3A7
ATOM	1224	CA	ASN	197	33.382	-13.455	36.068	1.00	0.00	3A7
ATOM	1225	CB	ASN	197	31.946	-12.846	36.138	1.00	0.00	3A7
ATOM	1226	CG	ASN	197	31.125	-13.111	34.865	1.00	0.00	3A7
ATOM	1227	OD1	ASN	197	31.170	-14.206	34.295	1.00	0.00	3A7
ATOM	1228	ND2	ASN	197	30.353	-12.069	34.431	1.00	0.00	3A7
ATOM	1229	C	ASN	197	34.255	-12.714	35.072	1.00	0.00	3A7
ATOM	1230	O	ASN	197	33.812	-11.770	34.419	1.00	0.00	3A7
ATOM	1231	N	ASN	198	35.541	-13.134	34.960	1.00	0.00	3A7
ATOM	1232	CA	ASN	198	36.520	-12.476	34.117	1.00	0.00	3A7
ATOM	1233	CB	ASN	198	37.878	-12.191	34.815	1.00	0.00	3A7
ATOM	1234	CG	ASN	198	37.631	-11.423	36.121	1.00	0.00	3A7
ATOM	1235	OD1	ASN	198	37.872	-11.949	37.214	1.00	0.00	3A7
ATOM	1236	ND2	ASN	198	37.143	-10.153	35.986	1.00	0.00	3A7
ATOM	1237	C	ASN	198	36.725	-13.246	32.825	1.00	0.00	3A7
ATOM	1238	O	ASN	198	36.624	-12.598	31.789	1.00	0.00	3A7
ATOM	1239	N	PRO	199	36.993	-14.562	32.735	1.00	0.00	3A7
ATOM	1240	CA	PRO	199	37.251	-15.242	31.473	1.00	0.00	3A7
ATOM	1241	CD	PRO	199	37.339	-15.415	33.865	1.00	0.00	3A7
ATOM	1242	CB	PRO	199	37.966	-16.553	31.866	1.00	0.00	3A7
ATOM	1243	CG	PRO	199	38.421	-16.338	33.313	1.00	0.00	3A7
ATOM	1244	C	PRO	199	35.959	-15.538	30.731	1.00	0.00	3A7
ATOM	1245	O	PRO	199	36.016	-15.766	29.524	1.00	0.00	3A7
ATOM	1246	N	GLN	200	34.800	-15.560	31.441	1.00	0.00	3A7
ATOM	1247	CA	GLN	200	33.519	-15.967	30.914	1.00	0.00	3A7
ATOM	1248	CB	GLN	200	32.614	-16.559	32.023	1.00	0.00	3A7
ATOM	1249	CG	GLN	200	31.297	-17.173	31.515	1.00	0.00	3A7
ATOM	1250	CD	GLN	200	30.581	-17.885	32.668	1.00	0.00	3A7
ATOM	1251	OE1	GLN	200	30.411	-19.110	32.645	1.00	0.00	3A7
ATOM	1252	NE2	GLN	200	30.150	-17.085	33.690	1.00	0.00	3A7

```
ATOM   1253  C   GLN   200      32.815 -14.819  30.232  1.00  0.00          3A7
ATOM   1254  O   GLN   200      32.140 -15.035  29.233  1.00  0.00          3A7
ATOM   1255  N   ASP   201      32.961 -13.568  30.743  1.00  0.00          3A7
ATOM   1256  CA  ASP   201      32.288 -12.384  30.219  1.00  0.00          3A7
ATOM   1257  CB  ASP   201      32.223 -11.254  31.288  1.00  0.00          3A7
ATOM   1258  CG  ASP   201      31.197 -10.174  30.927  1.00  0.00          3A7
ATOM   1259  OD1 ASP   201      31.610  -8.994  30.772  1.00  0.00          3A7
ATOM   1260  OD2 ASP   201      29.992 -10.520  30.805  1.00  0.00          3A7
ATOM   1261  C   ASP   201      32.876 -11.859  28.899  1.00  0.00          3A7
ATOM   1262  O   ASP   201      32.107 -11.342  28.095  1.00  0.00          3A7
ATOM   1263  N   PRO   202      34.177 -11.966  28.590  1.00  0.00          3A7
ATOM   1264  CA  PRO   202      34.768 -11.731  27.282  1.00  0.00          3A7
ATOM   1265  CD  PRO   202      35.191 -11.898  29.612  1.00  0.00          3A7
ATOM   1266  CB  PRO   202      36.280 -11.790  27.543  1.00  0.00          3A7
ATOM   1267  CG  PRO   202      36.411 -11.259  28.958  1.00  0.00          3A7
ATOM   1268  C   PRO   202      34.334 -12.755  26.270  1.00  0.00          3A7
ATOM   1269  O   PRO   202      34.099 -12.386  25.126  1.00  0.00          3A7
ATOM   1270  N   PHE   203      34.165 -14.041  26.662  1.00  0.00          3A7
ATOM   1271  CA  PHE   203      33.692 -15.113  25.807  1.00  0.00          3A7
ATOM   1272  CB  PHE   203      33.533 -16.402  26.628  1.00  0.00          3A7
ATOM   1273  CG  PHE   203      33.530 -17.655  25.800  1.00  0.00          3A7
ATOM   1274  CD1 PHE   203      34.701 -18.401  25.685  1.00  0.00          3A7
ATOM   1275  CD2 PHE   203      32.364 -18.126  25.192  1.00  0.00          3A7
ATOM   1276  CE1 PHE   203      34.713 -19.599  24.981  1.00  0.00          3A7
ATOM   1277  CE2 PHE   203      32.377 -19.316  24.471  1.00  0.00          3A7
ATOM   1278  CZ  PHE   203      33.547 -20.060  24.377  1.00  0.00          3A7
ATOM   1279  C   PHE   203      32.360 -14.780  25.173  1.00  0.00          3A7
ATOM   1280  O   PHE   203      32.125 -15.040  23.999  1.00  0.00          3A7
ATOM   1281  N   VAL   204      31.455 -14.147  25.959  1.00  0.00          3A7
ATOM   1282  CA  VAL   204      30.141 -13.686  25.564  1.00  0.00          3A7
ATOM   1283  CB  VAL   204      29.470 -12.914  26.710  1.00  0.00          3A7
ATOM   1284  CG1 VAL   204      28.141 -12.240  26.286  1.00  0.00          3A7
ATOM   1285  CG2 VAL   204      29.308 -13.845  27.927  1.00  0.00          3A7
ATOM   1286  C   VAL   204      30.210 -12.702  24.430  1.00  0.00          3A7
ATOM   1287  O   VAL   204      29.521 -12.835  23.424  1.00  0.00          3A7
ATOM   1288  N   GLU   205      31.077 -11.674  24.576  1.00  0.00          3A7
ATOM   1289  CA  GLU   205      31.235 -10.607  23.617  1.00  0.00          3A7
ATOM   1290  CB  GLU   205      32.215  -9.544  24.146  1.00  0.00          3A7
ATOM   1291  CG  GLU   205      32.242  -8.242  23.327  1.00  0.00          3A7
ATOM   1292  CD  GLU   205      33.217  -7.267  23.979  1.00  0.00          3A7
ATOM   1293  OE1 GLU   205      32.974  -6.880  25.153  1.00  0.00          3A7
ATOM   1294  OE2 GLU   205      34.219  -6.896  23.310  1.00  0.00          3A7
ATOM   1295  C   GLU   205      31.739 -11.106  22.289  1.00  0.00          3A7
ATOM   1296  O   GLU   205      31.308 -10.646  21.238  1.00  0.00          3A7
ATOM   1297  N   ASN   206      32.629 -12.123  22.316  1.00  0.00          3A7
ATOM   1298  CA  ASN   206      33.175 -12.741  21.134  1.00  0.00          3A7
ATOM   1299  CB  ASN   206      34.358 -13.657  21.467  1.00  0.00          3A7
ATOM   1300  CG  ASN   206      35.509 -12.819  22.025  1.00  0.00          3A7
ATOM   1301  OD1 ASN   206      35.798 -12.848  23.224  1.00  0.00          3A7
ATOM   1302  ND2 ASN   206      36.155 -12.023  21.120  1.00  0.00          3A7
ATOM   1303  C   ASN   206      32.151 -13.539  20.380  1.00  0.00          3A7
ATOM   1304  O   ASN   206      31.976 -13.337  19.182  1.00  0.00          3A7
ATOM   1305  N   THR   207      31.417 -14.452  21.067  1.00  0.00          3A7
ATOM   1306  CA  THR   207      30.406 -15.301  20.464  1.00  0.00          3A7
ATOM   1307  CB  THR   207      29.749 -16.188  21.502  1.00  0.00          3A7
ATOM   1308  OG1 THR   207      30.751 -16.917  22.199  1.00  0.00          3A7
ATOM   1309  CG2 THR   207      28.780 -17.201  20.851  1.00  0.00          3A7
ATOM   1310  C   THR   207      29.346 -14.492  19.768  1.00  0.00          3A7
ATOM   1311  O   THR   207      28.951 -14.790  18.646  1.00  0.00          3A7
ATOM   1312  N   LYS   208      28.929 -13.379  20.411  1.00  0.00          3A7
ATOM   1313  CA  LYS   208      27.951 -12.459  19.890  1.00  0.00          3A7
ATOM   1314  CB  LYS   208      27.604 -11.413  20.954  1.00  0.00          3A7
ATOM   1315  CG  LYS   208      26.398 -10.524  20.601  1.00  0.00          3A7
ATOM   1316  CD  LYS   208      25.914  -9.608  21.741  1.00  0.00          3A7
ATOM   1317  CE  LYS   208      26.801  -8.383  22.018  1.00  0.00          3A7
ATOM   1318  NZ  LYS   208      28.077  -8.751  22.673  1.00  0.00          3A7
ATOM   1319  C   LYS   208      28.389 -11.760  18.619  1.00  0.00          3A7
ATOM   1320  O   LYS   208      27.616 -11.653  17.675  1.00  0.00          3A7
ATOM   1321  N   LYS   209      29.664 -11.316  18.536  1.00  0.00          3A7
ATOM   1322  CA  LYS   209      30.209 -10.686  17.348  1.00  0.00          3A7
ATOM   1323  CB  LYS   209      31.622 -10.129  17.587  1.00  0.00          3A7
ATOM   1324  CG  LYS   209      31.660  -8.877  18.478  1.00  0.00          3A7
```

ATOM	1325	CD	LYS	209	33.007	-8.133	18.418	1.00	0.00	3A7
ATOM	1326	CE	LYS	209	34.227	-8.963	18.843	1.00	0.00	3A7
ATOM	1327	NZ	LYS	209	34.144	-9.343	20.270	1.00	0.00	3A7
ATOM	1328	C	LYS	209	30.275	-11.624	16.153	1.00	0.00	3A7
ATOM	1329	O	LYS	209	29.942	-11.252	15.031	1.00	0.00	3A7
ATOM	1330	N	LEU	210	30.662	-12.901	16.376	1.00	0.00	3A7
ATOM	1331	CA	LEU	210	30.592	-13.968	15.391	1.00	0.00	3A7
ATOM	1332	CB	LEU	210	30.985	-15.328	16.011	1.00	0.00	3A7
ATOM	1333	CG	LEU	210	31.127	-16.622	15.108	1.00	0.00	3A7
ATOM	1334	CD1	LEU	210	31.072	-17.872	16.013	1.00	0.00	3A7
ATOM	1335	CD2	LEU	210	30.134	-16.893	13.954	1.00	0.00	3A7
ATOM	1336	C	LEU	210	29.217	-14.131	14.809	1.00	0.00	3A7
ATOM	1337	O	LEU	210	29.056	-14.197	13.595	1.00	0.00	3A7
ATOM	1338	N	LEU	211	28.185	-14.172	15.680	1.00	0.00	3A7
ATOM	1339	CA	LEU	211	26.814	-14.406	15.302	1.00	0.00	3A7
ATOM	1340	CB	LEU	211	25.835	-14.273	16.480	1.00	0.00	3A7
ATOM	1341	CG	LEU	211	26.035	-15.159	17.726	1.00	0.00	3A7
ATOM	1342	CD1	LEU	211	24.820	-15.056	18.669	1.00	0.00	3A7
ATOM	1343	CD2	LEU	211	26.398	-16.614	17.396	1.00	0.00	3A7
ATOM	1344	C	LEU	211	26.271	-13.442	14.274	1.00	0.00	3A7
ATOM	1345	O	LEU	211	25.479	-13.847	13.418	1.00	0.00	3A7
ATOM	1346	N	ARG	212	26.667	-12.140	14.324	1.00	0.00	3A7
ATOM	1347	CA	ARG	212	26.196	-11.136	13.386	1.00	0.00	3A7
ATOM	1348	CB	ARG	212	25.985	-9.737	14.028	1.00	0.00	3A7
ATOM	1349	CG	ARG	212	27.103	-9.170	14.927	1.00	0.00	3A7
ATOM	1350	CD	ARG	212	28.270	-8.508	14.183	1.00	0.00	3A7
ATOM	1351	NE	ARG	212	29.078	-7.724	15.175	1.00	0.00	3A7
ATOM	1352	CZ	ARG	212	30.393	-7.406	14.970	1.00	0.00	3A7
ATOM	1353	NH1	ARG	212	31.075	-7.901	13.898	1.00	0.00	3A7
ATOM	1354	NH2	ARG	212	31.031	-6.581	15.851	1.00	0.00	3A7
ATOM	1355	C	ARG	212	27.097	-11.091	12.169	1.00	0.00	3A7
ATOM	1356	O	ARG	212	28.323	-11.083	12.272	1.00	0.00	3A7
ATOM	1357	N	PHE	213	26.441	-11.117	10.976	1.00	0.00	3A7
ATOM	1358	CA	PHE	213	26.943	-11.263	9.611	1.00	0.00	3A7
ATOM	1359	CB	PHE	213	27.428	-9.944	8.921	1.00	0.00	3A7
ATOM	1360	CG	PHE	213	28.597	-9.221	9.541	1.00	0.00	3A7
ATOM	1361	CD1	PHE	213	28.391	-8.264	10.535	1.00	0.00	3A7
ATOM	1362	CD2	PHE	213	29.890	-9.399	9.039	1.00	0.00	3A7
ATOM	1363	CE1	PHE	213	29.455	-7.517	11.032	1.00	0.00	3A7
ATOM	1364	CE2	PHE	213	30.959	-8.666	9.546	1.00	0.00	3A7
ATOM	1365	CZ	PHE	213	30.741	-7.723	10.544	1.00	0.00	3A7
ATOM	1366	C	PHE	213	27.926	-12.408	9.426	1.00	0.00	3A7
ATOM	1367	O	PHE	213	29.121	-12.215	9.209	1.00	0.00	3A7
ATOM	1368	N	ASN	214	27.395	-13.649	9.491	1.00	0.00	3A7
ATOM	1369	CA	ASN	214	28.142	-14.839	9.165	1.00	0.00	3A7
ATOM	1370	CB	ASN	214	29.054	-15.372	10.314	1.00	0.00	3A7
ATOM	1371	CG	ASN	214	29.994	-16.484	9.818	1.00	0.00	3A7
ATOM	1372	OD1	ASN	214	30.863	-16.242	8.972	1.00	0.00	3A7
ATOM	1373	ND2	ASN	214	29.800	-17.720	10.370	1.00	0.00	3A7
ATOM	1374	C	ASN	214	27.135	-15.863	8.671	1.00	0.00	3A7
ATOM	1375	O	ASN	214	27.356	-16.351	7.565	1.00	0.00	3A7
ATOM	1376	N	PRO	215	26.035	-16.260	9.344	1.00	0.00	3A7
ATOM	1377	CA	PRO	215	25.150	-17.305	8.858	1.00	0.00	3A7
ATOM	1378	CD	PRO	215	25.729	-15.929	10.728	1.00	0.00	3A7
ATOM	1379	CB	PRO	215	24.466	-17.865	10.125	1.00	0.00	3A7
ATOM	1380	CG	PRO	215	25.216	-17.241	11.310	1.00	0.00	3A7
ATOM	1381	C	PRO	215	24.158	-16.681	7.893	1.00	0.00	3A7
ATOM	1382	O	PRO	215	23.256	-15.982	8.353	1.00	0.00	3A7
ATOM	1383	N	LEU	216	24.323	-16.921	6.560	1.00	0.00	3A7
ATOM	1384	CA	LEU	216	23.496	-16.424	5.463	1.00	0.00	3A7
ATOM	1385	CB	LEU	216	21.971	-16.737	5.575	1.00	0.00	3A7
ATOM	1386	CG	LEU	216	21.559	-18.224	5.393	1.00	0.00	3A7
ATOM	1387	CD1	LEU	216	21.970	-18.782	4.017	1.00	0.00	3A7
ATOM	1388	CD2	LEU	216	22.012	-19.148	6.540	1.00	0.00	3A7
ATOM	1389	C	LEU	216	23.663	-14.925	5.304	1.00	0.00	3A7
ATOM	1390	O	LEU	216	22.996	-14.143	5.980	1.00	0.00	3A7
ATOM	1391	N	ASP	217	24.571	-14.501	4.392	1.00	0.00	3A7
ATOM	1392	CA	ASP	217	24.872	-13.102	4.192	1.00	0.00	3A7
ATOM	1393	CB	ASP	217	26.106	-12.608	5.013	1.00	0.00	3A7
ATOM	1394	CG	ASP	217	27.385	-13.427	4.786	1.00	0.00	3A7
ATOM	1395	OD1	ASP	217	28.378	-12.833	4.285	1.00	0.00	3A7
ATOM	1396	OD2	ASP	217	27.390	-14.641	5.118	1.00	0.00	3A7

ATOM	1397	C	ASP	217	25.056	-12.846	2.709	1.00	0.00	3A7
ATOM	1398	O	ASP	217	26.126	-13.118	2.166	1.00	0.00	3A7
ATOM	1399	N	PRO	218	24.053	-12.282	2.013	1.00	0.00	3A7
ATOM	1400	CA	PRO	218	24.193	-11.689	0.691	1.00	0.00	3A7
ATOM	1401	CD	PRO	218	22.655	-12.450	2.382	1.00	0.00	3A7
ATOM	1402	CB	PRO	218	22.746	-11.477	0.203	1.00	0.00	3A7
ATOM	1403	CG	PRO	218	21.908	-12.439	1.050	1.00	0.00	3A7
ATOM	1404	C	PRO	218	24.945	-10.372	0.782	1.00	0.00	3A7
ATOM	1405	O	PRO	218	24.911	-9.730	1.833	1.00	0.00	3A7
ATOM	1406	N	PHE	219	25.621	-9.950	-0.316	1.00	0.00	3A7
ATOM	1407	CA	PHE	219	26.432	-8.745	-0.344	1.00	0.00	3A7
ATOM	1408	CB	PHE	219	27.591	-8.800	-1.373	1.00	0.00	3A7
ATOM	1409	CG	PHE	219	28.495	-9.952	-1.047	1.00	0.00	3A7
ATOM	1410	CD1	PHE	219	29.296	-9.917	0.094	1.00	0.00	3A7
ATOM	1411	CD2	PHE	219	28.551	-11.070	-1.881	1.00	0.00	3A7
ATOM	1412	CE1	PHE	219	30.140	-10.981	0.400	1.00	0.00	3A7
ATOM	1413	CE2	PHE	219	29.393	-12.136	-1.578	1.00	0.00	3A7
ATOM	1414	CZ	PHE	219	30.189	-12.092	-0.437	1.00	0.00	3A7
ATOM	1415	C	PHE	219	25.587	-7.501	-0.570	1.00	0.00	3A7
ATOM	1416	O	PHE	219	25.626	-6.607	0.273	1.00	0.00	3A7
ATOM	1417	N	VAL	220	24.790	-7.366	-1.669	1.00	0.00	3A7
ATOM	1418	CA	VAL	220	24.617	-8.245	-2.807	1.00	0.00	3A7
ATOM	1419	CB	VAL	220	23.148	-8.591	-3.051	1.00	0.00	3A7
ATOM	1420	CG1	VAL	220	22.271	-7.323	-3.127	1.00	0.00	3A7
ATOM	1421	CG2	VAL	220	22.991	-9.517	-4.277	1.00	0.00	3A7
ATOM	1422	C	VAL	220	25.287	-7.570	-3.983	1.00	0.00	3A7
ATOM	1423	O	VAL	220	25.799	-8.235	-4.883	1.00	0.00	3A7
ATOM	1424	N	LEU	221	25.336	-6.211	-3.963	1.00	0.00	3A7
ATOM	1425	CA	LEU	221	26.163	-5.403	-4.835	1.00	0.00	3A7
ATOM	1426	CB	LEU	221	25.390	-4.284	-5.597	1.00	0.00	3A7
ATOM	1427	CG	LEU	221	24.479	-4.750	-6.764	1.00	0.00	3A7
ATOM	1428	CD1	LEU	221	25.258	-5.539	-7.835	1.00	0.00	3A7
ATOM	1429	CD2	LEU	221	23.213	-5.501	-6.317	1.00	0.00	3A7
ATOM	1430	C	LEU	221	27.196	-4.792	-3.913	1.00	0.00	3A7
ATOM	1431	O	LEU	221	27.565	-5.391	-2.904	1.00	0.00	3A7
ATOM	1432	N	SER	222	27.682	-3.567	-4.239	1.00	0.00	3A7
ATOM	1433	CA	SER	222	28.622	-2.816	-3.435	1.00	0.00	3A7
ATOM	1434	CB	SER	222	29.722	-2.139	-4.284	1.00	0.00	3A7
ATOM	1435	OG	SER	222	30.472	-3.121	-4.985	1.00	0.00	3A7
ATOM	1436	C	SER	222	27.841	-1.762	-2.698	1.00	0.00	3A7
ATOM	1437	O	SER	222	27.764	-0.612	-3.127	1.00	0.00	3A7
ATOM	1438	N	ILE	223	27.222	-2.164	-1.561	1.00	0.00	3A7
ATOM	1439	CA	ILE	223	26.322	-1.338	-0.788	1.00	0.00	3A7
ATOM	1440	CB	ILE	223	24.971	-2.017	-0.555	1.00	0.00	3A7
ATOM	1441	CG2	ILE	223	25.156	-3.487	-0.110	1.00	0.00	3A7
ATOM	1442	CG1	ILE	223	24.042	-1.193	0.374	1.00	0.00	3A7
ATOM	1443	CD	ILE	223	22.603	-1.718	0.416	1.00	0.00	3A7
ATOM	1444	C	ILE	223	27.019	-0.926	0.488	1.00	0.00	3A7
ATOM	1445	O	ILE	223	27.093	0.266	0.787	1.00	0.00	3A7
ATOM	1446	N	LYS	224	27.556	-1.893	1.271	1.00	0.00	3A7
ATOM	1447	CA	LYS	224	28.263	-1.581	2.490	1.00	0.00	3A7
ATOM	1448	CB	LYS	224	27.339	-1.185	3.674	1.00	0.00	3A7
ATOM	1449	CG	LYS	224	28.088	-0.528	4.849	1.00	0.00	3A7
ATOM	1450	CD	LYS	224	27.190	-0.187	6.049	1.00	0.00	3A7
ATOM	1451	CE	LYS	224	26.740	-1.411	6.861	1.00	0.00	3A7
ATOM	1452	NZ	LYS	224	27.901	-2.112	7.458	1.00	0.00	3A7
ATOM	1453	C	LYS	224	29.052	-2.796	2.890	1.00	0.00	3A7
ATOM	1454	O	LYS	224	30.070	-2.683	3.572	1.00	0.00	3A7
ATOM	1455	N	VAL	225	28.582	-4.008	2.483	1.00	0.00	3A7
ATOM	1456	CA	VAL	225	29.124	-5.288	2.907	1.00	0.00	3A7
ATOM	1457	CB	VAL	225	28.125	-6.430	2.746	1.00	0.00	3A7
ATOM	1458	CG1	VAL	225	28.683	-7.731	3.365	1.00	0.00	3A7
ATOM	1459	CG2	VAL	225	26.805	-6.017	3.429	1.00	0.00	3A7
ATOM	1460	C	VAL	225	30.398	-5.583	2.147	1.00	0.00	3A7
ATOM	1461	O	VAL	225	31.486	-5.449	2.708	1.00	0.00	3A7
ATOM	1462	N	PHE	226	30.271	-5.986	0.851	1.00	0.00	3A7
ATOM	1463	CA	PHE	226	31.349	-6.182	-0.106	1.00	0.00	3A7
ATOM	1464	CB	PHE	226	32.367	-4.997	-0.098	1.00	0.00	3A7
ATOM	1465	CG	PHE	226	33.203	-4.921	-1.346	1.00	0.00	3A7
ATOM	1466	CD1	PHE	226	34.585	-5.107	-1.283	1.00	0.00	3A7
ATOM	1467	CD2	PHE	226	32.615	-4.631	-2.578	1.00	0.00	3A7
ATOM	1468	CE1	PHE	226	35.365	-5.025	-2.432	1.00	0.00	3A7

ATOM	1469	CE2	PHE	226	33.393	-4.550	-3.730	1.00	0.00	3A7
ATOM	1470	CZ	PHE	226	34.768	-4.749	-3.658	1.00	0.00	3A7
ATOM	1471	C	PHE	226	32.059	-7.514	0.144	1.00	0.00	3A7
ATOM	1472	O	PHE	226	32.151	-7.943	1.295	1.00	0.00	3A7
ATOM	1473	N	PRO	227	32.610	-8.198	-0.871	1.00	0.00	3A7
ATOM	1474	CA	PRO	227	33.431	-9.392	-0.698	1.00	0.00	3A7
ATOM	1475	CD	PRO	227	32.111	-8.089	-2.237	1.00	0.00	3A7
ATOM	1476	CB	PRO	227	33.602	-9.944	-2.123	1.00	0.00	3A7
ATOM	1477	CG	PRO	227	32.349	-9.465	-2.857	1.00	0.00	3A7
ATOM	1478	C	PRO	227	34.778	-9.081	-0.061	1.00	0.00	3A7
ATOM	1479	O	PRO	227	35.140	-7.911	0.062	1.00	0.00	3A7
ATOM	1480	N	PHE	228	35.535	-10.132	0.346	1.00	0.00	3A7
ATOM	1481	CA	PHE	228	36.792	-10.004	1.060	1.00	0.00	3A7
ATOM	1482	CB	PHE	228	37.130	-11.255	1.926	1.00	0.00	3A7
ATOM	1483	CG	PHE	228	37.053	-12.560	1.172	1.00	0.00	3A7
ATOM	1484	CD1	PHE	228	35.821	-13.176	0.937	1.00	0.00	3A7
ATOM	1485	CD2	PHE	228	38.217	-13.193	0.733	1.00	0.00	3A7
ATOM	1486	CE1	PHE	228	35.753	-14.388	0.257	1.00	0.00	3A7
ATOM	1487	CE2	PHE	228	38.152	-14.405	0.053	1.00	0.00	3A7
ATOM	1488	CZ	PHE	228	36.919	-15.003	-0.187	1.00	0.00	3A7
ATOM	1489	C	PHE	228	37.924	-9.676	0.107	1.00	0.00	3A7
ATOM	1490	O	PHE	228	38.323	-10.488	-0.727	1.00	0.00	3A7
ATOM	1491	N	LEU	229	38.440	-8.432	0.225	1.00	0.00	3A7
ATOM	1492	CA	LEU	229	39.469	-7.914	-0.636	1.00	0.00	3A7
ATOM	1493	CB	LEU	229	38.924	-7.440	-2.010	1.00	0.00	3A7
ATOM	1494	CG	LEU	229	39.979	-6.871	-2.990	1.00	0.00	3A7
ATOM	1495	CD1	LEU	229	41.083	-7.892	-3.326	1.00	0.00	3A7
ATOM	1496	CD2	LEU	229	39.305	-6.347	-4.273	1.00	0.00	3A7
ATOM	1497	C	LEU	229	40.062	-6.752	0.105	1.00	0.00	3A7
ATOM	1498	O	LEU	229	41.281	-6.639	0.226	1.00	0.00	3A7
ATOM	1499	N	THR	230	39.186	-5.847	0.615	1.00	0.00	3A7
ATOM	1500	CA	THR	230	39.568	-4.636	1.308	1.00	0.00	3A7
ATOM	1501	CB	THR	230	38.715	-3.444	0.870	1.00	0.00	3A7
ATOM	1502	OG1	THR	230	39.184	-2.215	1.417	1.00	0.00	3A7
ATOM	1503	CG2	THR	230	37.220	-3.639	1.206	1.00	0.00	3A7
ATOM	1504	C	THR	230	39.476	-4.902	2.807	1.00	0.00	3A7
ATOM	1505	O	THR	230	38.513	-5.527	3.250	1.00	0.00	3A7
ATOM	1506	N	PRO	231	40.435	-4.450	3.626	1.00	0.00	3A7
ATOM	1507	CA	PRO	231	40.382	-4.534	5.074	1.00	0.00	3A7
ATOM	1508	CD	PRO	231	41.737	-3.996	3.151	1.00	0.00	3A7
ATOM	1509	CB	PRO	231	41.866	-4.556	5.472	1.00	0.00	3A7
ATOM	1510	CG	PRO	231	42.555	-3.696	4.409	1.00	0.00	3A7
ATOM	1511	C	PRO	231	39.661	-3.313	5.625	1.00	0.00	3A7
ATOM	1512	O	PRO	231	38.946	-2.637	4.885	1.00	0.00	3A7
ATOM	1513	N	ILE	232	39.877	-3.024	6.939	1.00	0.00	3A7
ATOM	1514	CA	ILE	232	39.462	-1.870	7.738	1.00	0.00	3A7
ATOM	1515	CB	ILE	232	40.410	-0.663	7.563	1.00	0.00	3A7
ATOM	1516	CG2	ILE	232	40.450	-0.093	6.123	1.00	0.00	3A7
ATOM	1517	CG1	ILE	232	40.186	0.463	8.608	1.00	0.00	3A7
ATOM	1518	CD	ILE	232	40.563	0.068	10.038	1.00	0.00	3A7
ATOM	1519	C	ILE	232	37.983	-1.493	7.610	1.00	0.00	3A7
ATOM	1520	O	ILE	232	37.631	-0.517	6.949	1.00	0.00	3A7
ATOM	1521	N	LEU	233	37.047	-2.244	8.259	1.00	0.00	3A7
ATOM	1522	CA	LEU	233	37.231	-3.488	8.977	1.00	0.00	3A7
ATOM	1523	CB	LEU	233	36.638	-3.490	10.418	1.00	0.00	3A7
ATOM	1524	CG	LEU	233	37.361	-2.613	11.475	1.00	0.00	3A7
ATOM	1525	CD1	LEU	233	38.832	-3.029	11.668	1.00	0.00	3A7
ATOM	1526	CD2	LEU	233	37.198	-1.098	11.249	1.00	0.00	3A7
ATOM	1527	C	LEU	233	36.518	-4.523	8.138	1.00	0.00	3A7
ATOM	1528	O	LEU	233	36.754	-4.608	6.933	1.00	0.00	3A7
ATOM	1529	N	GLU	234	35.621	-5.330	8.775	1.00	0.00	3A7
ATOM	1530	CA	GLU	234	34.755	-6.337	8.183	1.00	0.00	3A7
ATOM	1531	CB	GLU	234	33.985	-5.836	6.925	1.00	0.00	3A7
ATOM	1532	CG	GLU	234	32.750	-6.666	6.514	1.00	0.00	3A7
ATOM	1533	CD	GLU	234	33.141	-7.946	5.777	1.00	0.00	3A7
ATOM	1534	OE1	GLU	234	33.797	-7.837	4.707	1.00	0.00	3A7
ATOM	1535	OE2	GLU	234	32.780	-9.048	6.271	1.00	0.00	3A7
ATOM	1536	C	GLU	234	35.545	-7.587	7.877	1.00	0.00	3A7
ATOM	1537	O	GLU	234	36.385	-7.576	6.978	1.00	0.00	3A7
ATOM	1538	N	ALA	235	35.267	-8.681	8.642	1.00	0.00	3A7
ATOM	1539	CA	ALA	235	35.833	-10.014	8.499	1.00	0.00	3A7
ATOM	1540	CB	ALA	235	36.269	-10.390	7.067	1.00	0.00	3A7

ATOM	1541	C	ALA	235	37.017	-10.214	9.409	1.00	0.00	3A7
ATOM	1542	O	ALA	235	37.273	-11.312	9.899	1.00	0.00	3A7
ATOM	1543	N	LEU	236	37.790	-9.141	9.671	1.00	0.00	3A7
ATOM	1544	CA	LEU	236	38.971	-9.206	10.503	1.00	0.00	3A7
ATOM	1545	CB	LEU	236	39.828	-7.935	10.361	1.00	0.00	3A7
ATOM	1546	CG	LEU	236	40.242	-7.612	8.906	1.00	0.00	3A7
ATOM	1547	CD1	LEU	236	40.964	-6.254	8.836	1.00	0.00	3A7
ATOM	1548	CD2	LEU	236	41.094	-8.728	8.272	1.00	0.00	3A7
ATOM	1549	C	LEU	236	38.601	-9.366	11.956	1.00	0.00	3A7
ATOM	1550	O	LEU	236	39.204	-10.138	12.697	1.00	0.00	3A7
ATOM	1551	N	ASN	237	37.530	-8.664	12.387	1.00	0.00	3A7
ATOM	1552	CA	ASN	237	37.020	-8.738	13.741	1.00	0.00	3A7
ATOM	1553	CB	ASN	237	35.917	-7.685	13.982	1.00	0.00	3A7
ATOM	1554	CG	ASN	237	36.463	-6.273	13.746	1.00	0.00	3A7
ATOM	1555	OD1	ASN	237	35.922	-5.526	12.923	1.00	0.00	3A7
ATOM	1556	ND2	ASN	237	37.544	-5.910	14.500	1.00	0.00	3A7
ATOM	1557	C	ASN	237	36.444	-10.107	14.022	1.00	0.00	3A7
ATOM	1558	O	ASN	237	36.569	-10.658	15.111	1.00	0.00	3A7
ATOM	1559	N	ILE	238	35.832	-10.707	12.979	1.00	0.00	3A7
ATOM	1560	CA	ILE	238	35.229	-12.011	13.021	1.00	0.00	3A7
ATOM	1561	CB	ILE	238	34.447	-12.290	11.743	1.00	0.00	3A7
ATOM	1562	CG2	ILE	238	33.714	-13.648	11.845	1.00	0.00	3A7
ATOM	1563	CG1	ILE	238	33.451	-11.141	11.432	1.00	0.00	3A7
ATOM	1564	CD	ILE	238	32.367	-10.932	12.495	1.00	0.00	3A7
ATOM	1565	C	ILE	238	36.280	-13.064	13.260	1.00	0.00	3A7
ATOM	1566	O	ILE	238	36.094	-13.896	14.106	1.00	0.00	3A7
ATOM	1567	N	THR	239	37.422	-13.013	12.556	1.00	0.00	3A7
ATOM	1568	CA	THR	239	38.535	-13.929	12.699	1.00	0.00	3A7
ATOM	1569	CB	THR	239	39.546	-13.767	11.574	1.00	0.00	3A7
ATOM	1570	OG1	THR	239	38.870	-13.766	10.323	1.00	0.00	3A7
ATOM	1571	CG2	THR	239	40.562	-14.928	11.571	1.00	0.00	3A7
ATOM	1572	C	THR	239	39.226	-13.773	14.033	1.00	0.00	3A7
ATOM	1573	O	THR	239	39.720	-14.740	14.603	1.00	0.00	3A7
ATOM	1574	N	VAL	240	39.204	-12.555	14.619	1.00	0.00	3A7
ATOM	1575	CA	VAL	240	39.759	-12.276	15.932	1.00	0.00	3A7
ATOM	1576	CB	VAL	240	39.930	-10.784	16.162	1.00	0.00	3A7
ATOM	1577	CG1	VAL	240	40.276	-10.421	17.627	1.00	0.00	3A7
ATOM	1578	CG2	VAL	240	41.076	-10.316	15.239	1.00	0.00	3A7
ATOM	1579	C	VAL	240	38.911	-12.842	17.025	1.00	0.00	3A7
ATOM	1580	O	VAL	240	39.418	-13.460	17.956	1.00	0.00	3A7
ATOM	1581	N	PHE	241	37.578	-12.667	16.920	1.00	0.00	3A7
ATOM	1582	CA	PHE	241	36.634	-13.266	17.837	1.00	0.00	3A7
ATOM	1583	CB	PHE	241	35.170	-12.893	17.483	1.00	0.00	3A7
ATOM	1584	CG	PHE	241	34.222	-14.041	17.098	1.00	0.00	3A7
ATOM	1585	CD1	PHE	241	33.928	-15.104	17.973	1.00	0.00	3A7
ATOM	1586	CD2	PHE	241	34.038	-14.250	15.746	1.00	0.00	3A7
ATOM	1587	CE1	PHE	241	33.801	-16.400	17.483	1.00	0.00	3A7
ATOM	1588	CE2	PHE	241	34.006	-15.545	15.244	1.00	0.00	3A7
ATOM	1589	CZ	PHE	241	33.918	-16.626	16.119	1.00	0.00	3A7
ATOM	1590	C	PHE	241	36.784	-14.763	17.938	1.00	0.00	3A7
ATOM	1591	O	PHE	241	36.807	-15.276	19.050	1.00	0.00	3A7
ATOM	1592	N	PRO	242	36.833	-15.511	16.814	1.00	0.00	3A7
ATOM	1593	CA	PRO	242	36.972	-16.902	16.784	1.00	0.00	3A7
ATOM	1594	CD	PRO	242	37.457	-15.196	15.686	1.00	0.00	3A7
ATOM	1595	CB	PRO	242	36.945	-17.375	15.333	1.00	0.00	3A7
ATOM	1596	CG	PRO	242	37.313	-16.221	14.553	1.00	0.00	3A7
ATOM	1597	C	PRO	242	38.274	-17.310	17.435	1.00	0.00	3A7
ATOM	1598	O	PRO	242	38.251	-18.268	18.191	1.00	0.00	3A7
ATOM	1599	N	ARG	243	39.409	-16.603	17.262	1.00	0.00	3A7
ATOM	1600	CA	ARG	243	40.651	-16.892	17.893	1.00	0.00	3A7
ATOM	1601	CB	ARG	243	41.734	-15.942	17.355	1.00	0.00	3A7
ATOM	1602	CG	ARG	243	42.172	-16.265	15.917	1.00	0.00	3A7
ATOM	1603	CD	ARG	243	43.102	-15.187	15.348	1.00	0.00	3A7
ATOM	1604	NE	ARG	243	43.425	-15.532	13.927	1.00	0.00	3A7
ATOM	1605	CZ	ARG	243	44.062	-14.651	13.096	1.00	0.00	3A7
ATOM	1606	NH1	ARG	243	44.310	-15.003	11.800	1.00	0.00	3A7
ATOM	1607	NH2	ARG	243	44.444	-13.422	13.549	1.00	0.00	3A7
ATOM	1608	C	ARG	243	40.582	-16.769	19.398	1.00	0.00	3A7
ATOM	1609	O	ARG	243	41.152	-17.580	20.122	1.00	0.00	3A7
ATOM	1610	N	LYS	244	39.813	-15.774	19.905	1.00	0.00	3A7
ATOM	1611	CA	LYS	244	39.642	-15.565	21.327	1.00	0.00	3A7
ATOM	1612	CB	LYS	244	39.046	-14.178	21.648	1.00	0.00	3A7

ATOM	1613	CG	LYS	244	39.241	-13.772	23.119	1.00	0.00	3A7
ATOM	1614	CD	LYS	244	39.058	-12.271	23.402	1.00	0.00	3A7
ATOM	1615	CE	LYS	244	40.110	-11.365	22.745	1.00	0.00	3A7
ATOM	1616	NZ	LYS	244	41.474	-11.713	23.205	1.00	0.00	3A7
ATOM	1617	C	LYS	244	38.844	-16.684	21.965	1.00	0.00	3A7
ATOM	1618	O	LYS	244	39.175	-17.150	23.051	1.00	0.00	3A7
ATOM	1619	N	VAL	245	37.806	-17.201	21.259	1.00	0.00	3A7
ATOM	1620	CA	VAL	245	37.014	-18.341	21.692	1.00	0.00	3A7
ATOM	1621	CB	VAL	245	35.821	-18.595	20.774	1.00	0.00	3A7
ATOM	1622	CG1	VAL	245	35.055	-19.885	21.138	1.00	0.00	3A7
ATOM	1623	CG2	VAL	245	34.893	-17.368	20.861	1.00	0.00	3A7
ATOM	1624	C	VAL	245	37.868	-19.581	21.753	1.00	0.00	3A7
ATOM	1625	O	VAL	245	37.867	-20.306	22.748	1.00	0.00	3A7
ATOM	1626	N	ILE	246	38.674	-19.822	20.690	1.00	0.00	3A7
ATOM	1627	CA	ILE	246	39.563	-20.965	20.600	1.00	0.00	3A7
ATOM	1628	CB	ILE	246	40.252	-21.026	19.232	1.00	0.00	3A7
ATOM	1629	CG2	ILE	246	41.696	-21.593	19.259	1.00	0.00	3A7
ATOM	1630	CG1	ILE	246	39.414	-21.855	18.224	1.00	0.00	3A7
ATOM	1631	CD	ILE	246	38.083	-21.241	17.793	1.00	0.00	3A7
ATOM	1632	C	ILE	246	40.571	-20.966	21.724	1.00	0.00	3A7
ATOM	1633	O	ILE	246	40.828	-21.996	22.332	1.00	0.00	3A7
ATOM	1634	N	SER	247	41.133	-19.787	22.059	1.00	0.00	3A7
ATOM	1635	CA	SER	247	42.119	-19.652	23.098	1.00	0.00	3A7
ATOM	1636	CB	SER	247	42.734	-18.250	23.119	1.00	0.00	3A7
ATOM	1637	OG	SER	247	43.425	-18.000	21.903	1.00	0.00	3A7
ATOM	1638	C	SER	247	41.551	-19.917	24.461	1.00	0.00	3A7
ATOM	1639	O	SER	247	42.194	-20.579	25.271	1.00	0.00	3A7
ATOM	1640	N	PHE	248	40.320	-19.434	24.749	1.00	0.00	3A7
ATOM	1641	CA	PHE	248	39.670	-19.654	26.022	1.00	0.00	3A7
ATOM	1642	CB	PHE	248	38.328	-18.900	26.125	1.00	0.00	3A7
ATOM	1643	CG	PHE	248	38.514	-17.473	26.559	1.00	0.00	3A7
ATOM	1644	CD1	PHE	248	37.951	-16.425	25.828	1.00	0.00	3A7
ATOM	1645	CD2	PHE	248	39.191	-17.176	27.745	1.00	0.00	3A7
ATOM	1646	CE1	PHE	248	38.058	-15.111	26.274	1.00	0.00	3A7
ATOM	1647	CE2	PHE	248	39.316	-15.861	28.183	1.00	0.00	3A7
ATOM	1648	CZ	PHE	248	38.749	-14.827	27.447	1.00	0.00	3A7
ATOM	1649	C	PHE	248	39.389	-21.122	26.244	1.00	0.00	3A7
ATOM	1650	O	PHE	248	39.623	-21.663	27.323	1.00	0.00	3A7
ATOM	1651	N	LEU	249	38.919	-21.832	25.198	1.00	0.00	3A7
ATOM	1652	CA	LEU	249	38.585	-23.234	25.317	1.00	0.00	3A7
ATOM	1653	CB	LEU	249	37.717	-23.699	24.147	1.00	0.00	3A7
ATOM	1654	CG	LEU	249	36.376	-22.962	24.103	1.00	0.00	3A7
ATOM	1655	CD1	LEU	249	35.616	-23.308	22.821	1.00	0.00	3A7
ATOM	1656	CD2	LEU	249	35.503	-23.243	25.342	1.00	0.00	3A7
ATOM	1657	C	LEU	249	39.811	-24.111	25.396	1.00	0.00	3A7
ATOM	1658	O	LEU	249	39.841	-25.088	26.140	1.00	0.00	3A7
ATOM	1659	N	THR	250	40.891	-23.744	24.670	1.00	0.00	3A7
ATOM	1660	CA	THR	250	42.150	-24.464	24.706	1.00	0.00	3A7
ATOM	1661	CB	THR	250	43.131	-23.926	23.673	1.00	0.00	3A7
ATOM	1662	OG1	THR	250	42.595	-24.120	22.372	1.00	0.00	3A7
ATOM	1663	CG2	THR	250	44.496	-24.649	23.731	1.00	0.00	3A7
ATOM	1664	C	THR	250	42.765	-24.398	26.085	1.00	0.00	3A7
ATOM	1665	O	THR	250	43.326	-25.376	26.573	1.00	0.00	3A7
ATOM	1666	N	LYS	251	42.622	-23.243	26.777	1.00	0.00	3A7
ATOM	1667	CA	LYS	251	43.087	-23.060	28.132	1.00	0.00	3A7
ATOM	1668	CB	LYS	251	42.941	-21.601	28.592	1.00	0.00	3A7
ATOM	1669	CG	LYS	251	43.599	-21.282	29.945	1.00	0.00	3A7
ATOM	1670	CD	LYS	251	43.466	-19.803	30.335	1.00	0.00	3A7
ATOM	1671	CE	LYS	251	44.093	-19.494	31.700	1.00	0.00	3A7
ATOM	1672	NZ	LYS	251	43.930	-18.062	32.038	1.00	0.00	3A7
ATOM	1673	C	LYS	251	42.337	-23.933	29.091	1.00	0.00	3A7
ATOM	1674	O	LYS	251	42.946	-24.559	29.945	1.00	0.00	3A7
ATOM	1675	N	SER	252	40.996	-24.057	28.942	1.00	0.00	3A7
ATOM	1676	CA	SER	252	40.169	-24.912	29.776	1.00	0.00	3A7
ATOM	1677	CB	SER	252	38.679	-24.780	29.422	1.00	0.00	3A7
ATOM	1678	OG	SER	252	38.257	-23.431	29.562	1.00	0.00	3A7
ATOM	1679	C	SER	252	40.543	-26.371	29.662	1.00	0.00	3A7
ATOM	1680	O	SER	252	40.637	-27.089	30.653	1.00	0.00	3A7
ATOM	1681	N	VAL	253	40.836	-26.832	28.425	1.00	0.00	3A7
ATOM	1682	CA	VAL	253	41.211	-28.203	28.125	1.00	0.00	3A7
ATOM	1683	CB	VAL	253	41.292	-28.416	26.609	1.00	0.00	3A7
ATOM	1684	CG1	VAL	253	41.865	-29.803	26.237	1.00	0.00	3A7

```
ATOM   1685  CG2 VAL   253      39.886 -28.264  25.997  1.00  0.00          3A7
ATOM   1686  C   VAL   253      42.532 -28.553  28.758  1.00  0.00          3A7
ATOM   1687  O   VAL   253      42.684 -29.586  29.404  1.00  0.00          3A7
ATOM   1688  N   LYS   254      43.518 -27.644  28.616  1.00  0.00          3A7
ATOM   1689  CA  LYS   254      44.842 -27.794  29.162  1.00  0.00          3A7
ATOM   1690  CB  LYS   254      45.735 -26.640  28.706  1.00  0.00          3A7
ATOM   1691  CG  LYS   254      47.220 -26.788  29.086  1.00  0.00          3A7
ATOM   1692  CD  LYS   254      48.143 -25.705  28.496  1.00  0.00          3A7
ATOM   1693  CE  LYS   254      48.079 -24.338  29.199  1.00  0.00          3A7
ATOM   1694  NZ  LYS   254      46.811 -23.622  28.925  1.00  0.00          3A7
ATOM   1695  C   LYS   254      44.830 -27.834  30.665  1.00  0.00          3A7
ATOM   1696  O   LYS   254      45.412 -28.728  31.270  1.00  0.00          3A7
ATOM   1697  N   GLN   255      44.098 -26.892  31.313  1.00  0.00          3A7
ATOM   1698  CA  GLN   255      43.943 -26.855  32.753  1.00  0.00          3A7
ATOM   1699  CB  GLN   255      43.122 -25.635  33.238  1.00  0.00          3A7
ATOM   1700  CG  GLN   255      43.863 -24.302  33.045  1.00  0.00          3A7
ATOM   1701  CD  GLN   255      42.977 -23.153  33.535  1.00  0.00          3A7
ATOM   1702  OE1 GLN   255      43.332 -22.444  34.484  1.00  0.00          3A7
ATOM   1703  NE2 GLN   255      41.801 -22.974  32.860  1.00  0.00          3A7
ATOM   1704  C   GLN   255      43.283 -28.104  33.282  1.00  0.00          3A7
ATOM   1705  O   GLN   255      43.599 -28.568  34.372  1.00  0.00          3A7
ATOM   1706  N   ILE   256      42.375 -28.710  32.490  1.00  0.00          3A7
ATOM   1707  CA  ILE   256      41.679 -29.907  32.888  1.00  0.00          3A7
ATOM   1708  CB  ILE   256      40.404 -30.098  32.072  1.00  0.00          3A7
ATOM   1709  CG2 ILE   256      40.068 -31.597  31.831  1.00  0.00          3A7
ATOM   1710  CG1 ILE   256      39.198 -29.508  32.862  1.00  0.00          3A7
ATOM   1711  CD  ILE   256      39.270 -28.036  33.277  1.00  0.00          3A7
ATOM   1712  C   ILE   256      42.566 -31.136  32.826  1.00  0.00          3A7
ATOM   1713  O   ILE   256      42.411 -32.060  33.627  1.00  0.00          3A7
ATOM   1714  N   LYS   257      43.535 -31.169  31.881  1.00  0.00          3A7
ATOM   1715  CA  LYS   257      44.464 -32.272  31.759  1.00  0.00          3A7
ATOM   1716  CB  LYS   257      45.216 -32.240  30.418  1.00  0.00          3A7
ATOM   1717  CG  LYS   257      44.304 -32.548  29.218  1.00  0.00          3A7
ATOM   1718  CD  LYS   257      45.027 -32.676  27.864  1.00  0.00          3A7
ATOM   1719  CE  LYS   257      45.583 -31.365  27.283  1.00  0.00          3A7
ATOM   1720  NZ  LYS   257      46.799 -30.908  27.996  1.00  0.00          3A7
ATOM   1721  C   LYS   257      45.489 -32.284  32.873  1.00  0.00          3A7
ATOM   1722  O   LYS   257      45.944 -33.343  33.303  1.00  0.00          3A7
ATOM   1723  N   GLU   258      45.856 -31.083  33.378  1.00  0.00          3A7
ATOM   1724  CA  GLU   258      46.817 -30.925  34.446  1.00  0.00          3A7
ATOM   1725  CB  GLU   258      47.454 -29.519  34.428  1.00  0.00          3A7
ATOM   1726  CG  GLU   258      48.242 -29.217  33.141  1.00  0.00          3A7
ATOM   1727  CD  GLU   258      49.402 -30.199  33.003  1.00  0.00          3A7
ATOM   1728  OE1 GLU   258      50.286 -30.202  33.900  1.00  0.00          3A7
ATOM   1729  OE2 GLU   258      49.418 -30.958  31.997  1.00  0.00          3A7
ATOM   1730  C   GLU   258      46.174 -31.151  35.797  1.00  0.00          3A7
ATOM   1731  O   GLU   258      46.851 -31.501  36.763  1.00  0.00          3A7
ATOM   1732  N   GLY   259      44.829 -30.971  35.870  1.00  0.00          3A7
ATOM   1733  CA  GLY   259      44.026 -31.194  37.052  1.00  0.00          3A7
ATOM   1734  C   GLY   259      43.490 -32.598  37.051  1.00  0.00          3A7
ATOM   1735  O   GLY   259      44.004 -33.461  36.340  1.00  0.00          3A7
ATOM   1736  N   ARG   260      42.444 -32.842  37.887  1.00  0.00          3A7
ATOM   1737  CA  ARG   260      41.787 -34.118  38.133  1.00  0.00          3A7
ATOM   1738  CB  ARG   260      41.489 -34.954  36.853  1.00  0.00          3A7
ATOM   1739  CG  ARG   260      40.639 -36.233  37.027  1.00  0.00          3A7
ATOM   1740  CD  ARG   260      39.172 -36.004  37.425  1.00  0.00          3A7
ATOM   1741  NE  ARG   260      39.105 -35.667  38.882  1.00  0.00          3A7
ATOM   1742  CZ  ARG   260      37.949 -35.260  39.486  1.00  0.00          3A7
ATOM   1743  NH1 ARG   260      37.967 -34.927  40.809  1.00  0.00          3A7
ATOM   1744  NH2 ARG   260      36.784 -35.174  38.781  1.00  0.00          3A7
ATOM   1745  C   ARG   260      42.631 -34.898  39.116  1.00  0.00          3A7
ATOM   1746  O   ARG   260      43.344 -35.831  38.749  1.00  0.00          3A7
ATOM   1747  N   LEU   261      42.581 -34.475  40.403  1.00  0.00          3A7
ATOM   1748  CA  LEU   261      43.473 -34.943  41.438  1.00  0.00          3A7
ATOM   1749  CB  LEU   261      44.463 -33.853  41.945  1.00  0.00          3A7
ATOM   1750  CG  LEU   261      43.883 -32.584  42.630  1.00  0.00          3A7
ATOM   1751  CD1 LEU   261      45.023 -31.737  43.230  1.00  0.00          3A7
ATOM   1752  CD2 LEU   261      43.009 -31.708  41.709  1.00  0.00          3A7
ATOM   1753  C   LEU   261      42.675 -35.510  42.582  1.00  0.00          3A7
ATOM   1754  O   LEU   261      43.042 -36.544  43.138  1.00  0.00          3A7
ATOM   1755  N   LYS   262      41.569 -34.835  42.973  1.00  0.00          3A7
ATOM   1756  CA  LYS   262      40.788 -35.239  44.117  1.00  0.00          3A7
```

ATOM	1757	CB	LYS	262	41.421	-34.790	45.462	1.00	0.00	3A7
ATOM	1758	CG	LYS	262	40.810	-35.454	46.708	1.00	0.00	3A7
ATOM	1759	CD	LYS	262	41.515	-35.043	48.009	1.00	0.00	3A7
ATOM	1760	CE	LYS	262	41.066	-35.853	49.233	1.00	0.00	3A7
ATOM	1761	NZ	LYS	262	39.611	-35.711	49.468	1.00	0.00	3A7
ATOM	1762	C	LYS	262	39.442	-34.600	43.941	1.00	0.00	3A7
ATOM	1763	O	LYS	262	39.325	-33.548	43.313	1.00	0.00	3A7
ATOM	1764	N	GLU	263	38.381	-35.233	44.510	1.00	0.00	3A7
ATOM	1765	CA	GLU	263	37.009	-34.774	44.438	1.00	0.00	3A7
ATOM	1766	CB	GLU	263	36.001	-35.949	44.396	1.00	0.00	3A7
ATOM	1767	CG	GLU	263	36.178	-36.837	43.152	1.00	0.00	3A7
ATOM	1768	CD	GLU	263	35.147	-37.964	43.149	1.00	0.00	3A7
ATOM	1769	OE1	GLU	263	34.322	-38.035	44.098	1.00	0.00	3A7
ATOM	1770	OE2	GLU	263	35.174	-38.773	42.183	1.00	0.00	3A7
ATOM	1771	C	GLU	263	36.698	-33.900	45.630	1.00	0.00	3A7
ATOM	1772	O	GLU	263	35.910	-34.265	46.501	1.00	0.00	3A7
ATOM	1773	N	THR	264	37.333	-32.704	45.670	1.00	0.00	3A7
ATOM	1774	CA	THR	264	37.170	-31.721	46.715	1.00	0.00	3A7
ATOM	1775	CB	THR	264	38.280	-31.765	47.757	1.00	0.00	3A7
ATOM	1776	OG1	THR	264	38.329	-33.054	48.352	1.00	0.00	3A7
ATOM	1777	CG2	THR	264	38.047	-30.721	48.870	1.00	0.00	3A7
ATOM	1778	C	THR	264	37.164	-30.395	46.003	1.00	0.00	3A7
ATOM	1779	O	THR	264	36.480	-29.458	46.415	1.00	0.00	3A7
ATOM	1780	N	GLN	265	37.940	-30.300	44.890	1.00	0.00	3A7
ATOM	1781	CA	GLN	265	38.063	-29.123	44.052	1.00	0.00	3A7
ATOM	1782	CB	GLN	265	39.417	-29.038	43.298	1.00	0.00	3A7
ATOM	1783	CG	GLN	265	40.645	-28.808	44.201	1.00	0.00	3A7
ATOM	1784	CD	GLN	265	40.965	-30.055	45.032	1.00	0.00	3A7
ATOM	1785	OE1	GLN	265	41.070	-31.165	44.497	1.00	0.00	3A7
ATOM	1786	NE2	GLN	265	41.132	-29.849	46.374	1.00	0.00	3A7
ATOM	1787	C	GLN	265	36.953	-29.140	43.030	1.00	0.00	3A7
ATOM	1788	O	GLN	265	36.287	-28.132	42.802	1.00	0.00	3A7
ATOM	1789	N	LYS	266	36.738	-30.320	42.404	1.00	0.00	3A7
ATOM	1790	CA	LYS	266	35.642	-30.556	41.500	1.00	0.00	3A7
ATOM	1791	CB	LYS	266	36.035	-30.452	40.002	1.00	0.00	3A7
ATOM	1792	CG	LYS	266	37.305	-31.216	39.591	1.00	0.00	3A7
ATOM	1793	CD	LYS	266	37.703	-30.959	38.129	1.00	0.00	3A7
ATOM	1794	CE	LYS	266	38.982	-31.700	37.724	1.00	0.00	3A7
ATOM	1795	NZ	LYS	266	39.346	-31.401	36.320	1.00	0.00	3A7
ATOM	1796	C	LYS	266	35.129	-31.922	41.858	1.00	0.00	3A7
ATOM	1797	O	LYS	266	35.796	-32.934	41.655	1.00	0.00	3A7
ATOM	1798	N	HIS	267	33.902	-31.966	42.437	1.00	0.00	3A7
ATOM	1799	CA	HIS	267	33.272	-33.168	42.940	1.00	0.00	3A7
ATOM	1800	ND1	HIS	267	32.504	-35.052	45.499	1.00	0.00	3A7
ATOM	1801	CG	HIS	267	31.780	-34.098	44.815	1.00	0.00	3A7
ATOM	1802	CB	HIS	267	32.380	-32.874	44.174	1.00	0.00	3A7
ATOM	1803	NE2	HIS	267	30.385	-35.724	45.524	1.00	0.00	3A7
ATOM	1804	CD2	HIS	267	30.489	-34.526	44.840	1.00	0.00	3A7
ATOM	1805	CE1	HIS	267	31.620	-35.999	45.901	1.00	0.00	3A7
ATOM	1806	C	HIS	267	32.435	-33.802	41.858	1.00	0.00	3A7
ATOM	1807	O	HIS	267	32.255	-35.018	41.834	1.00	0.00	3A7
ATOM	1808	N	ARG	268	31.909	-32.963	40.929	1.00	0.00	3A7
ATOM	1809	CA	ARG	268	31.110	-33.390	39.804	1.00	0.00	3A7
ATOM	1810	CB	ARG	268	29.939	-32.419	39.501	1.00	0.00	3A7
ATOM	1811	CG	ARG	268	30.357	-30.974	39.172	1.00	0.00	3A7
ATOM	1812	CD	ARG	268	29.154	-30.049	38.948	1.00	0.00	3A7
ATOM	1813	NE	ARG	268	29.664	-28.690	38.573	1.00	0.00	3A7
ATOM	1814	CZ	ARG	268	28.818	-27.637	38.353	1.00	0.00	3A7
ATOM	1815	NH1	ARG	268	29.328	-26.423	37.993	1.00	0.00	3A7
ATOM	1816	NH2	ARG	268	27.470	-27.791	38.491	1.00	0.00	3A7
ATOM	1817	C	ARG	268	31.997	-33.501	38.593	1.00	0.00	3A7
ATOM	1818	O	ARG	268	33.012	-32.813	38.485	1.00	0.00	3A7
ATOM	1819	N	VAL	269	31.604	-34.383	37.643	1.00	0.00	3A7
ATOM	1820	CA	VAL	269	32.279	-34.566	36.378	1.00	0.00	3A7
ATOM	1821	CB	VAL	269	32.595	-36.021	36.063	1.00	0.00	3A7
ATOM	1822	CG1	VAL	269	33.733	-36.473	37.001	1.00	0.00	3A7
ATOM	1823	CG2	VAL	269	31.340	-36.903	36.220	1.00	0.00	3A7
ATOM	1824	C	VAL	269	31.408	-33.947	35.315	1.00	0.00	3A7
ATOM	1825	O	VAL	269	30.217	-33.712	35.519	1.00	0.00	3A7
ATOM	1826	N	ASP	270	32.030	-33.642	34.156	1.00	0.00	3A7
ATOM	1827	CA	ASP	270	31.450	-32.836	33.096	1.00	0.00	3A7
ATOM	1828	CB	ASP	270	31.980	-31.399	33.132	1.00	0.00	3A7

```
ATOM   1829  CG  ASP   270      33.510 -31.368  33.034  1.00  0.00           3A7
ATOM   1830  OD1 ASP   270      34.013 -30.868  31.995  1.00  0.00           3A7
ATOM   1831  OD2 ASP   270      34.191 -31.809  33.998  1.00  0.00           3A7
ATOM   1832  C   ASP   270      31.710 -33.510  31.781  1.00  0.00           3A7
ATOM   1833  O   ASP   270      32.369 -34.547  31.709  1.00  0.00           3A7
ATOM   1834  N   PHE   271      31.187 -32.915  30.684  1.00  0.00           3A7
ATOM   1835  CA  PHE   271      31.302 -33.474  29.357  1.00  0.00           3A7
ATOM   1836  CB  PHE   271      30.407 -32.722  28.356  1.00  0.00           3A7
ATOM   1837  CG  PHE   271      30.344 -33.517  27.080  1.00  0.00           3A7
ATOM   1838  CD1 PHE   271      30.012 -34.875  27.101  1.00  0.00           3A7
ATOM   1839  CD2 PHE   271      30.758 -32.938  25.887  1.00  0.00           3A7
ATOM   1840  CE1 PHE   271      30.211 -35.660  25.972  1.00  0.00           3A7
ATOM   1841  CE2 PHE   271      30.870 -33.707  24.737  1.00  0.00           3A7
ATOM   1842  CZ  PHE   271      30.646 -35.078  24.793  1.00  0.00           3A7
ATOM   1843  C   PHE   271      32.719 -33.478  28.848  1.00  0.00           3A7
ATOM   1844  O   PHE   271      33.150 -34.431  28.204  1.00  0.00           3A7
ATOM   1845  N   LEU   272      33.494 -32.417  29.146  1.00  0.00           3A7
ATOM   1846  CA  LEU   272      34.866 -32.326  28.716  1.00  0.00           3A7
ATOM   1847  CB  LEU   272      35.455 -30.979  29.100  1.00  0.00           3A7
ATOM   1848  CG  LEU   272      36.816 -30.698  28.482  1.00  0.00           3A7
ATOM   1849  CD1 LEU   272      36.864 -29.210  28.078  1.00  0.00           3A7
ATOM   1850  CD2 LEU   272      38.027 -31.011  29.363  1.00  0.00           3A7
ATOM   1851  C   LEU   272      35.735 -33.394  29.311  1.00  0.00           3A7
ATOM   1852  O   LEU   272      36.573 -33.979  28.634  1.00  0.00           3A7
ATOM   1853  N   GLN   273      35.522 -33.712  30.606  1.00  0.00           3A7
ATOM   1854  CA  GLN   273      36.255 -34.750  31.288  1.00  0.00           3A7
ATOM   1855  CB  GLN   273      35.890 -34.805  32.788  1.00  0.00           3A7
ATOM   1856  CG  GLN   273      36.853 -35.634  33.658  1.00  0.00           3A7
ATOM   1857  CD  GLN   273      38.222 -34.946  33.686  1.00  0.00           3A7
ATOM   1858  OE1 GLN   273      38.361 -33.845  34.234  1.00  0.00           3A7
ATOM   1859  NE2 GLN   273      39.247 -35.617  33.079  1.00  0.00           3A7
ATOM   1860  C   GLN   273      35.971 -36.088  30.668  1.00  0.00           3A7
ATOM   1861  O   GLN   273      36.882 -36.879  30.456  1.00  0.00           3A7
ATOM   1862  N   LEU   274      34.685 -36.340  30.310  1.00  0.00           3A7
ATOM   1863  CA  LEU   274      34.245 -37.560  29.669  1.00  0.00           3A7
ATOM   1864  CB  LEU   274      32.718 -37.631  29.471  1.00  0.00           3A7
ATOM   1865  CG  LEU   274      31.891 -37.798  30.761  1.00  0.00           3A7
ATOM   1866  CD1 LEU   274      30.398 -37.811  30.394  1.00  0.00           3A7
ATOM   1867  CD2 LEU   274      32.273 -39.060  31.558  1.00  0.00           3A7
ATOM   1868  C   LEU   274      34.854 -37.729  28.302  1.00  0.00           3A7
ATOM   1869  O   LEU   274      35.232 -38.832  27.930  1.00  0.00           3A7
ATOM   1870  N   MET   275      35.003 -36.636  27.521  1.00  0.00           3A7
ATOM   1871  CA  MET   275      35.607 -36.702  26.211  1.00  0.00           3A7
ATOM   1872  CB  MET   275      35.400 -35.428  25.399  1.00  0.00           3A7
ATOM   1873  CG  MET   275      33.958 -35.154  24.962  1.00  0.00           3A7
ATOM   1874  SD  MET   275      33.857 -33.829  23.713  1.00  0.00           3A7
ATOM   1875  CE  MET   275      34.315 -32.435  24.786  1.00  0.00           3A7
ATOM   1876  C   MET   275      37.090 -36.951  26.286  1.00  0.00           3A7
ATOM   1877  Q   MET   275      37.642 -37.666  25.458  1.00  0.00           3A7
ATOM   1878  N   ILE   276      37.778 -36.381  27.305  1.00  0.00           3A7
ATOM   1879  CA  ILE   276      39.215 -36.516  27.488  1.00  0.00           3A7
ATOM   1880  CB  ILE   276      39.723 -35.567  28.575  1.00  0.00           3A7
ATOM   1881  CG2 ILE   276      41.140 -35.906  29.105  1.00  0.00           3A7
ATOM   1882  CG1 ILE   276      39.717 -34.100  28.081  1.00  0.00           3A7
ATOM   1883  CD  ILE   276      40.767 -33.779  27.011  1.00  0.00           3A7
ATOM   1884  C   ILE   276      39.615 -37.926  27.833  1.00  0.00           3A7
ATOM   1885  O   ILE   276      40.701 -38.375  27.476  1.00  0.00           3A7
ATOM   1886  N   ASP   277      38.749 -38.659  28.548  1.00  0.00           3A7
ATOM   1887  CA  ASP   277      39.133 -39.958  29.016  1.00  0.00           3A7
ATOM   1888  CB  ASP   277      38.914 -40.156  30.516  1.00  0.00           3A7
ATOM   1889  CG  ASP   277      39.827 -39.210  31.302  1.00  0.00           3A7
ATOM   1890  OD1 ASP   277      40.999 -39.021  30.882  1.00  0.00           3A7
ATOM   1891  OD2 ASP   277      39.351 -38.657  32.329  1.00  0.00           3A7
ATOM   1892  C   ASP   277      38.346 -41.070  28.476  1.00  0.00           3A7
ATOM   1893  O   ASP   277      38.933 -42.095  28.164  1.00  0.00           3A7
ATOM   1894  N   SER   278      36.987 -41.031  28.602  1.00  0.00           3A7
ATOM   1895  CA  SER   278      36.186 -42.176  29.071  1.00  0.00           3A7
ATOM   1896  CB  SER   278      34.677 -41.818  29.196  1.00  0.00           3A7
ATOM   1897  OG  SER   278      34.091 -41.424  27.961  1.00  0.00           3A7
ATOM   1898  C   SER   278      36.329 -43.499  28.318  1.00  0.00           3A7
ATOM   1899  O   SER   278      35.567 -43.792  27.399  1.00  0.00           3A7
ATOM   1900  N   GLN   279      37.341 -44.307  28.750  1.00  0.00           3A7
```

ATOM	1901	CA	GLN	279	37.851	-45.539	28.167	1.00	0.00	3A7
ATOM	1902	CB	GLN	279	36.793	-46.503	27.561	1.00	0.00	3A7
ATOM	1903	CG	GLN	279	35.768	-47.000	28.593	1.00	0.00	3A7
ATOM	1904	CD	GLN	279	34.775	-47.928	27.887	1.00	0.00	3A7
ATOM	1905	OE1	GLN	279	35.143	-49.016	27.428	1.00	0.00	3A7
ATOM	1906	NE2	GLN	279	33.487	-47.472	27.805	1.00	0.00	3A7
ATOM	1907	C	GLN	279	38.889	-45.204	27.116	1.00	0.00	3A7
ATOM	1908	O	GLN	279	38.687	-45.481	25.937	1.00	0.00	3A7
ATOM	1909	N	ASN	280	40.027	-44.587	27.552	1.00	0.00	3A7
ATOM	1910	CA	ASN	280	41.202	-44.166	26.787	1.00	0.00	3A7
ATOM	1911	CB	ASN	280	42.008	-45.358	26.209	1.00	0.00	3A7
ATOM	1912	CG	ASN	280	42.430	-46.296	27.347	1.00	0.00	3A7
ATOM	1913	OD1	ASN	280	41.937	-47.427	27.447	1.00	0.00	3A7
ATOM	1914	ND2	ASN	280	43.366	-45.803	28.213	1.00	0.00	3A7
ATOM	1915	C	ASN	280	40.890	-43.183	25.664	1.00	0.00	3A7
ATOM	1916	O	ASN	280	40.934	-43.532	24.487	1.00	0.00	3A7
ATOM	1917	N	SER	281	40.551	-41.923	26.053	1.00	0.00	3A7
ATOM	1918	CA	SER	281	40.076	-40.803	25.252	1.00	0.00	3A7
ATOM	1919	CB	SER	281	40.924	-40.513	23.986	1.00	0.00	3A7
ATOM	1920	OG	SER	281	42.283	-40.298	24.340	1.00	0.00	3A7
ATOM	1921	C	SER	281	38.621	-40.951	24.837	1.00	0.00	3A7
ATOM	1922	O	SER	281	38.131	-40.172	24.021	1.00	0.00	3A7
ATOM	1923	N	LYS	282	37.924	-42.020	25.342	1.00	0.00	3A7
ATOM	1924	CA	LYS	282	36.818	-42.723	24.707	1.00	0.00	3A7
ATOM	1925	CB	LYS	282	35.459	-42.013	24.620	1.00	0.00	3A7
ATOM	1926	CG	LYS	282	34.288	-42.957	24.294	1.00	0.00	3A7
ATOM	1927	CD	LYS	282	32.914	-42.336	24.590	1.00	0.00	3A7
ATOM	1928	CE	LYS	282	31.744	-43.301	24.357	1.00	0.00	3A7
ATOM	1929	NZ	LYS	282	31.691	-43.746	22.946	1.00	0.00	3A7
ATOM	1930	C	LYS	282	37.194	-43.157	23.334	1.00	0.00	3A7
ATOM	1931	O	LYS	282	37.082	-42.407	22.364	1.00	0.00	3A7
ATOM	1932	N	ASP	283	37.706	-44.392	23.270	1.00	0.00	3A7
ATOM	1933	CA	ASP	283	38.125	-44.964	22.041	1.00	0.00	3A7
ATOM	1934	CB	ASP	283	39.663	-45.088	21.918	1.00	0.00	3A7
ATOM	1935	CG	ASP	283	40.442	-46.002	22.880	1.00	0.00	3A7
ATOM	1936	OD1	ASP	283	41.683	-46.097	22.672	1.00	0.00	3A7
ATOM	1937	OD2	ASP	283	39.853	-46.604	23.810	1.00	0.00	3A7
ATOM	1938	C	ASP	283	37.352	-46.233	21.948	1.00	0.00	3A7
ATOM	1939	O	ASP	283	37.675	-47.232	22.581	1.00	0.00	3A7
ATOM	1940	N	SER	284	36.258	-46.198	21.157	1.00	0.00	3A7
ATOM	1941	CA	SER	284	35.513	-47.378	20.782	1.00	0.00	3A7
ATOM	1942	CB	SER	284	34.115	-47.009	20.210	1.00	0.00	3A7
ATOM	1943	OG	SER	284	34.183	-45.995	19.212	1.00	0.00	3A7
ATOM	1944	C	SER	284	36.266	-48.277	19.834	1.00	0.00	3A7
ATOM	1945	O	SER	284	36.990	-49.180	20.242	1.00	0.00	3A7
ATOM	1946	N	GLU	285	36.113	-48.092	18.521	1.00	0.00	3A7
ATOM	1947	CA	GLU	285	36.639	-49.081	17.634	1.00	0.00	3A7
ATOM	1948	CB	GLU	285	35.795	-49.213	16.369	1.00	0.00	3A7
ATOM	1949	CG	GLU	285	35.628	-47.895	15.591	1.00	0.00	3A7
ATOM	1950	CD	GLU	285	34.752	-48.143	14.367	1.00	0.00	3A7
ATOM	1951	OE1	GLU	285	33.566	-48.527	14.555	1.00	0.00	3A7
ATOM	1952	OE2	GLU	285	35.255	-47.948	13.228	1.00	0.00	3A7
ATOM	1953	C	GLU	285	38.083	-48.834	17.309	1.00	0.00	3A7
ATOM	1954	O	GLU	285	38.621	-49.477	16.447	1.00	0.00	3A7
ATOM	1955	N	THR	286	38.744	-47.901	18.009	1.00	0.00	3A7
ATOM	1956	CA	THR	286	40.099	-47.398	17.894	1.00	0.00	3A7
ATOM	1957	CB	THR	286	41.251	-48.366	17.728	1.00	0.00	3A7
ATOM	1958	OG1	THR	286	41.071	-49.460	18.620	1.00	0.00	3A7
ATOM	1959	CG2	THR	286	42.623	-47.726	18.038	1.00	0.00	3A7
ATOM	1960	C	THR	286	40.161	-46.319	16.868	1.00	0.00	3A7
ATOM	1961	O	THR	286	41.095	-45.529	16.847	1.00	0.00	3A7
ATOM	1962	N	HIS	287	39.201	-46.294	15.904	1.00	0.00	3A7
ATOM	1963	CA	HIS	287	39.294	-45.529	14.676	1.00	0.00	3A7
ATOM	1964	ND1	HIS	287	37.806	-44.452	11.739	1.00	0.00	3A7
ATOM	1965	CG	HIS	287	38.588	-45.495	12.192	1.00	0.00	3A7
ATOM	1966	CB	HIS	287	38.440	-46.152	13.541	1.00	0.00	3A7
ATOM	1967	NE2	HIS	287	39.260	-44.903	10.120	1.00	0.00	3A7
ATOM	1968	CD2	HIS	287	39.470	-45.756	11.189	1.00	0.00	3A7
ATOM	1969	CE1	HIS	287	38.251	-44.140	10.497	1.00	0.00	3A7
ATOM	1970	C	HIS	287	38.868	-44.107	14.911	1.00	0.00	3A7
ATOM	1971	O	HIS	287	37.679	-43.797	14.904	1.00	0.00	3A7
ATOM	1972	N	LYS	288	39.880	-43.225	15.122	1.00	0.00	3A7

ATOM	1973	CA	LYS	288	39.776	-41.800	15.358	1.00	0.00	3A7
ATOM	1974	CB	LYS	288	38.889	-41.036	14.340	1.00	0.00	3A7
ATOM	1975	CG	LYS	288	39.415	-41.157	12.901	1.00	0.00	3A7
ATOM	1976	CD	LYS	288	38.528	-40.437	11.877	1.00	0.00	3A7
ATOM	1977	CE	LYS	288	39.036	-40.557	10.434	1.00	0.00	3A7
ATOM	1978	NZ	LYS	288	40.358	-39.909	10.282	1.00	0.00	3A7
ATOM	1979	C	LYS	288	39.309	-41.522	16.767	1.00	0.00	3A7
ATOM	1980	O	LYS	288	38.116	-41.380	17.030	1.00	0.00	3A7
ATOM	1981	N	ALA	289	40.290	-41.406	17.701	1.00	0.00	3A7
ATOM	1982	CA	ALA	289	40.092	-40.977	19.070	1.00	0.00	3A7
ATOM	1983	CB	ALA	289	41.158	-41.545	20.027	1.00	0.00	3A7
ATOM	1984	C	ALA	289	40.164	-39.473	19.078	1.00	0.00	3A7
ATOM	1985	O	ALA	289	40.670	-38.875	18.128	1.00	0.00	3A7
ATOM	1986	N	LEU	290	39.624	-38.812	20.137	1.00	0.00	3A7
ATOM	1987	CA	LEU	290	39.349	-37.401	20.081	1.00	0.00	3A7
ATOM	1988	CB	LEU	290	38.229	-37.004	21.014	1.00	0.00	3A7
ATOM	1989	CG	LEU	290	36.888	-37.703	20.701	1.00	0.00	3A7
ATOM	1990	CD1	LEU	290	35.892	-37.512	21.861	1.00	0.00	3A7
ATOM	1991	CD2	LEU	290	36.312	-37.221	19.355	1.00	0.00	3A7
ATOM	1992	C	LEU	290	40.550	-36.573	20.350	1.00	0.00	3A7
ATOM	1993	O	LEU	290	41.191	-36.642	21.390	1.00	0.00	3A7
ATOM	1994	N	SER	291	40.854	-35.731	19.352	1.00	0.00	3A7
ATOM	1995	CA	SER	291	41.954	-34.822	19.363	1.00	0.00	3A7
ATOM	1996	CB	SER	291	42.455	-34.592	17.928	1.00	0.00	3A7
ATOM	1997	OG	SER	291	41.422	-34.204	17.030	1.00	0.00	3A7
ATOM	1998	C	SER	291	41.471	-33.540	19.957	1.00	0.00	3A7
ATOM	1999	O	SER	291	40.275	-33.273	19.991	1.00	0.00	3A7
ATOM	2000	N	ASP	292	42.400	-32.681	20.410	1.00	0.00	3A7
ATOM	2001	CA	ASP	292	42.071	-31.438	21.064	1.00	0.00	3A7
ATOM	2002	CB	ASP	292	43.338	-30.745	21.556	1.00	0.00	3A7
ATOM	2003	CG	ASP	292	44.042	-31.647	22.570	1.00	0.00	3A7
ATOM	2004	OD1	ASP	292	43.426	-31.941	23.629	1.00	0.00	3A7
ATOM	2005	OD2	ASP	292	45.204	-32.050	22.298	1.00	0.00	3A7
ATOM	2006	C	ASP	292	41.334	-30.471	20.170	1.00	0.00	3A7
ATOM	2007	O	ASP	292	40.568	-29.641	20.643	1.00	0.00	3A7
ATOM	2008	N	LEU	293	41.506	-30.616	18.834	1.00	0.00	3A7
ATOM	2009	CA	LEU	293	40.836	-29.795	17.858	1.00	0.00	3A7
ATOM	2010	CB	LEU	293	41.527	-29.876	16.490	1.00	0.00	3A7
ATOM	2011	CG	LEU	293	43.011	-29.436	16.506	1.00	0.00	3A7
ATOM	2012	CD1	LEU	293	43.663	-29.663	15.129	1.00	0.00	3A7
ATOM	2013	CD2	LEU	293	43.189	-27.976	16.965	1.00	0.00	3A7
ATOM	2014	C	LEU	293	39.382	-30.187	17.711	1.00	0.00	3A7
ATOM	2015	O	LEU	293	38.493	-29.340	17.738	1.00	0.00	3A7
ATOM	2016	N	GLU	294	39.081	-31.502	17.619	1.00	0.00	3A7
ATOM	2017	CA	GLU	294	37.722	-31.998	17.504	1.00	0.00	3A7
ATOM	2018	CB	GLU	294	37.697	-33.523	17.310	1.00	0.00	3A7
ATOM	2019	CG	GLU	294	38.247	-33.957	15.942	1.00	0.00	3A7
ATOM	2020	CD	GLU	294	38.198	-35.480	15.850	1.00	0.00	3A7
ATOM	2021	OE1	GLU	294	37.070	-36.040	15.905	1.00	0.00	3A7
ATOM	2022	OE2	GLU	294	39.285	-36.104	15.722	1.00	0.00	3A7
ATOM	2023	C	GLU	294	36.901	-31.676	18.723	1.00	0.00	3A7
ATOM	2024	O	GLU	294	35.776	-31.192	18.632	1.00	0.00	3A7
ATOM	2025	N	LEU	295	37.506	-31.876	19.909	1.00	0.00	3A7
ATOM	2026	CA	LEU	295	36.915	-31.573	21.190	1.00	0.00	3A7
ATOM	2027	CB	LEU	295	37.911	-31.878	22.313	1.00	0.00	3A7
ATOM	2028	CG	LEU	295	38.311	-33.358	22.435	1.00	0.00	3A7
ATOM	2029	CD1	LEU	295	39.434	-33.555	23.470	1.00	0.00	3A7
ATOM	2030	CD2	LEU	295	37.094	-34.206	22.783	1.00	0.00	3A7
ATOM	2031	C	LEU	295	36.535	-30.119	21.312	1.00	0.00	3A7
ATOM	2032	O	LEU	295	35.404	-29.765	21.643	1.00	0.00	3A7
ATOM	2033	N	MET	296	37.488	-29.212	21.017	1.00	0.00	3A7
ATOM	2034	CA	MET	296	37.285	-27.783	21.050	1.00	0.00	3A7
ATOM	2035	CB	MET	296	38.580	-27.070	20.647	1.00	0.00	3A7
ATOM	2036	CG	MET	296	38.420	-25.578	20.350	1.00	0.00	3A7
ATOM	2037	SD	MET	296	40.016	-24.717	20.404	1.00	0.00	3A7
ATOM	2038	CE	MET	296	40.777	-25.540	18.974	1.00	0.00	3A7
ATOM	2039	C	MET	296	36.195	-27.341	20.113	1.00	0.00	3A7
ATOM	2040	O	MET	296	35.328	-26.566	20.489	1.00	0.00	3A7
ATOM	2041	N	ALA	297	36.174	-27.882	18.877	1.00	0.00	3A7
ATOM	2042	CA	ALA	297	35.172	-27.555	17.895	1.00	0.00	3A7
ATOM	2043	CB	ALA	297	35.493	-28.182	16.525	1.00	0.00	3A7
ATOM	2044	C	ALA	297	33.783	-27.978	18.300	1.00	0.00	3A7

ATOM	2045	O	ALA	297	32.817	-27.301	17.986	1.00	0.00	3A7
ATOM	2046	N	GLN	298	33.648	-29.071	19.085	1.00	0.00	3A7
ATOM	2047	CA	GLN	298	32.385	-29.501	19.640	1.00	0.00	3A7
ATOM	2048	CB	GLN	298	32.482	-30.905	20.248	1.00	0.00	3A7
ATOM	2049	CG	GLN	298	32.651	-32.025	19.207	1.00	0.00	3A7
ATOM	2050	CD	GLN	298	32.958	-33.345	19.922	1.00	0.00	3A7
ATOM	2051	OE1	GLN	298	34.080	-33.554	20.400	1.00	0.00	3A7
ATOM	2052	NE2	GLN	298	31.939	-34.253	19.977	1.00	0.00	3A7
ATOM	2053	C	GLN	298	31.922	-28.563	20.719	1.00	0.00	3A7
ATOM	2054	O	GLN	298	30.773	-28.142	20.728	1.00	0.00	3A7
ATOM	2055	N	SER	299	32.831	-28.160	21.630	1.00	0.00	3A7
ATOM	2056	CA	SER	299	32.535	-27.222	22.690	1.00	0.00	3A7
ATOM	2057	CB	SER	299	33.759	-27.023	23.597	1.00	0.00	3A7
ATOM	2058	OG	SER	299	34.175	-28.269	24.141	1.00	0.00	3A7
ATOM	2059	C	SER	299	32.097	-25.874	22.158	1.00	0.00	3A7
ATOM	2060	O	SER	299	31.185	-25.252	22.698	1.00	0.00	3A7
ATOM	2061	N	ILE	300	32.719	-25.399	21.047	1.00	0.00	3A7
ATOM	2062	CA	ILE	300	32.361	-24.170	20.361	1.00	0.00	3A7
ATOM	2063	CB	ILE	300	33.321	-23.832	19.229	1.00	0.00	3A7
ATOM	2064	CG2	ILE	300	32.843	-22.603	18.412	1.00	0.00	3A7
ATOM	2065	CG1	ILE	300	34.732	-23.560	19.774	1.00	0.00	3A7
ATOM	2066	CD	ILE	300	35.811	-23.539	18.691	1.00	0.00	3A7
ATOM	2067	C	ILE	300	30.987	-24.293	19.764	1.00	0.00	3A7
ATOM	2068	O	ILE	300	30.162	-23.398	19.914	1.00	0.00	3A7
ATOM	2069	N	ILE	301	30.695	-25.431	19.092	1.00	0.00	3A7
ATOM	2070	CA	ILE	301	29.418	-25.676	18.455	1.00	0.00	3A7
ATOM	2071	CB	ILE	301	29.475	-26.900	17.553	1.00	0.00	3A7
ATOM	2072	CG2	ILE	301	28.192	-27.772	17.525	1.00	0.00	3A7
ATOM	2073	CG1	ILE	301	29.774	-26.460	16.091	1.00	0.00	3A7
ATOM	2074	CD	ILE	301	31.053	-25.647	15.869	1.00	0.00	3A7
ATOM	2075	C	ILE	301	28.303	-25.792	19.465	1.00	0.00	3A7
ATOM	2076	O	ILE	301	27.182	-25.379	19.205	1.00	0.00	3A7
ATOM	2077	N	PHE	302	28.584	-26.318	20.673	1.00	0.00	3A7
ATOM	2078	CA	PHE	302	27.593	-26.507	21.709	1.00	0.00	3A7
ATOM	2079	CB	PHE	302	28.212	-27.306	22.878	1.00	0.00	3A7
ATOM	2080	CG	PHE	302	28.239	-28.790	22.660	1.00	0.00	3A7
ATOM	2081	CD1	PHE	302	28.348	-29.335	21.379	1.00	0.00	3A7
ATOM	2082	CD2	PHE	302	28.620	-29.577	23.757	1.00	0.00	3A7
ATOM	2083	CE1	PHE	302	28.914	-30.584	21.188	1.00	0.00	3A7
ATOM	2084	CE2	PHE	302	29.170	-30.829	23.567	1.00	0.00	3A7
ATOM	2085	CZ	PHE	302	29.356	-31.311	22.282	1.00	0.00	3A7
ATOM	2086	C	PHE	302	27.161	-25.150	22.252	1.00	0.00	3A7
ATOM	2087	O	PHE	302	25.980	-24.892	22.478	1.00	0.00	3A7
ATOM	2088	N	ILE	303	28.134	-24.221	22.452	1.00	0.00	3A7
ATOM	2089	CA	ILE	303	27.866	-22.889	22.966	1.00	0.00	3A7
ATOM	2090	CB	ILE	303	29.091	-22.188	23.539	1.00	0.00	3A7
ATOM	2091	CG2	ILE	303	28.716	-20.768	24.038	1.00	0.00	3A7
ATOM	2092	CG1	ILE	303	29.642	-23.043	24.700	1.00	0.00	3A7
ATOM	2093	CD	ILE	303	30.952	-22.513	25.280	1.00	0.00	3A7
ATOM	2094	C	ILE	303	27.215	-22.030	21.914	1.00	0.00	3A7
ATOM	2095	O	ILE	303	26.217	-21.376	22.173	1.00	0.00	3A7
ATOM	2096	N	PHE	304	27.728	-22.042	20.671	1.00	0.00	3A7
ATOM	2097	CA	PHE	304	27.197	-21.301	19.548	1.00	0.00	3A7
ATOM	2098	CB	PHE	304	28.117	-21.579	18.314	1.00	0.00	3A7
ATOM	2099	CG	PHE	304	27.669	-20.996	16.996	1.00	0.00	3A7
ATOM	2100	CD1	PHE	304	27.839	-19.644	16.704	1.00	0.00	3A7
ATOM	2101	CD2	PHE	304	27.091	-21.829	16.036	1.00	0.00	3A7
ATOM	2102	CE1	PHE	304	27.436	-19.134	15.472	1.00	0.00	3A7
ATOM	2103	CE2	PHE	304	26.678	-21.320	14.811	1.00	0.00	3A7
ATOM	2104	CZ	PHE	304	26.851	-19.970	14.526	1.00	0.00	3A7
ATOM	2105	C	PHE	304	25.772	-21.649	19.207	1.00	0.00	3A7
ATOM	2106	O	PHE	304	24.909	-20.780	19.129	1.00	0.00	3A7
ATOM	2107	N	ALA	305	25.493	-22.954	19.027	1.00	0.00	3A7
ATOM	2108	CA	ALA	305	24.183	-23.428	18.672	1.00	0.00	3A7
ATOM	2109	CB	ALA	305	24.206	-24.883	18.216	1.00	0.00	3A7
ATOM	2110	C	ALA	305	23.224	-23.354	19.820	1.00	0.00	3A7
ATOM	2111	O	ALA	305	22.041	-23.132	19.620	1.00	0.00	3A7
ATOM	2112	N	GLY	306	23.734	-23.533	21.051	1.00	0.00	3A7
ATOM	2113	CA	GLY	306	22.903	-23.642	22.219	1.00	0.00	3A7
ATOM	2114	C	GLY	306	22.541	-22.346	22.888	1.00	0.00	3A7
ATOM	2115	O	GLY	306	21.518	-22.258	23.561	1.00	0.00	3A7
ATOM	2116	N	TYR	307	23.359	-21.285	22.742	1.00	0.00	3A7

```
ATOM   2117  CA  TYR   307      23.134 -20.054  23.474  1.00  0.00          3A7
ATOM   2118  CB  TYR   307      24.473 -19.279  23.690  1.00  0.00          3A7
ATOM   2119  CG  TYR   307      24.492 -17.764  23.545  1.00  0.00          3A7
ATOM   2120  CD1 TYR   307      23.675 -16.927  24.308  1.00  0.00          3A7
ATOM   2121  CD2 TYR   307      25.364 -17.182  22.621  1.00  0.00          3A7
ATOM   2122  CE1 TYR   307      23.720 -15.545  24.144  1.00  0.00          3A7
ATOM   2123  CE2 TYR   307      25.420 -15.801  22.460  1.00  0.00          3A7
ATOM   2124  CZ  TYR   307      24.595 -14.980  23.222  1.00  0.00          3A7
ATOM   2125  OH  TYR   307      24.653 -13.578  23.066  1.00  0.00          3A7
ATOM   2126  C   TYR   307      22.056 -19.224  22.841  1.00  0.00          3A7
ATOM   2127  O   TYR   307      21.092 -18.851  23.498  1.00  0.00          3A7
ATOM   2128  N   GLU   308      22.222 -18.888  21.552  1.00  0.00          3A7
ATOM   2129  CA  GLU   308      21.442 -17.887  20.875  1.00  0.00          3A7
ATOM   2130  CB  GLU   308      22.048 -17.593  19.488  1.00  0.00          3A7
ATOM   2131  CG  GLU   308      22.280 -18.862  18.631  1.00  0.00          3A7
ATOM   2132  CD  GLU   308      23.057 -18.569  17.347  1.00  0.00          3A7
ATOM   2133  OE1 GLU   308      23.277 -17.372  17.030  1.00  0.00          3A7
ATOM   2134  OE2 GLU   308      23.430 -19.556  16.657  1.00  0.00          3A7
ATOM   2135  C   GLU   308      20.007 -18.253  20.661  1.00  0.00          3A7
ATOM   2136  O   GLU   308      19.119 -17.424  20.814  1.00  0.00          3A7
ATOM   2137  N   THR   309      19.741 -19.531  20.323  1.00  0.00          3A7
ATOM   2138  CA  THR   309      18.413 -20.055  20.080  1.00  0.00          3A7
ATOM   2139  CB  THR   309      18.504 -21.431  19.437  1.00  0.00          3A7
ATOM   2140  OG1 THR   309      17.244 -21.870  18.974  1.00  0.00          3A7
ATOM   2141  CG2 THR   309      19.256 -22.438  20.330  1.00  0.00          3A7
ATOM   2142  C   THR   309      17.592 -20.080  21.350  1.00  0.00          3A7
ATOM   2143  O   THR   309      16.436 -19.681  21.350  1.00  0.00          3A7
ATOM   2144  N   THR   310      18.187 -20.515  22.480  1.00  0.00          3A7
ATOM   2145  CA  THR   310      17.519 -20.567  23.760  1.00  0.00          3A7
ATOM   2146  CB  THR   310      18.271 -21.435  24.744  1.00  0.00          3A7
ATOM   2147  OG1 THR   310      18.739 -22.609  24.101  1.00  0.00          3A7
ATOM   2148  CG2 THR   310      17.383 -21.832  25.943  1.00  0.00          3A7
ATOM   2149  C   THR   310      17.233 -19.209  24.344  1.00  0.00          3A7
ATOM   2150  O   THR   310      16.168 -18.987  24.914  1.00  0.00          3A7
ATOM   2151  N   SER   311      18.147 -18.228  24.167  1.00  0.00          3A7
ATOM   2152  CA  SER   311      17.925 -16.885  24.659  1.00  0.00          3A7
ATOM   2153  CB  SER   311      19.171 -15.993  24.620  1.00  0.00          3A7
ATOM   2154  OG  SER   311      20.346 -16.710  24.906  1.00  0.00          3A7
ATOM   2155  C   SER   311      16.857 -16.191  23.854  1.00  0.00          3A7
ATOM   2156  O   SER   311      15.998 -15.515  24.407  1.00  0.00          3A7
ATOM   2157  N   SER   312      16.848 -16.368  22.505  1.00  0.00          3A7
ATOM   2158  CA  SER   312      15.858 -15.769  21.625  1.00  0.00          3A7
ATOM   2159  CB  SER   312      16.203 -15.894  20.128  1.00  0.00          3A7
ATOM   2160  OG  SER   312      16.398 -17.244  19.751  1.00  0.00          3A7
ATOM   2161  C   SER   312      14.473 -16.334  21.903  1.00  0.00          3A7
ATOM   2162  O   SER   312      13.477 -15.641  21.718  1.00  0.00          3A7
ATOM   2163  N   VAL   313      14.376 -17.602  22.376  1.00  0.00          3A7
ATOM   2164  CA  VAL   313      13.115 -18.232  22.678  1.00  0.00          3A7
ATOM   2165  CB  VAL   313      13.262 -19.732  22.736  1.00  0.00          3A7
ATOM   2166  CG1 VAL   313      12.003 -20.440  23.260  1.00  0.00          3A7
ATOM   2167  CG2 VAL   313      13.426 -20.126  21.263  1.00  0.00          3A7
ATOM   2168  C   VAL   313      12.555 -17.712  23.971  1.00  0.00          3A7
ATOM   2169  O   VAL   313      11.368 -17.425  24.059  1.00  0.00          3A7
ATOM   2170  N   LEU   314      13.406 -17.522  25.000  1.00  0.00          3A7
ATOM   2171  CA  LEU   314      13.003 -16.991  26.283  1.00  0.00          3A7
ATOM   2172  CB  LEU   314      14.178 -17.030  27.279  1.00  0.00          3A7
ATOM   2173  CG  LEU   314      14.712 -18.444  27.608  1.00  0.00          3A7
ATOM   2174  CD1 LEU   314      16.160 -18.400  28.135  1.00  0.00          3A7
ATOM   2175  CD2 LEU   314      13.817 -19.188  28.604  1.00  0.00          3A7
ATOM   2176  C   LEU   314      12.519 -15.573  26.181  1.00  0.00          3A7
ATOM   2177  O   LEU   314      11.490 -15.204  26.736  1.00  0.00          3A7
ATOM   2178  N   SER   315      13.252 -14.741  25.411  1.00  0.00          3A7
ATOM   2179  CA  SER   315      12.914 -13.355  25.165  1.00  0.00          3A7
ATOM   2180  CB  SER   315      14.033 -12.603  24.406  1.00  0.00          3A7
ATOM   2181  OG  SER   315      15.234 -12.612  25.166  1.00  0.00          3A7
ATOM   2182  C   SER   315      11.625 -13.209  24.374  1.00  0.00          3A7
ATOM   2183  O   SER   315      10.814 -12.336  24.676  1.00  0.00          3A7
ATOM   2184  N   PHE   316      11.391 -14.075  23.358  1.00  0.00          3A7
ATOM   2185  CA  PHE   316      10.164 -14.069  22.587  1.00  0.00          3A7
ATOM   2186  CB  PHE   316      10.264 -14.913  21.289  1.00  0.00          3A7
ATOM   2187  CG  PHE   316      10.697 -14.085  20.108  1.00  0.00          3A7
ATOM   2188  CD1 PHE   316      11.810 -14.439  19.342  1.00  0.00          3A7
```

ATOM	2189	CD2	PHE	316	9.933	-12.985	19.709	1.00	0.00	3A7
ATOM	2190	CE1	PHE	316	12.165	-13.699	18.217	1.00	0.00	3A7
ATOM	2191	CE2	PHE	316	10.281	-12.246	18.582	1.00	0.00	3A7
ATOM	2192	CZ	PHE	316	11.402	-12.600	17.837	1.00	0.00	3A7
ATOM	2193	C	PHE	316	9.015	-14.618	23.406	1.00	0.00	3A7
ATOM	2194	O	PHE	316	7.891	-14.133	23.296	1.00	0.00	3A7
ATOM	2195	N	ILE	317	9.257	-15.617	24.306	1.00	0.00	3A7
ATOM	2196	CA	ILE	317	8.200	-16.171	25.144	1.00	0.00	3A7
ATOM	2197	CB	ILE	317	8.522	-17.418	26.022	1.00	0.00	3A7
ATOM	2198	CG2	ILE	317	7.716	-17.454	27.357	1.00	0.00	3A7
ATOM	2199	CG1	ILE	317	8.150	-18.749	25.331	1.00	0.00	3A7
ATOM	2200	CD	ILE	317	9.210	-19.340	24.419	1.00	0.00	3A7
ATOM	2201	C	ILE	317	7.672	-15.117	26.091	1.00	0.00	3A7
ATOM	2202	O	ILE	317	6.464	-14.997	26.274	1.00	0.00	3A7
ATOM	2203	N	ILE	318	8.566	-14.313	26.715	1.00	0.00	3A7
ATOM	2204	CA	ILE	318	8.192	-13.252	27.635	1.00	0.00	3A7
ATOM	2205	CB	ILE	318	9.425	-12.624	28.274	1.00	0.00	3A7
ATOM	2206	CG2	ILE	318	9.076	-11.357	29.092	1.00	0.00	3A7
ATOM	2207	CG1	ILE	318	10.087	-13.689	29.181	1.00	0.00	3A7
ATOM	2208	CD	ILE	318	11.481	-13.295	29.665	1.00	0.00	3A7
ATOM	2209	C	ILE	318	7.339	-12.213	26.942	1.00	0.00	3A7
ATOM	2210	O	ILE	318	6.296	-11.802	27.441	1.00	0.00	3A7
ATOM	2211	N	TYR	319	7.731	-11.823	25.716	1.00	0.00	3A7
ATOM	2212	CA	TYR	319	6.987	-10.893	24.906	1.00	0.00	3A7
ATOM	2213	CB	TYR	319	7.729	-10.658	23.571	1.00	0.00	3A7
ATOM	2214	CG	TYR	319	6.940	-9.879	22.557	1.00	0.00	3A7
ATOM	2215	CD1	TYR	319	6.414	-8.628	22.863	1.00	0.00	3A7
ATOM	2216	CD2	TYR	319	6.693	-10.438	21.301	1.00	0.00	3A7
ATOM	2217	CE1	TYR	319	5.597	-7.976	21.949	1.00	0.00	3A7
ATOM	2218	CE2	TYR	319	5.898	-9.773	20.375	1.00	0.00	3A7
ATOM	2219	CZ	TYR	319	5.336	-8.544	20.704	1.00	0.00	3A7
ATOM	2220	OH	TYR	319	4.491	-7.887	19.783	1.00	0.00	3A7
ATOM	2221	C	TYR	319	5.568	-11.359	24.631	1.00	0.00	3A7
ATOM	2222	O	TYR	319	4.622	-10.588	24.752	1.00	0.00	3A7
ATOM	2223	N	GLU	320	5.404	-12.651	24.277	1.00	0.00	3A7
ATOM	2224	CA	GLU	320	4.118	-13.205	23.952	1.00	0.00	3A7
ATOM	2225	CB	GLU	320	4.190	-14.545	23.220	1.00	0.00	3A7
ATOM	2226	CG	GLU	320	4.824	-14.416	21.829	1.00	0.00	3A7
ATOM	2227	CD	GLU	320	3.795	-13.768	20.915	1.00	0.00	3A7
ATOM	2228	OE1	GLU	320	4.068	-12.634	20.435	1.00	0.00	3A7
ATOM	2229	OE2	GLU	320	2.723	-14.384	20.681	1.00	0.00	3A7
ATOM	2230	C	GLU	320	3.209	-13.345	25.140	1.00	0.00	3A7
ATOM	2231	O	GLU	320	2.018	-13.087	25.041	1.00	0.00	3A7
ATOM	2232	N	LEU	321	3.746	-13.705	26.321	1.00	0.00	3A7
ATOM	2233	CA	LEU	321	2.972	-13.799	27.537	1.00	0.00	3A7
ATOM	2234	CB	LEU	321	3.805	-14.427	28.662	1.00	0.00	3A7
ATOM	2235	CG	LEU	321	4.011	-15.941	28.472	1.00	0.00	3A7
ATOM	2236	CD1	LEU	321	5.072	-16.456	29.453	1.00	0.00	3A7
ATOM	2237	CD2	LEU	321	2.687	-16.706	28.641	1.00	0.00	3A7
ATOM	2238	C	LEU	321	2.505	-12.447	28.007	1.00	0.00	3A7
ATOM	2239	O	LEU	321	1.395	-12.302	28.509	1.00	0.00	3A7
ATOM	2240	N	ALA	322	3.360	-11.421	27.837	1.00	0.00	3A7
ATOM	2241	CA	ALA	322	3.065	-10.068	28.220	1.00	0.00	3A7
ATOM	2242	CB	ALA	322	4.351	-9.229	28.225	1.00	0.00	3A7
ATOM	2243	C	ALA	322	2.044	-9.469	27.279	1.00	0.00	3A7
ATOM	2244	O	ALA	322	1.166	-8.702	27.668	1.00	0.00	3A7
ATOM	2245	N	THR	323	2.110	-9.863	25.996	1.00	0.00	3A7
ATOM	2246	CA	THR	323	1.174	-9.402	25.006	1.00	0.00	3A7
ATOM	2247	CB	THR	323	1.714	-9.509	23.612	1.00	0.00	3A7
ATOM	2248	OG1	THR	323	2.224	-10.786	23.282	1.00	0.00	3A7
ATOM	2249	CG2	THR	323	2.782	-8.417	23.418	1.00	0.00	3A7
ATOM	2250	C	THR	323	-0.164	-10.105	25.063	1.00	0.00	3A7
ATOM	2251	O	THR	323	-1.132	-9.627	24.486	1.00	0.00	3A7
ATOM	2252	N	HIS	324	-0.258	-11.241	25.774	1.00	0.00	3A7
ATOM	2253	CA	HIS	324	-1.475	-12.018	25.882	1.00	0.00	3A7
ATOM	2254	ND1	HIS	324	-2.250	-12.554	22.767	1.00	0.00	3A7
ATOM	2255	CG	HIS	324	-1.279	-13.139	23.576	1.00	0.00	3A7
ATOM	2256	CB	HIS	324	-1.248	-13.311	25.087	1.00	0.00	3A7
ATOM	2257	NE2	HIS	324	-0.359	-12.447	21.617	1.00	0.00	3A7
ATOM	2258	CD2	HIS	324	-0.126	-13.016	22.856	1.00	0.00	3A7
ATOM	2259	CE1	HIS	324	-1.648	-12.187	21.610	1.00	0.00	3A7
ATOM	2260	C	HIS	324	-1.699	-12.327	27.334	1.00	0.00	3A7

```
ATOM   2261  O   HIS   324      -1.410 -13.448  27.764  1.00  0.00          3A7
ATOM   2262  N   PRO   325      -2.246 -11.398  28.139  1.00  0.00          3A7
ATOM   2263  CA  PRO   325      -2.362 -11.530  29.587  1.00  0.00          3A7
ATOM   2264  CD  PRO   325      -2.664 -10.073  27.697  1.00  0.00          3A7
ATOM   2265  CB  PRO   325      -3.005 -10.217  30.049  1.00  0.00          3A7
ATOM   2266  CG  PRO   325      -2.634  -9.212  28.959  1.00  0.00          3A7
ATOM   2267  C   PRO   325      -3.219 -12.703  30.001  1.00  0.00          3A7
ATOM   2268  O   PRO   325      -2.994 -13.255  31.072  1.00  0.00          3A7
ATOM   2269  N   ASP   326      -4.183 -13.144  29.162  1.00  0.00          3A7
ATOM   2270  CA  ASP   326      -5.016 -14.290  29.448  1.00  0.00          3A7
ATOM   2271  CB  ASP   326      -6.108 -14.480  28.372  1.00  0.00          3A7
ATOM   2272  CG  ASP   326      -7.091 -13.305  28.363  1.00  0.00          3A7
ATOM   2273  OD1 ASP   326      -7.016 -12.435  29.271  1.00  0.00          3A7
ATOM   2274  OD2 ASP   326      -7.946 -13.276  27.437  1.00  0.00          3A7
ATOM   2275  C   ASP   326      -4.191 -15.557  29.518  1.00  0.00          3A7
ATOM   2276  O   ASP   326      -4.391 -16.408  30.379  1.00  0.00          3A7
ATOM   2277  N   VAL   327      -3.192 -15.680  28.617  1.00  0.00          3A7
ATOM   2278  CA  VAL   327      -2.308 -16.822  28.551  1.00  0.00          3A7
ATOM   2279  CB  VAL   327      -1.522 -16.855  27.249  1.00  0.00          3A7
ATOM   2280  CG1 VAL   327      -0.634 -18.114  27.189  1.00  0.00          3A7
ATOM   2281  CG2 VAL   327      -2.526 -16.830  26.078  1.00  0.00          3A7
ATOM   2282  C   VAL   327      -1.357 -16.811  29.718  1.00  0.00          3A7
ATOM   2283  O   VAL   327      -1.126 -17.833  30.353  1.00  0.00          3A7
ATOM   2284  N   GLN   328      -0.822 -15.622  30.057  1.00  0.00          3A7
ATOM   2285  CA  GLN   328       0.054 -15.440  31.190  1.00  0.00          3A7
ATOM   2286  CB  GLN   328       0.551 -13.994  31.280  1.00  0.00          3A7
ATOM   2287  CG  GLN   328       1.927 -13.874  31.956  1.00  0.00          3A7
ATOM   2288  CD  GLN   328       2.430 -12.432  31.850  1.00  0.00          3A7
ATOM   2289  OE1 GLN   328       1.677 -11.512  31.507  1.00  0.00          3A7
ATOM   2290  NE2 GLN   328       3.749 -12.247  32.162  1.00  0.00          3A7
ATOM   2291  C   GLN   328      -0.565 -15.809  32.500  1.00  0.00          3A7
ATOM   2292  O   GLN   328       0.057 -16.448  33.339  1.00  0.00          3A7
ATOM   2293  N   GLN   329      -1.847 -15.438  32.692  1.00  0.00          3A7
ATOM   2294  CA  GLN   329      -2.599 -15.749  33.879  1.00  0.00          3A7
ATOM   2295  CB  GLN   329      -3.961 -15.032  33.870  1.00  0.00          3A7
ATOM   2296  CG  GLN   329      -3.832 -13.525  34.148  1.00  0.00          3A7
ATOM   2297  CD  GLN   329      -5.215 -12.882  34.023  1.00  0.00          3A7
ATOM   2298  OE1 GLN   329      -6.121 -13.175  34.813  1.00  0.00          3A7
ATOM   2299  NE2 GLN   329      -5.369 -11.987  33.000  1.00  0.00          3A7
ATOM   2300  C   GLN   329      -2.821 -17.226  34.022  1.00  0.00          3A7
ATOM   2301  O   GLN   329      -2.653 -17.780  35.102  1.00  0.00          3A7
ATOM   2302  N   LYS   330      -3.153 -17.913  32.907  1.00  0.00          3A7
ATOM   2303  CA  LYS   330      -3.370 -19.343  32.883  1.00  0.00          3A7
ATOM   2304  CB  LYS   330      -3.917 -19.754  31.503  1.00  0.00          3A7
ATOM   2305  CG  LYS   330      -4.508 -21.169  31.446  1.00  0.00          3A7
ATOM   2306  CD  LYS   330      -5.246 -21.428  30.124  1.00  0.00          3A7
ATOM   2307  CE  LYS   330      -5.927 -22.799  30.054  1.00  0.00          3A7
ATOM   2308  NZ  LYS   330      -6.952 -22.943  31.113  1.00  0.00          3A7
ATOM   2309  C   LYS   330      -2.097 -20.090  33.241  1.00  0.00          3A7
ATOM   2310  O   LYS   330      -2.090 -21.027  34.040  1.00  0.00          3A7
ATOM   2311  N   VAL   331      -0.946 -19.618  32.704  1.00  0.00          3A7
ATOM   2312  CA  VAL   331       0.363 -20.189  32.957  1.00  0.00          3A7
ATOM   2313  CB  VAL   331       1.419 -19.605  32.030  1.00  0.00          3A7
ATOM   2314  CG1 VAL   331       2.843 -20.076  32.382  1.00  0.00          3A7
ATOM   2315  CG2 VAL   331       1.080 -20.072  30.601  1.00  0.00          3A7
ATOM   2316  C   VAL   331       0.782 -19.992  34.390  1.00  0.00          3A7
ATOM   2317  O   VAL   331       1.274 -20.919  35.023  1.00  0.00          3A7
ATOM   2318  N   GLN   332       0.561 -18.783  34.951  1.00  0.00          3A7
ATOM   2319  CA  GLN   332       0.896 -18.455  36.319  1.00  0.00          3A7
ATOM   2320  CB  GLN   332       0.668 -16.968  36.628  1.00  0.00          3A7
ATOM   2321  CG  GLN   332       1.756 -16.072  36.011  1.00  0.00          3A7
ATOM   2322  CD  GLN   332       1.457 -14.601  36.311  1.00  0.00          3A7
ATOM   2323  OE1 GLN   332       2.196 -13.947  37.057  1.00  0.00          3A7
ATOM   2324  NE2 GLN   332       0.350 -14.079  35.701  1.00  0.00          3A7
ATOM   2325  C   GLN   332       0.082 -19.234  37.311  1.00  0.00          3A7
ATOM   2326  O   GLN   332       0.592 -19.634  38.351  1.00  0.00          3A7
ATOM   2327  N   LYS   333      -1.200 -19.512  36.991  1.00  0.00          3A7
ATOM   2328  CA  LYS   333      -2.087 -20.320  37.797  1.00  0.00          3A7
ATOM   2329  CB  LYS   333      -3.508 -20.312  37.204  1.00  0.00          3A7
ATOM   2330  CG  LYS   333      -4.571 -21.052  38.035  1.00  0.00          3A7
ATOM   2331  CD  LYS   333      -5.986 -20.945  37.441  1.00  0.00          3A7
ATOM   2332  CE  LYS   333      -6.125 -21.617  36.068  1.00  0.00          3A7
```

```
ATOM   2333  NZ  LYS   333      -7.518 -21.516  35.576  1.00  0.00          3A7
ATOM   2334  C   LYS   333      -1.600 -21.746  37.882  1.00  0.00          3A7
ATOM   2335  O   LYS   333      -1.547 -22.344  38.954  1.00  0.00          3A7
ATOM   2336  N   GLU   334      -1.171 -22.295  36.728  1.00  0.00          3A7
ATOM   2337  CA  GLU   334      -0.533 -23.579  36.649  1.00  0.00          3A7
ATOM   2338  CB  GLU   334      -0.149 -23.952  35.224  1.00  0.00          3A7
ATOM   2339  CG  GLU   334      -0.038 -25.481  35.122  1.00  0.00          3A7
ATOM   2340  CD  GLU   334       0.087 -25.922  33.672  1.00  0.00          3A7
ATOM   2341  OE1 GLU   334      -0.736 -26.779  33.251  1.00  0.00          3A7
ATOM   2342  OE2 GLU   334       1.007 -25.424  32.971  1.00  0.00          3A7
ATOM   2343  C   GLU   334       0.701 -23.722  37.472  1.00  0.00          3A7
ATOM   2344  O   GLU   334       0.825 -24.667  38.236  1.00  0.00          3A7
ATOM   2345  N   ILE   335       1.627 -22.744  37.370  1.00  0.00          3A7
ATOM   2346  CA  ILE   335       2.874 -22.692  38.098  1.00  0.00          3A7
ATOM   2347  CB  ILE   335       3.672 -21.474  37.679  1.00  0.00          3A7
ATOM   2348  CG2 ILE   335       4.884 -21.230  38.599  1.00  0.00          3A7
ATOM   2349  CG1 ILE   335       4.128 -21.660  36.215  1.00  0.00          3A7
ATOM   2350  CD  ILE   335       4.634 -20.360  35.597  1.00  0.00          3A7
ATOM   2351  C   ILE   335       2.643 -22.684  39.587  1.00  0.00          3A7
ATOM   2352  O   ILE   335       3.219 -23.480  40.320  1.00  0.00          3A7
ATOM   2353  N   ASP   336       1.727 -21.822  40.071  1.00  0.00          3A7
ATOM   2354  CA  ASP   336       1.416 -21.706  41.476  1.00  0.00          3A7
ATOM   2355  CB  ASP   336       0.411 -20.565  41.750  1.00  0.00          3A7
ATOM   2356  CG  ASP   336       1.021 -19.199  41.420  1.00  0.00          3A7
ATOM   2357  OD1 ASP   336       2.243 -19.127  41.123  1.00  0.00          3A7
ATOM   2358  OD2 ASP   336       0.255 -18.199  41.470  1.00  0.00          3A7
ATOM   2359  C   ASP   336       0.838 -22.996  42.010  1.00  0.00          3A7
ATOM   2360  O   ASP   336       1.183 -23.420  43.106  1.00  0.00          3A7
ATOM   2361  N   THR   337      -0.022 -23.674  41.213  1.00  0.00          3A7
ATOM   2362  CA  THR   337      -0.701 -24.903  41.571  1.00  0.00          3A7
ATOM   2363  CB  THR   337      -1.854 -25.156  40.609  1.00  0.00          3A7
ATOM   2364  OG1 THR   337      -2.791 -24.092  40.721  1.00  0.00          3A7
ATOM   2365  CG2 THR   337      -2.601 -26.473  40.896  1.00  0.00          3A7
ATOM   2366  C   THR   337       0.216 -26.114  41.595  1.00  0.00          3A7
ATOM   2367  O   THR   337       0.055 -27.000  42.433  1.00  0.00          3A7
ATOM   2368  N   VAL   338       1.202 -26.189  40.667  1.00  0.00          3A7
ATOM   2369  CA  VAL   338       2.055 -27.349  40.503  1.00  0.00          3A7
ATOM   2370  CB  VAL   338       2.466 -27.564  39.051  1.00  0.00          3A7
ATOM   2371  CG1 VAL   338       3.403 -28.783  38.900  1.00  0.00          3A7
ATOM   2372  CG2 VAL   338       1.182 -27.789  38.226  1.00  0.00          3A7
ATOM   2373  C   VAL   338       3.261 -27.232  41.404  1.00  0.00          3A7
ATOM   2374  O   VAL   338       3.589 -28.178  42.113  1.00  0.00          3A7
ATOM   2375  N   LEU   339       3.950 -26.065  41.421  1.00  0.00          3A7
ATOM   2376  CA  LEU   339       5.053 -25.835  42.331  1.00  0.00          3A7
ATOM   2377  CB  LEU   339       6.213 -25.014  41.736  1.00  0.00          3A7
ATOM   2378  CG  LEU   339       7.082 -25.819  40.766  1.00  0.00          3A7
ATOM   2379  CD1 LEU   339       8.159 -24.904  40.176  1.00  0.00          3A7
ATOM   2380  CD2 LEU   339       7.715 -27.051  41.439  1.00  0.00          3A7
ATOM   2381  C   LEU   339       4.552 -25.038  43.521  1.00  0.00          3A7
ATOM   2382  O   LEU   339       4.197 -23.878  43.325  1.00  0.00          3A7
ATOM   2383  N   PRO   340       4.486 -25.565  44.752  1.00  0.00          3A7
ATOM   2384  CA  PRO   340       3.973 -24.851  45.907  1.00  0.00          3A7
ATOM   2385  CD  PRO   340       4.660 -26.986  45.025  1.00  0.00          3A7
ATOM   2386  CB  PRO   340       3.483 -25.968  46.840  1.00  0.00          3A7
ATOM   2387  CG  PRO   340       4.398 -27.154  46.523  1.00  0.00          3A7
ATOM   2388  C   PRO   340       5.084 -24.042  46.550  1.00  0.00          3A7
ATOM   2389  O   PRO   340       6.241 -24.463  46.512  1.00  0.00          3A7
ATOM   2390  N   ASN   341       4.716 -22.893  47.182  1.00  0.00          3A7
ATOM   2391  CA  ASN   341       5.537 -22.073  48.065  1.00  0.00          3A7
ATOM   2392  CB  ASN   341       6.167 -22.872  49.244  1.00  0.00          3A7
ATOM   2393  CG  ASN   341       5.072 -23.614  50.023  1.00  0.00          3A7
ATOM   2394  OD1 ASN   341       5.051 -24.850  50.059  1.00  0.00          3A7
ATOM   2395  ND2 ASN   341       4.155 -22.826  50.663  1.00  0.00          3A7
ATOM   2396  C   ASN   341       6.625 -21.330  47.312  1.00  0.00          3A7
ATOM   2397  O   ASN   341       6.423 -20.897  46.178  1.00  0.00          3A7
ATOM   2398  N   LYS   342       7.813 -21.175  47.953  1.00  0.00          3A7
ATOM   2399  CA  LYS   342       8.980 -20.529  47.396  1.00  0.00          3A7
ATOM   2400  CB  LYS   342       9.578 -19.456  48.339  1.00  0.00          3A7
ATOM   2401  CG  LYS   342       8.601 -18.309  48.647  1.00  0.00          3A7
ATOM   2402  CD  LYS   342       9.210 -17.205  49.527  1.00  0.00          3A7
ATOM   2403  CE  LYS   342       9.570 -17.674  50.944  1.00  0.00          3A7
ATOM   2404  NZ  LYS   342      10.133 -16.560  51.741  1.00  0.00          3A7
```

```
ATOM   2405  C   LYS   342      10.016 -21.594  47.146  1.00  0.00          3A7
ATOM   2406  O   LYS   342      11.181 -21.442  47.515  1.00  0.00          3A7
ATOM   2407  N   ALA   343       9.595 -22.711  46.501  1.00  0.00          3A7
ATOM   2408  CA  ALA   343      10.434 -23.839  46.171  1.00  0.00          3A7
ATOM   2409  CB  ALA   343       9.750 -25.189  46.468  1.00  0.00          3A7
ATOM   2410  C   ALA   343      10.737 -23.763  44.700  1.00  0.00          3A7
ATOM   2411  O   ALA   343       9.824 -23.520  43.911  1.00  0.00          3A7
ATOM   2412  N   PRO   344      11.980 -24.000  44.274  1.00  0.00          3A7
ATOM   2413  CA  PRO   344      12.353 -24.110  42.875  1.00  0.00          3A7
ATOM   2414  CD  PRO   344      13.149 -23.771  45.118  1.00  0.00          3A7
ATOM   2415  CB  PRO   344      13.894 -24.072  42.880  1.00  0.00          3A7
ATOM   2416  CG  PRO   344      14.248 -23.318  44.160  1.00  0.00          3A7
ATOM   2417  C   PRO   344      11.838 -25.414  42.274  1.00  0.00          3A7
ATOM   2418  O   PRO   344      11.420 -26.289  43.033  1.00  0.00          3A7
ATOM   2419  N   PRO   345      11.880 -25.589  40.953  1.00  0.00          3A7
ATOM   2420  CA  PRO   345      11.325 -26.737  40.270  1.00  0.00          3A7
ATOM   2421  CD  PRO   345      12.098 -24.479  40.043  1.00  0.00          3A7
ATOM   2422  CB  PRO   345      11.402 -26.382  38.778  1.00  0.00          3A7
ATOM   2423  CG  PRO   345      11.412 -24.857  38.731  1.00  0.00          3A7
ATOM   2424  C   PRO   345      12.117 -27.996  40.521  1.00  0.00          3A7
ATOM   2425  O   PRO   345      13.329 -27.934  40.723  1.00  0.00          3A7
ATOM   2426  N   THR   346      11.432 -29.156  40.428  1.00  0.00          3A7
ATOM   2427  CA  THR   346      12.073 -30.434  40.286  1.00  0.00          3A7
ATOM   2428  CB  THR   346      11.485 -31.522  41.180  1.00  0.00          3A7
ATOM   2429  OG1 THR   346      10.071 -31.633  41.047  1.00  0.00          3A7
ATOM   2430  CG2 THR   346      11.830 -31.183  42.644  1.00  0.00          3A7
ATOM   2431  C   THR   346      11.920 -30.751  38.827  1.00  0.00          3A7
ATOM   2432  O   THR   346      11.346 -29.983  38.054  1.00  0.00          3A7
ATOM   2433  N   TYR   347      12.422 -31.922  38.405  1.00  0.00          3A7
ATOM   2434  CA  TYR   347      12.345 -32.298  37.022  1.00  0.00          3A7
ATOM   2435  CB  TYR   347      13.345 -33.383  36.599  1.00  0.00          3A7
ATOM   2436  CG  TYR   347      13.830 -34.221  37.758  1.00  0.00          3A7
ATOM   2437  CD1 TYR   347      13.226 -35.455  38.007  1.00  0.00          3A7
ATOM   2438  CD2 TYR   347      14.880 -33.809  38.584  1.00  0.00          3A7
ATOM   2439  CE1 TYR   347      13.653 -36.258  39.060  1.00  0.00          3A7
ATOM   2440  CE2 TYR   347      15.310 -34.609  39.638  1.00  0.00          3A7
ATOM   2441  CZ  TYR   347      14.697 -35.835  39.877  1.00  0.00          3A7
ATOM   2442  OH  TYR   347      15.133 -36.649  40.945  1.00  0.00          3A7
ATOM   2443  C   TYR   347      10.986 -32.842  36.741  1.00  0.00          3A7
ATOM   2444  O   TYR   347      10.471 -32.653  35.655  1.00  0.00          3A7
ATOM   2445  N   ASP   348      10.354 -33.487  37.746  1.00  0.00          3A7
ATOM   2446  CA  ASP   348       9.033 -34.072  37.677  1.00  0.00          3A7
ATOM   2447  CB  ASP   348       8.708 -34.785  38.996  1.00  0.00          3A7
ATOM   2448  CG  ASP   348       9.678 -35.950  39.163  1.00  0.00          3A7
ATOM   2449  OD1 ASP   348       9.665 -36.846  38.277  1.00  0.00          3A7
ATOM   2450  OD2 ASP   348      10.439 -35.959  40.167  1.00  0.00          3A7
ATOM   2451  C   ASP   348       7.939 -33.064  37.424  1.00  0.00          3A7
ATOM   2452  O   ASP   348       6.884 -33.393  36.890  1.00  0.00          3A7
ATOM   2453  N   THR   349       8.224 -31.784  37.764  1.00  0.00          3A7
ATOM   2454  CA  THR   349       7.414 -30.615  37.512  1.00  0.00          3A7
ATOM   2455  CB  THR   349       8.047 -29.394  38.153  1.00  0.00          3A7
ATOM   2456  OG1 THR   349       8.345 -29.682  39.512  1.00  0.00          3A7
ATOM   2457  CG2 THR   349       7.118 -28.168  38.103  1.00  0.00          3A7
ATOM   2458  C   THR   349       7.246 -30.355  36.030  1.00  0.00          3A7
ATOM   2459  O   THR   349       6.224 -29.855  35.582  1.00  0.00          3A7
ATOM   2460  N   VAL   350       8.243 -30.735  35.203  1.00  0.00          3A7
ATOM   2461  CA  VAL   350       8.261 -30.585  33.760  1.00  0.00          3A7
ATOM   2462  CB  VAL   350       9.589 -31.111  33.245  1.00  0.00          3A7
ATOM   2463  CG1 VAL   350       9.700 -31.257  31.710  1.00  0.00          3A7
ATOM   2464  CG2 VAL   350      10.704 -30.188  33.784  1.00  0.00          3A7
ATOM   2465  C   VAL   350       7.128 -31.305  33.054  1.00  0.00          3A7
ATOM   2466  O   VAL   350       6.691 -30.900  31.980  1.00  0.00          3A7
ATOM   2467  N   LEU   351       6.619 -32.397  33.667  1.00  0.00          3A7
ATOM   2468  CA  LEU   351       5.583 -33.220  33.098  1.00  0.00          3A7
ATOM   2469  CB  LEU   351       5.689 -34.682  33.599  1.00  0.00          3A7
ATOM   2470  CG  LEU   351       7.076 -35.324  33.359  1.00  0.00          3A7
ATOM   2471  CD1 LEU   351       7.162 -36.712  34.024  1.00  0.00          3A7
ATOM   2472  CD2 LEU   351       7.441 -35.402  31.865  1.00  0.00          3A7
ATOM   2473  C   LEU   351       4.203 -32.710  33.432  1.00  0.00          3A7
ATOM   2474  O   LEU   351       3.248 -32.996  32.716  1.00  0.00          3A7
ATOM   2475  N   GLN   352       4.059 -31.949  34.546  1.00  0.00          3A7
ATOM   2476  CA  GLN   352       2.775 -31.491  35.037  1.00  0.00          3A7
```

ATOM	2477	CB	GLN	352	2.625	-31.677	36.565	1.00	0.00	3A7
ATOM	2478	CG	GLN	352	2.109	-33.072	36.977	1.00	0.00	3A7
ATOM	2479	CD	GLN	352	3.125	-34.176	36.678	1.00	0.00	3A7
ATOM	2480	OE1	GLN	352	2.971	-34.938	35.716	1.00	0.00	3A7
ATOM	2481	NE2	GLN	352	4.173	-34.268	37.551	1.00	0.00	3A7
ATOM	2482	C	GLN	352	2.540	-30.043	34.711	1.00	0.00	3A7
ATOM	2483	O	GLN	352	1.702	-29.394	35.333	1.00	0.00	3A7
ATOM	2484	N	LEU	353	3.254	-29.494	33.712	1.00	0.00	3A7
ATOM	2485	CA	LEU	353	3.130	-28.104	33.338	1.00	0.00	3A7
ATOM	2486	CB	LEU	353	4.489	-27.396	33.371	1.00	0.00	3A7
ATOM	2487	CG	LEU	353	4.991	-27.076	34.789	1.00	0.00	3A7
ATOM	2488	CD1	LEU	353	6.496	-26.787	34.712	1.00	0.00	3A7
ATOM	2489	CD2	LEU	353	4.215	-25.911	35.433	1.00	0.00	3A7
ATOM	2490	C	LEU	353	2.588	-28.000	31.951	1.00	0.00	3A7
ATOM	2491	O	LEU	353	3.198	-27.396	31.071	1.00	0.00	3A7
ATOM	2492	N	GLU	354	1.380	-28.556	31.747	1.00	0.00	3A7
ATOM	2493	CA	GLU	354	0.702	-28.679	30.481	1.00	0.00	3A7
ATOM	2494	CB	GLU	354	-0.697	-29.284	30.692	1.00	0.00	3A7
ATOM	2495	CG	GLU	354	-0.745	-30.790	31.013	1.00	0.00	3A7
ATOM	2496	CD	GLU	354	-0.273	-31.081	32.431	1.00	0.00	3A7
ATOM	2497	OE1	GLU	354	0.614	-31.962	32.579	1.00	0.00	3A7
ATOM	2498	OE2	GLU	354	-0.801	-30.446	33.382	1.00	0.00	3A7
ATOM	2499	C	GLU	354	0.533	-27.384	29.710	1.00	0.00	3A7
ATOM	2500	O	GLU	354	0.869	-27.315	28.531	1.00	0.00	3A7
ATOM	2501	N	TYR	355	0.017	-26.319	30.358	1.00	0.00	3A7
ATOM	2502	CA	TYR	355	-0.255	-25.056	29.708	1.00	0.00	3A7
ATOM	2503	CB	TYR	355	-1.107	-24.126	30.584	1.00	0.00	3A7
ATOM	2504	CG	TYR	355	-2.413	-24.797	30.922	1.00	0.00	3A7
ATOM	2505	CD1	TYR	355	-2.853	-24.843	32.245	1.00	0.00	3A7
ATOM	2506	CD2	TYR	355	-3.183	-25.427	29.938	1.00	0.00	3A7
ATOM	2507	CE1	TYR	355	-4.029	-25.504	32.585	1.00	0.00	3A7
ATOM	2508	CE2	TYR	355	-4.354	-26.101	30.275	1.00	0.00	3A7
ATOM	2509	CZ	TYR	355	-4.779	-26.138	31.599	1.00	0.00	3A7
ATOM	2510	OH	TYR	355	-5.972	-26.813	31.940	1.00	0.00	3A7
ATOM	2511	C	TYR	355	1.014	-24.314	29.358	1.00	0.00	3A7
ATOM	2512	O	TYR	355	1.093	-23.672	28.320	1.00	0.00	3A7
ATOM	2513	N	LEU	356	2.069	-24.432	30.194	1.00	0.00	3A7
ATOM	2514	CA	LEU	356	3.372	-23.853	29.929	1.00	0.00	3A7
ATOM	2515	CB	LEU	356	4.307	-24.000	31.136	1.00	0.00	3A7
ATOM	2516	CG	LEU	356	5.331	-22.859	31.211	1.00	0.00	3A7
ATOM	2517	CD1	LEU	356	5.499	-22.429	32.674	1.00	0.00	3A7
ATOM	2518	CD2	LEU	356	6.699	-23.187	30.588	1.00	0.00	3A7
ATOM	2519	C	LEU	356	4.082	-24.430	28.735	1.00	0.00	3A7
ATOM	2520	O	LEU	356	4.610	-23.709	27.891	1.00	0.00	3A7
ATOM	2521	N	ASP	357	4.076	-25.778	28.619	1.00	0.00	3A7
ATOM	2522	CA	ASP	357	4.652	-26.516	27.513	1.00	0.00	3A7
ATOM	2523	CB	ASP	357	4.362	-28.050	27.598	1.00	0.00	3A7
ATOM	2524	CG	ASP	357	5.259	-28.771	28.597	1.00	0.00	3A7
ATOM	2525	OD1	ASP	357	5.958	-29.726	28.159	1.00	0.00	3A7
ATOM	2526	OD2	ASP	357	5.258	-28.397	29.796	1.00	0.00	3A7
ATOM	2527	C	ASP	357	4.055	-26.136	26.182	1.00	0.00	3A7
ATOM	2528	O	ASP	357	4.748	-25.985	25.183	1.00	0.00	3A7
ATOM	2529	N	MET	358	2.719	-25.956	26.163	1.00	0.00	3A7
ATOM	2530	CA	MET	358	1.969	-25.573	24.997	1.00	0.00	3A7
ATOM	2531	CB	MET	358	0.466	-25.711	25.263	1.00	0.00	3A7
ATOM	2532	CG	MET	358	0.027	-27.178	25.430	1.00	0.00	3A7
ATOM	2533	SD	MET	358	-1.535	-27.420	26.341	1.00	0.00	3A7
ATOM	2534	CE	MET	358	-2.631	-26.461	25.262	1.00	0.00	3A7
ATOM	2535	C	MET	358	2.269	-24.149	24.601	1.00	0.00	3A7
ATOM	2536	O	MET	358	2.344	-23.825	23.421	1.00	0.00	3A7
ATOM	2537	N	VAL	359	2.505	-23.255	25.594	1.00	0.00	3A7
ATOM	2538	CA	VAL	359	2.885	-21.869	25.376	1.00	0.00	3A7
ATOM	2539	CB	VAL	359	2.885	-21.083	26.684	1.00	0.00	3A7
ATOM	2540	CG1	VAL	359	3.710	-19.776	26.626	1.00	0.00	3A7
ATOM	2541	CG2	VAL	359	1.412	-20.783	27.005	1.00	0.00	3A7
ATOM	2542	C	VAL	359	4.233	-21.791	24.701	1.00	0.00	3A7
ATOM	2543	O	VAL	359	4.408	-21.063	23.725	1.00	0.00	3A7
ATOM	2544	N	VAL	360	5.224	-22.575	25.182	1.00	0.00	3A7
ATOM	2545	CA	VAL	360	6.556	-22.600	24.616	1.00	0.00	3A7
ATOM	2546	CB	VAL	360	7.506	-23.421	25.479	1.00	0.00	3A7
ATOM	2547	CG1	VAL	360	8.897	-23.573	24.831	1.00	0.00	3A7
ATOM	2548	CG2	VAL	360	7.633	-22.713	26.844	1.00	0.00	3A7

ATOM	2549	C	VAL	360	6.520	-23.153	23.207	1.00	0.00	3A7
ATOM	2550	O	VAL	360	7.168	-22.609	22.323	1.00	0.00	3A7
ATOM	2551	N	ASN	361	5.711	-24.208	22.949	1.00	0.00	3A7
ATOM	2552	CA	ASN	361	5.556	-24.789	21.630	1.00	0.00	3A7
ATOM	2553	CB	ASN	361	4.650	-26.030	21.669	1.00	0.00	3A7
ATOM	2554	CG	ASN	361	5.417	-27.219	22.258	1.00	0.00	3A7
ATOM	2555	OD1	ASN	361	6.641	-27.329	22.121	1.00	0.00	3A7
ATOM	2556	ND2	ASN	361	4.654	-28.135	22.930	1.00	0.00	3A7
ATOM	2557	C	ASN	361	4.952	-23.808	20.655	1.00	0.00	3A7
ATOM	2558	O	ASN	361	5.410	-23.694	19.523	1.00	0.00	3A7
ATOM	2559	N	GLU	362	3.925	-23.044	21.087	1.00	0.00	3A7
ATOM	2560	CA	GLU	362	3.338	-21.994	20.287	1.00	0.00	3A7
ATOM	2561	CB	GLU	362	2.013	-21.499	20.896	1.00	0.00	3A7
ATOM	2562	CG	GLU	362	1.224	-20.515	20.011	1.00	0.00	3A7
ATOM	2563	CD	GLU	362	0.583	-21.183	18.798	1.00	0.00	3A7
ATOM	2564	OE1	GLU	362	0.987	-22.314	18.429	1.00	0.00	3A7
ATOM	2565	OE2	GLU	362	-0.309	-20.534	18.190	1.00	0.00	3A7
ATOM	2566	C	GLU	362	4.241	-20.837	20.000	1.00	0.00	3A7
ATOM	2567	O	GLU	362	4.205	-20.266	18.913	1.00	0.00	3A7
ATOM	2568	N	THR	363	5.135	-20.478	20.946	1.00	0.00	3A7
ATOM	2569	CA	THR	363	6.090	-19.416	20.720	1.00	0.00	3A7
ATOM	2570	CB	THR	363	6.793	-19.002	21.991	1.00	0.00	3A7
ATOM	2571	OG1	THR	363	5.804	-18.623	22.938	1.00	0.00	3A7
ATOM	2572	CG2	THR	363	7.691	-17.778	21.706	1.00	0.00	3A7
ATOM	2573	C	THR	363	7.091	-19.831	19.666	1.00	0.00	3A7
ATOM	2574	O	THR	363	7.464	-19.042	18.805	1.00	0.00	3A7
ATOM	2575	N	LEU	364	7.504	-21.115	19.676	1.00	0.00	3A7
ATOM	2576	CA	LEU	364	8.417	-21.641	18.695	1.00	0.00	3A7
ATOM	2577	CB	LEU	364	8.957	-23.014	19.086	1.00	0.00	3A7
ATOM	2578	CG	LEU	364	9.921	-23.018	20.283	1.00	0.00	3A7
ATOM	2579	CD1	LEU	364	10.242	-24.462	20.696	1.00	0.00	3A7
ATOM	2580	CD2	LEU	364	11.219	-22.259	19.974	1.00	0.00	3A7
ATOM	2581	C	LEU	364	7.769	-21.746	17.338	1.00	0.00	3A7
ATOM	2582	O	LEU	364	8.410	-21.492	16.324	1.00	0.00	3A7
ATOM	2583	N	ARG	365	6.467	-22.094	17.264	1.00	0.00	3A7
ATOM	2584	CA	ARG	365	5.743	-22.109	16.003	1.00	0.00	3A7
ATOM	2585	CB	ARG	365	4.300	-22.612	16.169	1.00	0.00	3A7
ATOM	2586	CG	ARG	365	3.614	-22.980	14.858	1.00	0.00	3A7
ATOM	2587	CD	ARG	365	2.117	-23.285	15.005	1.00	0.00	3A7
ATOM	2588	NE	ARG	365	1.371	-21.987	15.068	1.00	0.00	3A7
ATOM	2589	CZ	ARG	365	0.011	-21.942	15.201	1.00	0.00	3A7
ATOM	2590	NH1	ARG	365	-0.637	-20.742	15.124	1.00	0.00	3A7
ATOM	2591	NH2	ARG	365	-0.703	-23.084	15.418	1.00	0.00	3A7
ATOM	2592	C	ARG	365	5.648	-20.756	15.371	1.00	0.00	3A7
ATOM	2593	O	ARG	365	5.941	-20.573	14.192	1.00	0.00	3A7
ATOM	2594	N	LEU	366	5.239	-19.760	16.176	1.00	0.00	3A7
ATOM	2595	CA	LEU	366	5.030	-18.410	15.729	1.00	0.00	3A7
ATOM	2596	CB	LEU	366	4.204	-17.608	16.752	1.00	0.00	3A7
ATOM	2597	CG	LEU	366	3.017	-16.833	16.122	1.00	0.00	3A7
ATOM	2598	CD1	LEU	366	2.029	-16.361	17.201	1.00	0.00	3A7
ATOM	2599	CD2	LEU	366	3.452	-15.648	15.240	1.00	0.00	3A7
ATOM	2600	C	LEU	366	6.295	-17.670	15.380	1.00	0.00	3A7
ATOM	2601	O	LEU	366	6.339	-16.992	14.359	1.00	0.00	3A7
ATOM	2602	N	PHE	367	7.367	-17.798	16.193	1.00	0.00	3A7
ATOM	2603	CA	PHE	367	8.619	-17.136	15.897	1.00	0.00	3A7
ATOM	2604	CB	PHE	367	8.999	-16.072	16.907	1.00	0.00	3A7
ATOM	2605	CG	PHE	367	7.886	-15.081	17.042	1.00	0.00	3A7
ATOM	2606	CD1	PHE	367	6.921	-15.250	18.035	1.00	0.00	3A7
ATOM	2607	CD2	PHE	367	7.781	-13.998	16.170	1.00	0.00	3A7
ATOM	2608	CE1	PHE	367	5.855	-14.365	18.137	1.00	0.00	3A7
ATOM	2609	CE2	PHE	367	6.723	-13.100	16.285	1.00	0.00	3A7
ATOM	2610	CZ	PHE	367	5.757	-13.284	17.269	1.00	0.00	3A7
ATOM	2611	C	PHE	367	9.740	-18.121	15.878	1.00	0.00	3A7
ATOM	2612	O	PHE	367	10.525	-18.207	16.823	1.00	0.00	3A7
ATOM	2613	N	PRO	368	9.897	-18.877	14.814	1.00	0.00	3A7
ATOM	2614	CA	PRO	368	10.926	-19.868	14.730	1.00	0.00	3A7
ATOM	2615	CD	PRO	368	8.891	-19.039	13.788	1.00	0.00	3A7
ATOM	2616	CB	PRO	368	10.570	-20.710	13.544	1.00	0.00	3A7
ATOM	2617	CG	PRO	368	9.531	-19.942	12.757	1.00	0.00	3A7
ATOM	2618	C	PRO	368	12.257	-19.200	14.589	1.00	0.00	3A7
ATOM	2619	O	PRO	368	12.479	-18.434	13.657	1.00	0.00	3A7
ATOM	2620	N	VAL	369	13.143	-19.481	15.561	1.00	0.00	3A7

ATOM	2621	CA	VAL	369	14.427	-18.858	15.709	1.00	0.00	3A7
ATOM	2622	CB	VAL	369	15.058	-19.329	16.991	1.00	0.00	3A7
ATOM	2623	CG1	VAL	369	16.449	-18.705	17.115	1.00	0.00	3A7
ATOM	2624	CG2	VAL	369	14.135	-18.876	18.133	1.00	0.00	3A7
ATOM	2625	C	VAL	369	15.330	-19.141	14.529	1.00	0.00	3A7
ATOM	2626	O	VAL	369	16.105	-18.284	14.109	1.00	0.00	3A7
ATOM	2627	N	ALA	370	15.232	-20.349	13.946	1.00	0.00	3A7
ATOM	2628	CA	ALA	370	15.984	-20.686	12.775	1.00	0.00	3A7
ATOM	2629	CB	ALA	370	16.677	-22.035	12.966	1.00	0.00	3A7
ATOM	2630	C	ALA	370	15.038	-20.739	11.619	1.00	0.00	3A7
ATOM	2631	O	ALA	370	14.503	-21.792	11.309	1.00	0.00	3A7
ATOM	2632	N	MET	371	14.813	-19.597	10.938	1.00	0.00	3A7
ATOM	2633	CA	MET	371	13.787	-19.436	9.924	1.00	0.00	3A7
ATOM	2634	CB	MET	371	13.599	-17.940	9.616	1.00	0.00	3A7
ATOM	2635	CG	MET	371	14.852	-17.053	9.800	1.00	0.00	3A7
ATOM	2636	SD	MET	371	16.175	-17.276	8.566	1.00	0.00	3A7
ATOM	2637	CE	MET	371	15.303	-16.484	7.182	1.00	0.00	3A7
ATOM	2638	C	MET	371	14.093	-20.142	8.625	1.00	0.00	3A7
ATOM	2639	O	MET	371	13.208	-20.260	7.783	1.00	0.00	3A7
ATOM	2640	N	ARG	372	15.346	-20.621	8.432	1.00	0.00	3A7
ATOM	2641	CA	ARG	372	15.716	-21.368	7.254	1.00	0.00	3A7
ATOM	2642	CB	ARG	372	16.208	-20.480	6.088	1.00	0.00	3A7
ATOM	2643	CG	ARG	372	15.140	-19.769	5.248	1.00	0.00	3A7
ATOM	2644	CD	ARG	372	15.828	-19.020	4.096	1.00	0.00	3A7
ATOM	2645	NE	ARG	372	14.871	-18.673	2.996	1.00	0.00	3A7
ATOM	2646	CZ	ARG	372	14.486	-19.599	2.066	1.00	0.00	3A7
ATOM	2647	NH1	ARG	372	13.971	-19.194	0.870	1.00	0.00	3A7
ATOM	2648	NH2	ARG	372	14.646	-20.930	2.301	1.00	0.00	3A7
ATOM	2649	C	ARG	372	16.832	-22.309	7.639	1.00	0.00	3A7
ATOM	2650	O	ARG	372	17.619	-22.029	8.542	1.00	0.00	3A7
ATOM	2651	N	LEU	373	16.916	-23.453	6.907	1.00	0.00	3A7
ATOM	2652	CA	LEU	373	17.947	-24.462	7.034	1.00	0.00	3A7
ATOM	2653	CB	LEU	373	17.400	-25.879	7.360	1.00	0.00	3A7
ATOM	2654	CG	LEU	373	16.633	-26.016	8.700	1.00	0.00	3A7
ATOM	2655	CD1	LEU	373	17.347	-25.305	9.860	1.00	0.00	3A7
ATOM	2656	CD2	LEU	373	15.150	-25.605	8.611	1.00	0.00	3A7
ATOM	2657	C	LEU	373	18.641	-24.532	5.697	1.00	0.00	3A7
ATOM	2658	O	LEU	373	18.145	-23.979	4.717	1.00	0.00	3A7
ATOM	2659	N	GLU	374	19.806	-25.232	5.619	1.00	0.00	3A7
ATOM	2660	CA	GLU	374	20.496	-25.477	4.356	1.00	0.00	3A7
ATOM	2661	CB	GLU	374	21.788	-24.637	4.153	1.00	0.00	3A7
ATOM	2662	CG	GLU	374	21.575	-23.121	4.279	1.00	0.00	3A7
ATOM	2663	CD	GLU	374	22.909	-22.422	4.038	1.00	0.00	3A7
ATOM	2664	OE1	GLU	374	23.435	-21.801	5.000	1.00	0.00	3A7
ATOM	2665	OE2	GLU	374	23.420	-22.501	2.889	1.00	0.00	3A7
ATOM	2666	C	GLU	374	20.862	-26.936	4.222	1.00	0.00	3A7
ATOM	2667	O	GLU	374	21.393	-27.553	5.141	1.00	0.00	3A7
ATOM	2668	N	ARG	375	20.591	-27.510	3.026	1.00	0.00	3A7
ATOM	2669	CA	ARG	375	20.879	-28.878	2.666	1.00	0.00	3A7
ATOM	2670	CB	ARG	375	19.614	-29.770	2.636	1.00	0.00	3A7
ATOM	2671	CG	ARG	375	19.033	-30.018	4.037	1.00	0.00	3A7
ATOM	2672	CD	ARG	375	17.789	-30.919	4.035	1.00	0.00	3A7
ATOM	2673	NE	ARG	375	17.499	-31.381	5.436	1.00	0.00	3A7
ATOM	2674	CZ	ARG	375	16.930	-30.590	6.396	1.00	0.00	3A7
ATOM	2675	NH1	ARG	375	16.734	-31.096	7.650	1.00	0.00	3A7
ATOM	2676	NH2	ARG	375	16.558	-29.307	6.125	1.00	0.00	3A7
ATOM	2677	C	ARG	375	21.494	-28.826	1.293	1.00	0.00	3A7
ATOM	2678	O	ARG	375	21.347	-27.846	0.569	1.00	0.00	3A7
ATOM	2679	N	VAL	376	22.225	-29.890	0.889	1.00	0.00	3A7
ATOM	2680	CA	VAL	376	22.836	-29.949	-0.420	1.00	0.00	3A7
ATOM	2681	CB	VAL	376	24.347	-29.725	-0.397	1.00	0.00	3A7
ATOM	2682	CG1	VAL	376	24.936	-29.796	-1.822	1.00	0.00	3A7
ATOM	2683	CG2	VAL	376	24.638	-28.346	0.234	1.00	0.00	3A7
ATOM	2684	C	VAL	376	22.508	-31.316	-0.934	1.00	0.00	3A7
ATOM	2685	O	VAL	376	22.653	-32.316	-0.233	1.00	0.00	3A7
ATOM	2686	N	CYS	377	22.071	-31.397	-2.212	1.00	0.00	3A7
ATOM	2687	CA	CYS	377	21.721	-32.642	-2.851	1.00	0.00	3A7
ATOM	2688	CB	CYS	377	20.821	-32.435	-4.083	1.00	0.00	3A7
ATOM	2689	SG	CYS	377	19.174	-31.876	-3.569	1.00	0.00	3A7
ATOM	2690	C	CYS	377	22.964	-33.392	-3.254	1.00	0.00	3A7
ATOM	2691	O	CYS	377	23.919	-32.843	-3.794	1.00	0.00	3A7
ATOM	2692	N	LYS	378	22.964	-34.705	-2.955	1.00	0.00	3A7

ATOM	2693	CA	LYS	378	24.083	-35.594	-3.143	1.00	0.00	3A7
ATOM	2694	CB	LYS	378	24.073	-36.718	-2.075	1.00	0.00	3A7
ATOM	2695	CG	LYS	378	23.127	-36.428	-0.894	1.00	0.00	3A7
ATOM	2696	CD	LYS	378	23.024	-37.592	0.101	1.00	0.00	3A7
ATOM	2697	CE	LYS	378	21.948	-37.375	1.174	1.00	0.00	3A7
ATOM	2698	NZ	LYS	378	22.223	-36.159	1.974	1.00	0.00	3A7
ATOM	2699	C	LYS	378	24.040	-36.202	-4.524	1.00	0.00	3A7
ATOM	2700	O	LYS	378	25.062	-36.609	-5.075	1.00	0.00	3A7
ATOM	2701	N	LYS	379	22.814	-36.285	-5.081	1.00	0.00	3A7
ATOM	2702	CA	LYS	379	22.547	-36.939	-6.329	1.00	0.00	3A7
ATOM	2703	CB	LYS	379	22.121	-38.417	-6.127	1.00	0.00	3A7
ATOM	2704	CG	LYS	379	20.935	-38.609	-5.161	1.00	0.00	3A7
ATOM	2705	CD	LYS	379	20.582	-40.083	-4.899	1.00	0.00	3A7
ATOM	2706	CE	LYS	379	21.665	-40.842	-4.120	1.00	0.00	3A7
ATOM	2707	NZ	LYS	379	21.236	-42.233	-3.850	1.00	0.00	3A7
ATOM	2708	C	LYS	379	21.450	-36.155	-6.981	1.00	0.00	3A7
ATOM	2709	O	LYS	379	21.014	-35.119	-6.483	1.00	0.00	3A7
ATOM	2710	N	ASP	380	20.951	-36.650	-8.134	1.00	0.00	3A7
ATOM	2711	CA	ASP	380	19.820	-36.071	-8.818	1.00	0.00	3A7
ATOM	2712	CB	ASP	380	19.811	-36.404	-10.323	1.00	0.00	3A7
ATOM	2713	CG	ASP	380	21.092	-35.921	-10.999	1.00	0.00	3A7
ATOM	2714	OD1	ASP	380	21.347	-34.689	-10.981	1.00	0.00	3A7
ATOM	2715	OD2	ASP	380	21.824	-36.782	-11.556	1.00	0.00	3A7
ATOM	2716	C	ASP	380	18.562	-36.616	-8.182	1.00	0.00	3A7
ATOM	2717	O	ASP	380	18.496	-37.798	-7.848	1.00	0.00	3A7
ATOM	2718	N	VAL	381	17.554	-35.744	-7.966	1.00	0.00	3A7
ATOM	2719	CA	VAL	381	16.378	-36.118	-7.224	1.00	0.00	3A7
ATOM	2720	CB	VAL	381	16.557	-35.910	-5.720	1.00	0.00	3A7
ATOM	2721	CG1	VAL	381	16.853	-34.439	-5.360	1.00	0.00	3A7
ATOM	2722	CG2	VAL	381	15.353	-36.489	-4.947	1.00	0.00	3A7
ATOM	2723	C	VAL	381	15.248	-35.308	-7.781	1.00	0.00	3A7
ATOM	2724	O	VAL	381	15.417	-34.151	-8.142	1.00	0.00	3A7
ATOM	2725	N	GLU	382	14.045	-35.908	-7.874	1.00	0.00	3A7
ATOM	2726	CA	GLU	382	12.888	-35.247	-8.420	1.00	0.00	3A7
ATOM	2727	CB	GLU	382	12.165	-36.100	-9.485	1.00	0.00	3A7
ATOM	2728	CG	GLU	382	12.963	-36.325	-10.781	1.00	0.00	3A7
ATOM	2729	CD	GLU	382	14.109	-37.311	-10.571	1.00	0.00	3A7
ATOM	2730	OE1	GLU	382	13.827	-38.470	-10.163	1.00	0.00	3A7
ATOM	2731	OE2	GLU	382	15.281	-36.921	-10.822	1.00	0.00	3A7
ATOM	2732	C	GLU	382	11.952	-34.980	-7.271	1.00	0.00	3A7
ATOM	2733	O	GLU	382	11.531	-35.909	-6.587	1.00	0.00	3A7
ATOM	2734	N	ILE	383	11.615	-33.690	-7.028	1.00	0.00	3A7
ATOM	2735	CA	ILE	383	10.762	-33.270	-5.937	1.00	0.00	3A7
ATOM	2736	CB	ILE	383	11.449	-32.299	-4.973	1.00	0.00	3A7
ATOM	2737	CG2	ILE	383	10.543	-32.043	-3.747	1.00	0.00	3A7
ATOM	2738	CG1	ILE	383	12.865	-32.774	-4.555	1.00	0.00	3A7
ATOM	2739	CD	ILE	383	12.883	-34.026	-3.677	1.00	0.00	3A7
ATOM	2740	C	ILE	383	9.578	-32.594	-6.567	1.00	0.00	3A7
ATOM	2741	O	ILE	383	9.686	-31.493	-7.103	1.00	0.00	3A7
ATOM	2742	N	ASN	384	8.399	-33.254	-6.521	1.00	0.00	3A7
ATOM	2743	CA	ASN	384	7.130	-32.719	-6.976	1.00	0.00	3A7
ATOM	2744	CB	ASN	384	6.732	-31.411	-6.222	1.00	0.00	3A7
ATOM	2745	CG	ASN	384	5.218	-31.147	-6.283	1.00	0.00	3A7
ATOM	2746	OD1	ASN	384	4.758	-30.251	-7.000	1.00	0.00	3A7
ATOM	2747	ND2	ASN	384	4.443	-31.956	-5.498	1.00	0.00	3A7
ATOM	2748	C	ASN	384	7.100	-32.504	-8.480	1.00	0.00	3A7
ATOM	2749	O	ASN	384	6.410	-31.623	-8.988	1.00	0.00	3A7
ATOM	2750	N	GLY	385	7.870	-33.322	-9.231	1.00	0.00	3A7
ATOM	2751	CA	GLY	385	7.911	-33.246	-10.666	1.00	0.00	3A7
ATOM	2752	C	GLY	385	9.013	-32.342	-11.156	1.00	0.00	3A7
ATOM	2753	O	GLY	385	9.217	-32.266	-12.366	1.00	0.00	3A7
ATOM	2754	N	MET	386	9.762	-31.631	-10.264	1.00	0.00	3A7
ATOM	2755	CA	MET	386	10.855	-30.773	-10.695	1.00	0.00	3A7
ATOM	2756	CB	MET	386	10.660	-29.264	-10.426	1.00	0.00	3A7
ATOM	2757	CG	MET	386	10.337	-28.845	-8.990	1.00	0.00	3A7
ATOM	2758	SD	MET	386	9.854	-27.091	-8.895	1.00	0.00	3A7
ATOM	2759	CE	MET	386	11.448	-26.373	-9.388	1.00	0.00	3A7
ATOM	2760	C	MET	386	12.159	-31.305	-10.187	1.00	0.00	3A7
ATOM	2761	O	MET	386	12.335	-31.654	-9.025	1.00	0.00	3A7
ATOM	2762	N	PHE	387	13.122	-31.396	-11.125	1.00	0.00	3A7
ATOM	2763	CA	PHE	387	14.382	-32.074	-10.982	1.00	0.00	3A7
ATOM	2764	CB	PHE	387	14.935	-32.474	-12.378	1.00	0.00	3A7

ATOM	2765	CG	PHE	387	14.102	-33.505	-13.091	1.00	0.00	3A7
ATOM	2766	CD1	PHE	387	14.645	-34.767	-13.344	1.00	0.00	3A7
ATOM	2767	CD2	PHE	387	12.827	-33.213	-13.585	1.00	0.00	3A7
ATOM	2768	CE1	PHE	387	13.920	-35.727	-14.045	1.00	0.00	3A7
ATOM	2769	CE2	PHE	387	12.097	-34.173	-14.280	1.00	0.00	3A7
ATOM	2770	CZ	PHE	387	12.642	-35.433	-14.507	1.00	0.00	3A7
ATOM	2771	C	PHE	387	15.405	-31.180	-10.312	1.00	0.00	3A7
ATOM	2772	O	PHE	387	15.631	-30.043	-10.726	1.00	0.00	3A7
ATOM	2773	N	ILE	388	16.066	-31.706	-9.251	1.00	0.00	3A7
ATOM	2774	CA	ILE	388	17.145	-31.049	-8.544	1.00	0.00	3A7
ATOM	2775	CB	ILE	388	16.994	-31.071	-7.032	1.00	0.00	3A7
ATOM	2776	CG2	ILE	388	18.144	-30.276	-6.387	1.00	0.00	3A7
ATOM	2777	CG1	ILE	388	15.641	-30.487	-6.591	1.00	0.00	3A7
ATOM	2778	CD	ILE	388	15.434	-29.010	-6.913	1.00	0.00	3A7
ATOM	2779	C	ILE	388	18.438	-31.746	-8.935	1.00	0.00	3A7
ATOM	2780	O	ILE	388	18.576	-32.952	-8.728	1.00	0.00	3A7
ATOM	2781	N	PRO	389	19.415	-31.021	-9.496	1.00	0.00	3A7
ATOM	2782	CA	PRO	389	20.698	-31.581	-9.867	1.00	0.00	3A7
ATOM	2783	CD	PRO	389	19.063	-29.901	-10.375	1.00	0.00	3A7
ATOM	2784	CB	PRO	389	21.290	-30.549	-10.822	1.00	0.00	3A7
ATOM	2785	CG	PRO	389	20.081	-29.931	-11.509	1.00	0.00	3A7
ATOM	2786	C	PRO	389	21.614	-31.785	-8.684	1.00	0.00	3A7
ATOM	2787	O	PRO	389	21.474	-31.121	-7.659	1.00	0.00	3A7
ATOM	2788	N	LYS	390	22.627	-32.663	-8.836	1.00	0.00	3A7
ATOM	2789	CA	LYS	390	23.654	-32.884	-7.847	1.00	0.00	3A7
ATOM	2790	CB	LYS	390	24.733	-33.851	-8.363	1.00	0.00	3A7
ATOM	2791	CG	LYS	390	24.234	-35.053	-9.176	1.00	0.00	3A7
ATOM	2792	CD	LYS	390	25.372	-36.029	-9.517	1.00	0.00	3A7
ATOM	2793	CE	LYS	390	24.921	-37.258	-10.316	1.00	0.00	3A7
ATOM	2794	NZ	LYS	390	23.959	-38.073	-9.538	1.00	0.00	3A7
ATOM	2795	C	LYS	390	24.346	-31.584	-7.486	1.00	0.00	3A7
ATOM	2796	O	LYS	390	24.631	-30.776	-8.366	1.00	0.00	3A7
ATOM	2797	N	GLY	391	24.558	-31.329	-6.177	1.00	0.00	3A7
ATOM	2798	CA	GLY	391	25.250	-30.153	-5.707	1.00	0.00	3A7
ATOM	2799	C	GLY	391	24.397	-28.926	-5.567	1.00	0.00	3A7
ATOM	2800	O	GLY	391	24.924	-27.848	-5.320	1.00	0.00	3A7
ATOM	2801	N	VAL	392	23.052	-29.029	-5.690	1.00	0.00	3A7
ATOM	2802	CA	VAL	392	22.159	-27.896	-5.522	1.00	0.00	3A7
ATOM	2803	CB	VAL	392	20.829	-28.126	-6.224	1.00	0.00	3A7
ATOM	2804	CG1	VAL	392	19.765	-27.062	-5.883	1.00	0.00	3A7
ATOM	2805	CG2	VAL	392	21.074	-28.134	-7.744	1.00	0.00	3A7
ATOM	2806	C	VAL	392	21.922	-27.684	-4.050	1.00	0.00	3A7
ATOM	2807	O	VAL	392	21.849	-28.644	-3.290	1.00	0.00	3A7
ATOM	2808	N	VAL	393	21.787	-26.403	-3.629	1.00	0.00	3A7
ATOM	2809	CA	VAL	393	21.491	-26.024	-2.268	1.00	0.00	3A7
ATOM	2810	CB	VAL	393	22.118	-24.695	-1.900	1.00	0.00	3A7
ATOM	2811	CG1	VAL	393	21.828	-24.336	-0.425	1.00	0.00	3A7
ATOM	2812	CG2	VAL	393	23.636	-24.785	-2.160	1.00	0.00	3A7
ATOM	2813	C	VAL	393	19.992	-25.964	-2.130	1.00	0.00	3A7
ATOM	2814	O	VAL	393	19.308	-25.288	-2.891	1.00	0.00	3A7
ATOM	2815	N	VAL	394	19.457	-26.712	-1.145	1.00	0.00	3A7
ATOM	2816	CA	VAL	394	18.049	-26.825	-0.864	1.00	0.00	3A7
ATOM	2817	CB	VAL	394	17.609	-28.282	-0.810	1.00	0.00	3A7
ATOM	2818	CG1	VAL	394	16.104	-28.411	-0.510	1.00	0.00	3A7
ATOM	2819	CG2	VAL	394	17.948	-28.936	-2.163	1.00	0.00	3A7
ATOM	2820	C	VAL	394	17.840	-26.177	0.471	1.00	0.00	3A7
ATOM	2821	O	VAL	394	18.601	-26.423	1.400	1.00	0.00	3A7
ATOM	2822	N	MET	395	16.800	-25.325	0.609	1.00	0.00	3A7
ATOM	2823	CA	MET	395	16.529	-24.656	1.856	1.00	0.00	3A7
ATOM	2824	CB	MET	395	16.818	-23.145	1.809	1.00	0.00	3A7
ATOM	2825	CG	MET	395	18.304	-22.812	1.578	1.00	0.00	3A7
ATOM	2826	SD	MET	395	18.747	-21.101	2.015	1.00	0.00	3A7
ATOM	2827	CE	MET	395	17.770	-20.277	0.725	1.00	0.00	3A7
ATOM	2828	C	MET	395	15.093	-24.885	2.216	1.00	0.00	3A7
ATOM	2829	O	MET	395	14.195	-24.925	1.389	1.00	0.00	3A7
ATOM	2830	N	ILE	396	14.842	-25.076	3.515	1.00	0.00	3A7
ATOM	2831	CA	ILE	396	13.536	-25.356	4.059	1.00	0.00	3A7
ATOM	2832	CB	ILE	396	13.599	-26.610	4.904	1.00	0.00	3A7
ATOM	2833	CG2	ILE	396	12.490	-26.667	5.983	1.00	0.00	3A7
ATOM	2834	CG1	ILE	396	13.729	-27.897	4.057	1.00	0.00	3A7
ATOM	2835	CD	ILE	396	15.087	-28.104	3.373	1.00	0.00	3A7
ATOM	2836	C	ILE	396	13.188	-24.182	4.902	1.00	0.00	3A7

ATOM	2837	O	ILE	396	13.874	-23.964	5.894	1.00	0.00	3A7
ATOM	2838	N	PRO	397	12.167	-23.398	4.590	1.00	0.00	3A7
ATOM	2839	CA	PRO	397	11.790	-22.297	5.462	1.00	0.00	3A7
ATOM	2840	CD	PRO	397	11.961	-23.022	3.209	1.00	0.00	3A7
ATOM	2841	CB	PRO	397	11.201	-21.252	4.533	1.00	0.00	3A7
ATOM	2842	CG	PRO	397	10.809	-22.043	3.293	1.00	0.00	3A7
ATOM	2843	C	PRO	397	10.834	-22.717	6.544	1.00	0.00	3A7
ATOM	2844	O	PRO	397	9.629	-22.732	6.310	1.00	0.00	3A7
ATOM	2845	N	SER	398	11.352	-22.981	7.767	1.00	0.00	3A7
ATOM	2846	CA	SER	398	10.575	-23.392	8.914	1.00	0.00	3A7
ATOM	2847	CB	SER	398	11.471	-23.676	10.138	1.00	0.00	3A7
ATOM	2848	OG	SER	398	12.135	-22.517	10.613	1.00	0.00	3A7
ATOM	2849	C	SER	398	9.531	-22.379	9.316	1.00	0.00	3A7
ATOM	2850	O	SER	398	8.422	-22.745	9.668	1.00	0.00	3A7
ATOM	2851	N	TYR	399	9.838	-21.053	9.231	1.00	0.00	3A7
ATOM	2852	CA	TYR	399	8.913	-19.958	9.507	1.00	0.00	3A7
ATOM	2853	CB	TYR	399	9.578	-18.562	9.264	1.00	0.00	3A7
ATOM	2854	CG	TYR	399	9.084	-17.492	10.212	1.00	0.00	3A7
ATOM	2855	CD1	TYR	399	9.933	-16.936	11.172	1.00	0.00	3A7
ATOM	2856	CD2	TYR	399	7.775	-17.008	10.123	1.00	0.00	3A7
ATOM	2857	CE1	TYR	399	9.473	-15.959	12.051	1.00	0.00	3A7
ATOM	2858	CE2	TYR	399	7.308	-16.041	11.007	1.00	0.00	3A7
ATOM	2859	CZ	TYR	399	8.156	-15.520	11.975	1.00	0.00	3A7
ATOM	2860	OH	TYR	399	7.673	-14.553	12.880	1.00	0.00	3A7
ATOM	2861	C	TYR	399	7.688	-20.038	8.647	1.00	0.00	3A7
ATOM	2862	O	TYR	399	6.567	-19.765	9.067	1.00	0.00	3A7
ATOM	2863	N	VAL	400	7.911	-20.472	7.398	1.00	0.00	3A7
ATOM	2864	CA	VAL	400	6.877	-20.616	6.436	1.00	0.00	3A7
ATOM	2865	CB	VAL	400	7.444	-20.658	5.045	1.00	0.00	3A7
ATOM	2866	CG1	VAL	400	6.294	-20.758	4.020	1.00	0.00	3A7
ATOM	2867	CG2	VAL	400	8.183	-19.308	4.899	1.00	0.00	3A7
ATOM	2868	C	VAL	400	6.002	-21.827	6.653	1.00	0.00	3A7
ATOM	2869	O	VAL	400	4.781	-21.734	6.547	1.00	0.00	3A7
ATOM	2870	N	LEU	401	6.602	-22.992	6.970	1.00	0.00	3A7
ATOM	2871	CA	LEU	401	5.875	-24.224	7.175	1.00	0.00	3A7
ATOM	2872	CB	LEU	401	6.790	-25.449	7.318	1.00	0.00	3A7
ATOM	2873	CG	LEU	401	8.101	-25.453	6.535	1.00	0.00	3A7
ATOM	2874	CD1	LEU	401	8.877	-26.722	6.915	1.00	0.00	3A7
ATOM	2875	CD2	LEU	401	7.904	-25.294	5.023	1.00	0.00	3A7
ATOM	2876	C	LEU	401	5.031	-24.186	8.449	1.00	0.00	3A7
ATOM	2877	O	LEU	401	3.918	-24.705	8.504	1.00	0.00	3A7
ATOM	2878	N	HIS	402	5.545	-23.512	9.509	1.00	0.00	3A7
ATOM	2879	CA	HIS	402	4.879	-23.303	10.782	1.00	0.00	3A7
ATOM	2880	ND1	HIS	402	7.090	-24.809	12.042	1.00	0.00	3A7
ATOM	2881	CG	HIS	402	6.758	-23.553	12.480	1.00	0.00	3A7
ATOM	2882	CB	HIS	402	5.843	-22.628	11.778	1.00	0.00	3A7
ATOM	2883	NE2	HIS	402	8.734	-24.122	13.375	1.00	0.00	3A7
ATOM	2884	CD2	HIS	402	7.762	-23.155	13.305	1.00	0.00	3A7
ATOM	2885	CE1	HIS	402	8.289	-25.085	12.595	1.00	0.00	3A7
ATOM	2886	C	HIS	402	3.648	-22.420	10.674	1.00	0.00	3A7
ATOM	2887	O	HIS	402	2.844	-22.343	11.602	1.00	0.00	3A7
ATOM	2888	N	HIS	403	3.485	-21.730	9.522	1.00	0.00	3A7
ATOM	2889	CA	HIS	403	2.382	-20.839	9.280	1.00	0.00	3A7
ATOM	2890	ND1	HIS	403	4.537	-19.115	10.966	1.00	0.00	3A7
ATOM	2891	CG	HIS	403	3.389	-18.746	10.299	1.00	0.00	3A7
ATOM	2892	CB	HIS	403	2.858	-19.394	9.048	1.00	0.00	3A7
ATOM	2893	NE2	HIS	403	3.638	-17.451	12.131	1.00	0.00	3A7
ATOM	2894	CD2	HIS	403	2.852	-17.730	11.028	1.00	0.00	3A7
ATOM	2895	CE1	HIS	403	4.638	-18.308	12.051	1.00	0.00	3A7
ATOM	2896	C	HIS	403	1.564	-21.280	8.096	1.00	0.00	3A7
ATOM	2897	O	HIS	403	0.830	-20.492	7.500	1.00	0.00	3A7
ATOM	2898	N	ASP	404	1.605	-22.588	7.740	1.00	0.00	3A7
ATOM	2899	CA	ASP	404	0.811	-23.143	6.662	1.00	0.00	3A7
ATOM	2900	CB	ASP	404	1.274	-24.585	6.322	1.00	0.00	3A7
ATOM	2901	CG	ASP	404	0.584	-25.218	5.103	1.00	0.00	3A7
ATOM	2902	OD1	ASP	404	-0.209	-24.540	4.402	1.00	0.00	3A7
ATOM	2903	OD2	ASP	404	0.879	-26.417	4.850	1.00	0.00	3A7
ATOM	2904	C	ASP	404	-0.645	-23.164	7.105	1.00	0.00	3A7
ATOM	2905	O	ASP	404	-0.941	-23.809	8.108	1.00	0.00	3A7
ATOM	2906	N	PRO	405	-1.568	-22.474	6.421	1.00	0.00	3A7
ATOM	2907	CA	PRO	405	-2.958	-22.344	6.827	1.00	0.00	3A7
ATOM	2908	CD	PRO	405	-1.277	-21.674	5.237	1.00	0.00	3A7

ATOM	2909	CB	PRO	405	-3.543	-21.309	5.854	1.00	0.00	3A7
ATOM	2910	CG	PRO	405	-2.641	-21.373	4.621	1.00	0.00	3A7
ATOM	2911	C	PRO	405	-3.739	-23.646	6.756	1.00	0.00	3A7
ATOM	2912	O	PRO	405	-4.766	-23.734	7.420	1.00	0.00	3A7
ATOM	2913	N	LYS	406	-3.297	-24.674	5.989	1.00	0.00	3A7
ATOM	2914	CA	LYS	406	-3.983	-25.942	5.892	1.00	0.00	3A7
ATOM	2915	CB	LYS	406	-3.545	-26.748	4.646	1.00	0.00	3A7
ATOM	2916	CG	LYS	406	-3.805	-26.004	3.326	1.00	0.00	3A7
ATOM	2917	CD	LYS	406	-3.234	-26.692	2.072	1.00	0.00	3A7
ATOM	2918	CE	LYS	406	-3.939	-27.993	1.650	1.00	0.00	3A7
ATOM	2919	NZ	LYS	406	-3.601	-29.127	2.541	1.00	0.00	3A7
ATOM	2920	C	LYS	406	-3.730	-26.791	7.115	1.00	0.00	3A7
ATOM	2921	O	LYS	406	-4.554	-27.622	7.479	1.00	0.00	3A7
ATOM	2922	N	TYR	407	-2.572	-26.584	7.783	1.00	0.00	3A7
ATOM	2923	CA	TYR	407	-2.174	-27.340	8.948	1.00	0.00	3A7
ATOM	2924	CB	TYR	407	-0.677	-27.703	8.898	1.00	0.00	3A7
ATOM	2925	CG	TYR	407	-0.579	-28.906	8.000	1.00	0.00	3A7
ATOM	2926	CD1	TYR	407	-0.674	-28.783	6.613	1.00	0.00	3A7
ATOM	2927	CD2	TYR	407	-0.492	-30.184	8.557	1.00	0.00	3A7
ATOM	2928	CE1	TYR	407	-0.693	-29.912	5.799	1.00	0.00	3A7
ATOM	2929	CE2	TYR	407	-0.483	-31.314	7.746	1.00	0.00	3A7
ATOM	2930	CZ	TYR	407	-0.585	-31.179	6.365	1.00	0.00	3A7
ATOM	2931	OH	TYR	407	-0.583	-32.324	5.538	1.00	0.00	3A7
ATOM	2932	C	TYR	407	-2.474	-26.584	10.218	1.00	0.00	3A7
ATOM	2933	O	TYR	407	-2.827	-27.189	11.229	1.00	0.00	3A7
ATOM	2934	N	TRP	408	-2.334	-25.240	10.202	1.00	0.00	3A7
ATOM	2935	CA	TRP	408	-2.553	-24.414	11.368	1.00	0.00	3A7
ATOM	2936	CB	TRP	408	-1.243	-23.786	11.891	1.00	0.00	3A7
ATOM	2937	CG	TRP	408	-0.242	-24.837	12.291	1.00	0.00	3A7
ATOM	2938	CD2	TRP	408	-0.524	-25.818	13.304	1.00	0.00	3A7
ATOM	2939	CD1	TRP	408	1.005	-25.107	11.823	1.00	0.00	3A7
ATOM	2940	NE1	TRP	408	1.515	-26.195	12.482	1.00	0.00	3A7
ATOM	2941	CE2	TRP	408	0.574	-26.677	13.353	1.00	0.00	3A7
ATOM	2942	CE3	TRP	408	-1.619	-26.011	14.121	1.00	0.00	3A7
ATOM	2943	CZ2	TRP	408	0.578	-27.783	14.170	1.00	0.00	3A7
ATOM	2944	CZ3	TRP	408	-1.597	-27.102	14.983	1.00	0.00	3A7
ATOM	2945	CH2	TRP	408	-0.524	-27.989	14.995	1.00	0.00	3A7
ATOM	2946	C	TRP	408	-3.541	-23.347	10.974	1.00	0.00	3A7
ATOM	2947	O	TRP	408	-3.197	-22.324	10.383	1.00	0.00	3A7
ATOM	2948	N	THR	409	-4.838	-23.556	11.320	1.00	0.00	3A7
ATOM	2949	CA	THR	409	-5.897	-22.587	11.078	1.00	0.00	3A7
ATOM	2950	CB	THR	409	-7.275	-23.197	11.275	1.00	0.00	3A7
ATOM	2951	OG1	THR	409	-8.322	-22.316	10.873	1.00	0.00	3A7
ATOM	2952	CG2	THR	409	-7.503	-23.671	12.727	1.00	0.00	3A7
ATOM	2953	C	THR	409	-5.686	-21.354	11.951	1.00	0.00	3A7
ATOM	2954	O	THR	409	-5.295	-21.439	13.116	1.00	0.00	3A7
ATOM	2955	N	GLU	410	-5.888	-20.153	11.363	1.00	0.00	3A7
ATOM	2956	CA	GLU	410	-5.519	-18.880	11.957	1.00	0.00	3A7
ATOM	2957	CB	GLU	410	-6.432	-18.485	13.138	1.00	0.00	3A7
ATOM	2958	CG	GLU	410	-7.920	-18.447	12.751	1.00	0.00	3A7
ATOM	2959	CD	GLU	410	-8.744	-18.043	13.970	1.00	0.00	3A7
ATOM	2960	OE1	GLU	410	-8.705	-18.790	14.985	1.00	0.00	3A7
ATOM	2961	OE2	GLU	410	-9.423	-16.984	13.903	1.00	0.00	3A7
ATOM	2962	C	GLU	410	-4.059	-18.872	12.399	1.00	0.00	3A7
ATOM	2963	O	GLU	410	-3.756	-18.654	13.572	1.00	0.00	3A7
ATOM	2964	N	PRO	411	-3.140	-19.188	11.476	1.00	0.00	3A7
ATOM	2965	CA	PRO	411	-1.722	-19.438	11.747	1.00	0.00	3A7
ATOM	2966	CD	PRO	411	-3.394	-19.045	10.041	1.00	0.00	3A7
ATOM	2967	CB	PRO	411	-1.144	-19.794	10.370	1.00	0.00	3A7
ATOM	2968	CG	PRO	411	-2.020	-19.039	9.368	1.00	0.00	3A7
ATOM	2969	C	PRO	411	-1.022	-18.216	12.290	1.00	0.00	3A7
ATOM	2970	O	PRO	411	0.020	-18.335	12.931	1.00	0.00	3A7
ATOM	2971	N	GLU	412	-1.592	-17.019	12.058	1.00	0.00	3A7
ATOM	2972	CA	GLU	412	-1.018	-15.791	12.493	1.00	0.00	3A7
ATOM	2973	CB	GLU	412	-1.368	-14.650	11.516	1.00	0.00	3A7
ATOM	2974	CG	GLU	412	-0.914	-14.895	10.063	1.00	0.00	3A7
ATOM	2975	CD	GLU	412	0.609	-14.849	9.920	1.00	0.00	3A7
ATOM	2976	OE1	GLU	412	1.093	-15.190	8.807	1.00	0.00	3A7
ATOM	2977	OE2	GLU	412	1.306	-14.468	10.897	1.00	0.00	3A7
ATOM	2978	C	GLU	412	-1.450	-15.419	13.903	1.00	0.00	3A7
ATOM	2979	O	GLU	412	-1.079	-14.360	14.405	1.00	0.00	3A7
ATOM	2980	N	LYS	413	-2.226	-16.290	14.589	1.00	0.00	3A7

ATOM	2981	CA	LYS	413	-2.691	-16.035	15.932	1.00	0.00	3A7
ATOM	2982	CB	LYS	413	-4.204	-16.281	16.093	1.00	0.00	3A7
ATOM	2983	CG	LYS	413	-5.059	-15.300	15.276	1.00	0.00	3A7
ATOM	2984	CD	LYS	413	-6.569	-15.457	15.519	1.00	0.00	3A7
ATOM	2985	CE	LYS	413	-7.012	-15.075	16.938	1.00	0.00	3A7
ATOM	2986	NZ	LYS	413	-8.477	-15.230	17.084	1.00	0.00	3A7
ATOM	2987	C	LYS	413	-1.939	-16.896	16.917	1.00	0.00	3A7
ATOM	2988	O	LYS	413	-1.731	-18.089	16.718	1.00	0.00	3A7
ATOM	2989	N	PHE	414	-1.550	-16.288	18.059	1.00	0.00	3A7
ATOM	2990	CA	PHE	414	-0.981	-16.968	19.200	1.00	0.00	3A7
ATOM	2991	CB	PHE	414	-0.298	-15.950	20.125	1.00	0.00	3A7
ATOM	2992	CG	PHE	414	0.563	-16.580	21.179	1.00	0.00	3A7
ATOM	2993	CD1	PHE	414	1.763	-17.214	20.878	1.00	0.00	3A7
ATOM	2994	CD2	PHE	414	0.126	-16.541	22.505	1.00	0.00	3A7
ATOM	2995	CE1	PHE	414	2.507	-17.815	21.887	1.00	0.00	3A7
ATOM	2996	CE2	PHE	414	0.864	-17.148	23.513	1.00	0.00	3A7
ATOM	2997	CZ	PHE	414	2.048	-17.802	23.199	1.00	0.00	3A7
ATOM	2998	C	PHE	414	-2.045	-17.668	19.981	1.00	0.00	3A7
ATOM	2999	O	PHE	414	-2.819	-17.039	20.697	1.00	0.00	3A7
ATOM	3000	N	LEU	415	-2.093	-19.006	19.847	1.00	0.00	3A7
ATOM	3001	CA	LEU	415	-3.087	-19.816	20.488	1.00	0.00	3A7
ATOM	3002	CB	LEU	415	-4.201	-20.254	19.504	1.00	0.00	3A7
ATOM	3003	CG	LEU	415	-5.081	-19.105	18.954	1.00	0.00	3A7
ATOM	3004	CD1	LEU	415	-5.988	-19.603	17.812	1.00	0.00	3A7
ATOM	3005	CD2	LEU	415	-5.911	-18.424	20.058	1.00	0.00	3A7
ATOM	3006	C	LEU	415	-2.421	-21.064	20.998	1.00	0.00	3A7
ATOM	3007	O	LEU	415	-2.308	-22.038	20.252	1.00	0.00	3A7
ATOM	3008	N	PRO	416	-2.010	-21.141	22.271	1.00	0.00	3A7
ATOM	3009	CA	PRO	416	-1.339	-22.301	22.847	1.00	0.00	3A7
ATOM	3010	CD	PRO	416	-1.874	-19.967	23.122	1.00	0.00	3A7
ATOM	3011	CB	PRO	416	-1.071	-21.888	24.299	1.00	0.00	3A7
ATOM	3012	CG	PRO	416	-0.878	-20.375	24.207	1.00	0.00	3A7
ATOM	3013	C	PRO	416	-2.201	-23.547	22.780	1.00	0.00	3A7
ATOM	3014	O	PRO	416	-1.669	-24.651	22.766	1.00	0.00	3A7
ATOM	3015	N	GLU	417	-3.535	-23.381	22.682	1.00	0.00	3A7
ATOM	3016	CA	GLU	417	-4.480	-24.458	22.678	1.00	0.00	3A7
ATOM	3017	CB	GLU	417	-5.921	-23.933	22.878	1.00	0.00	3A7
ATOM	3018	CG	GLU	417	-6.072	-23.126	24.179	1.00	0.00	3A7
ATOM	3019	CD	GLU	417	-7.521	-22.672	24.323	1.00	0.00	3A7
ATOM	3020	OE1	GLU	417	-8.172	-23.077	25.322	1.00	0.00	3A7
ATOM	3021	OE2	GLU	417	-7.994	-21.911	23.436	1.00	0.00	3A7
ATOM	3022	C	GLU	417	-4.459	-25.295	21.427	1.00	0.00	3A7
ATOM	3023	O	GLU	417	-4.883	-26.446	21.478	1.00	0.00	3A7
ATOM	3024	N	ARG	418	-3.988	-24.733	20.282	1.00	0.00	3A7
ATOM	3025	CA	ARG	418	-4.140	-25.279	18.944	1.00	0.00	3A7
ATOM	3026	CB	ARG	418	-3.753	-24.206	17.890	1.00	0.00	3A7
ATOM	3027	CG	ARG	418	-4.118	-24.508	16.422	1.00	0.00	3A7
ATOM	3028	CD	ARG	418	-5.605	-24.343	16.069	1.00	0.00	3A7
ATOM	3029	NE	ARG	418	-6.397	-25.466	16.668	1.00	0.00	3A7
ATOM	3030	CZ	ARG	418	-7.765	-25.471	16.670	1.00	0.00	3A7
ATOM	3031	NH1	ARG	418	-8.433	-26.503	17.264	1.00	0.00	3A7
ATOM	3032	NH2	ARG	418	-8.465	-24.456	16.087	1.00	0.00	3A7
ATOM	3033	C	ARG	418	-3.324	-26.538	18.706	1.00	0.00	3A7
ATOM	3034	O	ARG	418	-2.209	-26.489	18.187	1.00	0.00	3A7
ATOM	3035	N	PHE	419	-3.919	-27.699	19.103	1.00	0.00	3A7
ATOM	3036	CA	PHE	419	-3.457	-29.076	18.984	1.00	0.00	3A7
ATOM	3037	CB	PHE	419	-3.390	-29.565	17.516	1.00	0.00	3A7
ATOM	3038	CG	PHE	419	-4.772	-29.517	16.915	1.00	0.00	3A7
ATOM	3039	CD1	PHE	419	-5.049	-28.723	15.799	1.00	0.00	3A7
ATOM	3040	CD2	PHE	419	-5.806	-30.278	17.466	1.00	0.00	3A7
ATOM	3041	CE1	PHE	419	-6.325	-28.691	15.246	1.00	0.00	3A7
ATOM	3042	CE2	PHE	419	-7.085	-30.245	16.919	1.00	0.00	3A7
ATOM	3043	CZ	PHE	419	-7.345	-29.452	15.806	1.00	0.00	3A7
ATOM	3044	C	PHE	419	-2.135	-29.334	19.681	1.00	0.00	3A7
ATOM	3045	O	PHE	419	-1.066	-28.961	19.199	1.00	0.00	3A7
ATOM	3046	N	SER	420	-2.220	-30.000	20.861	1.00	0.00	3A7
ATOM	3047	CA	SER	420	-1.120	-30.259	21.764	1.00	0.00	3A7
ATOM	3048	CB	SER	420	-1.589	-30.137	23.241	1.00	0.00	3A7
ATOM	3049	OG	SER	420	-0.513	-30.208	24.172	1.00	0.00	3A7
ATOM	3050	C	SER	420	-0.568	-31.644	21.508	1.00	0.00	3A7
ATOM	3051	O	SER	420	-1.267	-32.527	21.013	1.00	0.00	3A7
ATOM	3052	N	LYS	421	0.722	-31.842	21.877	1.00	0.00	3A7

ATOM	3053	CA	LYS	421	1.404	-33.112	21.813	1.00	0.00	3A7
ATOM	3054	CB	LYS	421	2.506	-33.196	20.717	1.00	0.00	3A7
ATOM	3055	CG	LYS	421	3.804	-32.380	20.921	1.00	0.00	3A7
ATOM	3056	CD	LYS	421	3.679	-30.845	20.996	1.00	0.00	3A7
ATOM	3057	CE	LYS	421	3.332	-30.147	19.673	1.00	0.00	3A7
ATOM	3058	NZ	LYS	421	1.927	-30.385	19.273	1.00	0.00	3A7
ATOM	3059	C	LYS	421	2.007	-33.350	23.167	1.00	0.00	3A7
ATOM	3060	O	LYS	421	2.165	-32.424	23.962	1.00	0.00	3A7
ATOM	3061	N	LYS	422	2.373	-34.620	23.448	1.00	0.00	3A7
ATOM	3062	CA	LYS	422	3.032	-34.986	24.675	1.00	0.00	3A7
ATOM	3063	CB	LYS	422	2.048	-35.203	25.856	1.00	0.00	3A7
ATOM	3064	CG	LYS	422	2.715	-35.433	27.225	1.00	0.00	3A7
ATOM	3065	CD	LYS	422	3.520	-34.222	27.727	1.00	0.00	3A7
ATOM	3066	CE	LYS	422	4.151	-34.436	29.109	1.00	0.00	3A7
ATOM	3067	NZ	LYS	422	5.140	-35.537	29.071	1.00	0.00	3A7
ATOM	3068	C	LYS	422	3.767	-36.262	24.379	1.00	0.00	3A7
ATOM	3069	O	LYS	422	4.874	-36.483	24.867	1.00	0.00	3A7
ATOM	3070	N	ASN	423	3.138	-37.137	23.555	1.00	0.00	3A7
ATOM	3071	CA	ASN	423	3.658	-38.427	23.165	1.00	0.00	3A7
ATOM	3072	CB	ASN	423	2.646	-39.581	23.442	1.00	0.00	3A7
ATOM	3073	CG	ASN	423	1.264	-39.329	22.812	1.00	0.00	3A7
ATOM	3074	OD1	ASN	423	0.498	-38.476	23.277	1.00	0.00	3A7
ATOM	3075	ND2	ASN	423	0.950	-40.110	21.734	1.00	0.00	3A7
ATOM	3076	C	ASN	423	4.031	-38.367	21.703	1.00	0.00	3A7
ATOM	3077	O	ASN	423	3.916	-37.323	21.061	1.00	0.00	3A7
ATOM	3078	N	LYS	424	4.481	-39.522	21.148	1.00	0.00	3A7
ATOM	3079	CA	LYS	424	4.861	-39.684	19.760	1.00	0.00	3A7
ATOM	3080	CB	LYS	424	5.998	-40.724	19.591	1.00	0.00	3A7
ATOM	3081	CG	LYS	424	6.530	-40.859	18.153	1.00	0.00	3A7
ATOM	3082	CD	LYS	424	7.676	-41.874	18.013	1.00	0.00	3A7
ATOM	3083	CE	LYS	424	8.960	-41.460	18.744	1.00	0.00	3A7
ATOM	3084	NZ	LYS	424	10.027	-42.465	18.534	1.00	0.00	3A7
ATOM	3085	C	LYS	424	3.649	-40.125	18.981	1.00	0.00	3A7
ATOM	3086	O	LYS	424	3.011	-41.116	19.335	1.00	0.00	3A7
ATOM	3087	N	ASP	425	3.321	-39.353	17.910	1.00	0.00	3A7
ATOM	3088	CA	ASP	425	2.171	-39.492	17.032	1.00	0.00	3A7
ATOM	3089	CB	ASP	425	1.794	-40.959	16.658	1.00	0.00	3A7
ATOM	3090	CG	ASP	425	0.795	-41.005	15.496	1.00	0.00	3A7
ATOM	3091	OD1	ASP	425	-0.322	-41.550	15.698	1.00	0.00	3A7
ATOM	3092	OD2	ASP	425	1.142	-40.497	14.397	1.00	0.00	3A7
ATOM	3093	C	ASP	425	1.009	-38.771	17.679	1.00	0.00	3A7
ATOM	3094	O	ASP	425	0.241	-39.355	18.444	1.00	0.00	3A7
ATOM	3095	N	ASN	426	0.881	-37.457	17.372	1.00	0.00	3A7
ATOM	3096	CA	ASN	426	-0.110	-36.573	17.945	1.00	0.00	3A7
ATOM	3097	CB	ASN	426	0.515	-35.250	18.487	1.00	0.00	3A7
ATOM	3098	CG	ASN	426	1.320	-34.458	17.438	1.00	0.00	3A7
ATOM	3099	OD1	ASN	426	2.282	-34.963	16.848	1.00	0.00	3A7
ATOM	3100	ND2	ASN	426	0.912	-33.168	17.234	1.00	0.00	3A7
ATOM	3101	C	ASN	426	-1.189	-36.329	16.915	1.00	0.00	3A7
ATOM	3102	O	ASN	426	-1.547	-37.229	16.157	1.00	0.00	3A7
ATOM	3103	N	ILE	427	-1.746	-35.090	16.880	1.00	0.00	3A7
ATOM	3104	CA	ILE	427	-2.849	-34.709	16.022	1.00	0.00	3A7
ATOM	3105	CB	ILE	427	-3.731	-33.632	16.647	1.00	0.00	3A7
ATOM	3106	CG2	ILE	427	-4.975	-33.389	15.762	1.00	0.00	3A7
ATOM	3107	CG1	ILE	427	-4.130	-34.009	18.097	1.00	0.00	3A7
ATOM	3108	CD	ILE	427	-4.944	-35.302	18.218	1.00	0.00	3A7
ATOM	3109	C	ILE	427	-2.306	-34.224	14.699	1.00	0.00	3A7
ATOM	3110	O	ILE	427	-2.782	-34.635	13.641	1.00	0.00	3A7
ATOM	3111	N	ASP	428	-1.289	-33.326	14.741	1.00	0.00	3A7
ATOM	3112	CA	ASP	428	-0.691	-32.752	13.555	1.00	0.00	3A7
ATOM	3113	CB	ASP	428	-1.067	-31.262	13.360	1.00	0.00	3A7
ATOM	3114	CG	ASP	428	-2.578	-31.131	13.173	1.00	0.00	3A7
ATOM	3115	OD1	ASP	428	-3.101	-31.683	12.169	1.00	0.00	3A7
ATOM	3116	OD2	ASP	428	-3.224	-30.473	14.030	1.00	0.00	3A7
ATOM	3117	C	ASP	428	0.815	-32.877	13.650	1.00	0.00	3A7
ATOM	3118	O	ASP	428	1.471	-31.935	14.093	1.00	0.00	3A7
ATOM	3119	N	PRO	429	1.414	-34.003	13.251	1.00	0.00	3A7
ATOM	3120	CA	PRO	429	2.856	-34.177	13.157	1.00	0.00	3A7
ATOM	3121	CD	PRO	429	0.694	-35.245	12.998	1.00	0.00	3A7
ATOM	3122	CB	PRO	429	3.026	-35.701	13.258	1.00	0.00	3A7
ATOM	3123	CG	PRO	429	1.763	-36.266	12.604	1.00	0.00	3A7
ATOM	3124	C	PRO	429	3.490	-33.658	11.858	1.00	0.00	3A7

ATOM	3125	O	PRO	429	2.892	-33.616	10.780	1.00	0.00	3A7
ATOM	3126	N	TYR	430	4.793	-33.325	11.967	1.00	0.00	3A7
ATOM	3127	CA	TYR	430	5.745	-33.153	10.884	1.00	0.00	3A7
ATOM	3128	CB	TYR	430	5.621	-34.248	9.770	1.00	0.00	3A7
ATOM	3129	CG	TYR	430	6.889	-34.285	8.969	1.00	0.00	3A7
ATOM	3130	CD1	TYR	430	8.048	-34.836	9.516	1.00	0.00	3A7
ATOM	3131	CD2	TYR	430	6.967	-33.566	7.779	1.00	0.00	3A7
ATOM	3132	CE1	TYR	430	9.284	-34.596	8.926	1.00	0.00	3A7
ATOM	3133	CE2	TYR	430	8.205	-33.267	7.232	1.00	0.00	3A7
ATOM	3134	CZ	TYR	430	9.366	-33.774	7.806	1.00	0.00	3A7
ATOM	3135	OH	TYR	430	10.620	-33.421	7.266	1.00	0.00	3A7
ATOM	3136	C	TYR	430	5.763	-31.761	10.274	1.00	0.00	3A7
ATOM	3137	O	TYR	430	6.683	-31.428	9.529	1.00	0.00	3A7
ATOM	3138	N	ILE	431	4.795	-30.877	10.599	1.00	0.00	3A7
ATOM	3139	CA	ILE	431	4.842	-29.502	10.146	1.00	0.00	3A7
ATOM	3140	CB	ILE	431	3.495	-28.893	9.784	1.00	0.00	3A7
ATOM	3141	CG2	ILE	431	2.954	-29.661	8.570	1.00	0.00	3A7
ATOM	3142	CG1	ILE	431	2.477	-28.800	10.949	1.00	0.00	3A7
ATOM	3143	CD	ILE	431	1.966	-30.124	11.513	1.00	0.00	3A7
ATOM	3144	C	ILE	431	5.480	-28.630	11.193	1.00	0.00	3A7
ATOM	3145	O	ILE	431	5.889	-27.509	10.893	1.00	0.00	3A7
ATOM	3146	N	TYR	432	5.562	-29.122	12.460	1.00	0.00	3A7
ATOM	3147	CA	TYR	432	6.198	-28.443	13.571	1.00	0.00	3A7
ATOM	3148	CB	TYR	432	5.758	-28.969	14.973	1.00	0.00	3A7
ATOM	3149	CG	TYR	432	4.498	-28.367	15.505	1.00	0.00	3A7
ATOM	3150	CD1	TYR	432	3.438	-29.190	15.886	1.00	0.00	3A7
ATOM	3151	CD2	TYR	432	4.439	-27.004	15.799	1.00	0.00	3A7
ATOM	3152	CE1	TYR	432	2.350	-28.665	16.575	1.00	0.00	3A7
ATOM	3153	CE2	TYR	432	3.348	-26.477	16.484	1.00	0.00	3A7
ATOM	3154	CZ	TYR	432	2.304	-27.307	16.878	1.00	0.00	3A7
ATOM	3155	OH	TYR	432	1.204	-26.773	17.586	1.00	0.00	3A7
ATOM	3156	C	TYR	432	7.676	-28.741	13.531	1.00	0.00	3A7
ATOM	3157	O	TYR	432	8.161	-29.675	14.169	1.00	0.00	3A7
ATOM	3158	N	THR	433	8.425	-27.919	12.778	1.00	0.00	3A7
ATOM	3159	CA	THR	433	9.824	-28.119	12.506	1.00	0.00	3A7
ATOM	3160	CB	THR	433	10.074	-28.167	10.995	1.00	0.00	3A7
ATOM	3161	OG1	THR	433	9.638	-26.980	10.336	1.00	0.00	3A7
ATOM	3162	CG2	THR	433	9.309	-29.368	10.401	1.00	0.00	3A7
ATOM	3163	C	THR	433	10.729	-27.070	13.107	1.00	0.00	3A7
ATOM	3164	O	THR	433	11.720	-26.744	12.459	1.00	0.00	3A7
ATOM	3165	N	PRO	434	10.544	-26.494	14.305	1.00	0.00	3A7
ATOM	3166	CA	PRO	434	11.476	-25.526	14.854	1.00	0.00	3A7
ATOM	3167	CD	PRO	434	9.603	-26.944	15.329	1.00	0.00	3A7
ATOM	3168	CB	PRO	434	10.738	-25.003	16.098	1.00	0.00	3A7
ATOM	3169	CG	PRO	434	9.981	-26.220	16.622	1.00	0.00	3A7
ATOM	3170	C	PRO	434	12.807	-26.180	15.226	1.00	0.00	3A7
ATOM	3171	O	PRO	434	13.809	-25.477	15.300	1.00	0.00	3A7
ATOM	3172	N	PHE	435	12.847	-27.518	15.456	1.00	0.00	3A7
ATOM	3173	CA	PHE	435	14.041	-28.253	15.844	1.00	0.00	3A7
ATOM	3174	CB	PHE	435	13.670	-29.173	17.045	1.00	0.00	3A7
ATOM	3175	CG	PHE	435	13.744	-28.509	18.358	1.00	0.00	3A7
ATOM	3176	CD1	PHE	435	14.729	-27.557	18.520	1.00	0.00	3A7
ATOM	3177	CD2	PHE	435	12.731	-28.261	19.269	1.00	0.00	3A7
ATOM	3178	CE1	PHE	435	14.264	-26.403	19.460	1.00	0.00	3A7
ATOM	3179	CE2	PHE	435	14.105	-27.600	20.460	1.00	0.00	3A7
ATOM	3180	CZ	PHE	435	13.408	-26.726	20.695	1.00	0.00	3A7
ATOM	3181	C	PHE	435	14.509	-29.099	14.689	1.00	0.00	3A7
ATOM	3182	O	PHE	435	15.352	-29.980	14.855	1.00	0.00	3A7
ATOM	3183	N	GLY	436	13.993	-28.834	13.469	1.00	0.00	3A7
ATOM	3184	CA	GLY	436	14.463	-29.495	12.269	1.00	0.00	3A7
ATOM	3185	C	GLY	436	13.733	-30.777	12.129	1.00	0.00	3A7
ATOM	3186	O	GLY	436	12.792	-31.061	12.870	1.00	0.00	3A7
ATOM	3187	N	SER	437	14.147	-31.599	11.152	1.00	0.00	3A7
ATOM	3188	CA	SER	437	13.525	-32.872	10.944	1.00	0.00	3A7
ATOM	3189	CB	SER	437	12.322	-32.829	9.974	1.00	0.00	3A7
ATOM	3190	OG	SER	437	11.247	-32.079	10.518	1.00	0.00	3A7
ATOM	3191	C	SER	437	14.585	-33.730	10.351	1.00	0.00	3A7
ATOM	3192	O	SER	437	15.352	-33.291	9.494	1.00	0.00	3A7
ATOM	3193	N	GLY	438	14.623	-35.006	10.788	1.00	0.00	3A7
ATOM	3194	CA	GLY	438	15.462	-36.010	10.184	1.00	0.00	3A7
ATOM	3195	C	GLY	438	16.610	-36.414	11.067	1.00	0.00	3A7
ATOM	3196	O	GLY	438	16.526	-36.346	12.293	1.00	0.00	3A7

ATOM	3197	N	PRO	439	17.704	-36.873	10.443	1.00	0.00	3A7
ATOM	3198	CA	PRO	439	18.897	-37.275	11.180	1.00	0.00	3A7
ATOM	3199	CD	PRO	439	17.653	-37.555	9.152	1.00	0.00	3A7
ATOM	3200	CB	PRO	439	19.741	-38.079	10.170	1.00	0.00	3A7
ATOM	3201	CG	PRO	439	18.702	-38.666	9.220	1.00	0.00	3A7
ATOM	3202	C	PRO	439	19.700	-36.119	11.729	1.00	0.00	3A7
ATOM	3203	O	PRO	439	20.523	-36.342	12.614	1.00	0.00	3A7
ATOM	3204	N	ARG	440	19.490	-34.889	11.217	1.00	0.00	3A7
ATOM	3205	CA	ARG	440	20.212	-33.720	11.642	1.00	0.00	3A7
ATOM	3206	CB	ARG	440	20.704	-32.913	10.433	1.00	0.00	3A7
ATOM	3207	CG	ARG	440	21.775	-33.662	9.617	1.00	0.00	3A7
ATOM	3208	CD	ARG	440	21.846	-33.224	8.148	1.00	0.00	3A7
ATOM	3209	NE	ARG	440	20.618	-33.741	7.458	1.00	0.00	3A7
ATOM	3210	CZ	ARG	440	20.391	-33.552	6.123	1.00	0.00	3A7
ATOM	3211	NH1	ARG	440	19.299	-34.126	5.537	1.00	0.00	3A7
ATOM	3212	NH2	ARG	440	21.244	-32.799	5.371	1.00	0.00	3A7
ATOM	3213	C	ARG	440	19.307	-32.855	12.480	1.00	0.00	3A7
ATOM	3214	O	ARG	440	19.471	-31.639	12.565	1.00	0.00	3A7
ATOM	3215	N	ASN	441	18.322	-33.480	13.163	1.00	0.00	3A7
ATOM	3216	CA	ASN	441	17.420	-32.809	14.066	1.00	0.00	3A7
ATOM	3217	CB	ASN	441	16.263	-33.734	14.515	1.00	0.00	3A7
ATOM	3218	CG	ASN	441	16.713	-34.970	15.324	1.00	0.00	3A7
ATOM	3219	OD1	ASN	441	17.527	-35.781	14.869	1.00	0.00	3A7
ATOM	3220	ND2	ASN	441	16.154	-35.093	16.567	1.00	0.00	3A7
ATOM	3221	C	ASN	441	18.197	-32.339	15.260	1.00	0.00	3A7
ATOM	3222	O	ASN	441	19.263	-32.884	15.550	1.00	0.00	3A7
ATOM	3223	N	CYS	442	17.690	-31.324	15.990	1.00	0.00	3A7
ATOM	3224	CA	CYS	442	18.409	-30.739	17.097	1.00	0.00	3A7
ATOM	3225	CB	CYS	442	17.629	-29.548	17.676	1.00	0.00	3A7
ATOM	3226	SG	CYS	442	18.592	-28.606	18.905	1.00	0.00	3A7
ATOM	3227	C	CYS	442	18.683	-31.758	18.181	1.00	0.00	3A7
ATOM	3228	O	CYS	442	17.779	-32.410	18.699	1.00	0.00	3A7
ATOM	3229	N	ILE	443	19.971	-31.894	18.535	1.00	0.00	3A7
ATOM	3230	CA	ILE	443	20.405	-32.830	19.531	1.00	0.00	3A7
ATOM	3231	CB	ILE	443	21.872	-33.211	19.324	1.00	0.00	3A7
ATOM	3232	CG2	ILE	443	22.414	-34.095	20.472	1.00	0.00	3A7
ATOM	3233	CG1	ILE	443	22.046	-33.916	17.955	1.00	0.00	3A7
ATOM	3234	CD	ILE	443	21.378	-35.291	17.849	1.00	0.00	3A7
ATOM	3235	C	ILE	443	20.167	-32.223	20.902	1.00	0.00	3A7
ATOM	3236	O	ILE	443	20.008	-32.929	21.894	1.00	0.00	3A7
ATOM	3237	N	GLY	444	20.106	-30.876	20.975	1.00	0.00	3A7
ATOM	3238	CA	GLY	444	19.894	-30.159	22.204	1.00	0.00	3A7
ATOM	3239	C	GLY	444	18.471	-29.893	22.535	1.00	0.00	3A7
ATOM	3240	O	GLY	444	18.222	-29.153	23.479	1.00	0.00	3A7
ATOM	3241	N	MET	445	17.493	-30.471	21.788	1.00	0.00	3A7
ATOM	3242	CA	MET	445	16.056	-30.254	21.939	1.00	0.00	3A7
ATOM	3243	CB	MET	445	15.279	-31.201	21.002	1.00	0.00	3A7
ATOM	3244	CG	MET	445	13.742	-31.222	21.137	1.00	0.00	3A7
ATOM	3245	SD	MET	445	12.898	-32.098	19.780	1.00	0.00	3A7
ATOM	3246	CE	MET	445	13.584	-33.749	20.107	1.00	0.00	3A7
ATOM	3247	C	MET	445	15.558	-30.454	23.349	1.00	0.00	3A7
ATOM	3248	O	MET	445	14.887	-29.598	23.919	1.00	0.00	3A7
ATOM	3249	N	ARG	446	15.928	-31.580	23.976	1.00	0.00	3A7
ATOM	3250	CA	ARG	446	15.476	-31.910	25.309	1.00	0.00	3A7
ATOM	3251	CB	ARG	446	15.826	-33.368	25.684	1.00	0.00	3A7
ATOM	3252	CG	ARG	446	15.490	-34.340	24.538	1.00	0.00	3A7
ATOM	3253	CD	ARG	446	15.588	-35.824	24.911	1.00	0.00	3A7
ATOM	3254	NE	ARG	446	14.428	-36.164	25.799	1.00	0.00	3A7
ATOM	3255	CZ	ARG	446	14.005	-37.451	25.986	1.00	0.00	3A7
ATOM	3256	NH1	ARG	446	12.921	-37.696	26.780	1.00	0.00	3A7
ATOM	3257	NH2	ARG	446	14.658	-38.492	25.394	1.00	0.00	3A7
ATOM	3258	C	ARG	446	16.001	-30.952	26.348	1.00	0.00	3A7
ATOM	3259	O	ARG	446	15.276	-30.542	27.248	1.00	0.00	3A7
ATOM	3260	N	PHE	447	17.267	-30.512	26.201	1.00	0.00	3A7
ATOM	3261	CA	PHE	447	17.865	-29.566	27.113	1.00	0.00	3A7
ATOM	3262	CB	PHE	447	19.408	-29.515	27.061	1.00	0.00	3A7
ATOM	3263	CG	PHE	447	19.952	-30.827	26.613	1.00	0.00	3A7
ATOM	3264	CD1	PHE	447	20.810	-30.828	25.520	1.00	0.00	3A7
ATOM	3265	CD2	PHE	447	19.433	-32.037	27.086	1.00	0.00	3A7
ATOM	3266	CE1	PHE	447	20.971	-31.985	24.778	1.00	0.00	3A7
ATOM	3267	CE2	PHE	447	19.526	-33.173	26.291	1.00	0.00	3A7
ATOM	3268	CZ	PHE	447	20.229	-33.109	25.096	1.00	0.00	3A7

ATOM	3269	C	PHE	447	17.285	-28.185	26.918	1.00	0.00	3A7
ATOM	3270	O	PHE	447	17.071	-27.458	27.881	1.00	0.00	3A7
ATOM	3271	N	ALA	448	16.949	-27.798	25.656	1.00	0.00	3A7
ATOM	3272	CA	ALA	448	16.406	-26.493	25.374	1.00	0.00	3A7
ATOM	3273	CB	ALA	448	16.379	-26.216	23.882	1.00	0.00	3A7
ATOM	3274	C	ALA	448	15.020	-26.344	25.914	1.00	0.00	3A7
ATOM	3275	O	ALA	448	14.679	-25.313	26.493	1.00	0.00	3A7
ATOM	3276	N	LEU	449	14.197	-27.406	25.800	1.00	0.00	3A7
ATOM	3277	CA	LEU	449	12.842	-27.402	26.309	1.00	0.00	3A7
ATOM	3278	CB	LEU	449	12.029	-28.605	25.813	1.00	0.00	3A7
ATOM	3279	CG	LEU	449	11.639	-28.523	24.324	1.00	0.00	3A7
ATOM	3280	CD1	LEU	449	11.120	-29.879	23.807	1.00	0.00	3A7
ATOM	3281	CD2	LEU	449	10.621	-27.401	24.038	1.00	0.00	3A7
ATOM	3282	C	LEU	449	12.800	-27.422	27.811	1.00	0.00	3A7
ATOM	3283	O	LEU	449	11.936	-26.797	28.417	1.00	0.00	3A7
ATOM	3284	N	VAL	450	13.770	-28.111	28.454	1.00	0.00	3A7
ATOM	3285	CA	VAL	450	13.883	-28.171	29.893	1.00	0.00	3A7
ATOM	3286	CB	VAL	450	14.890	-29.213	30.345	1.00	0.00	3A7
ATOM	3287	CG1	VAL	450	15.177	-29.141	31.862	1.00	0.00	3A7
ATOM	3288	CG2	VAL	450	14.262	-30.592	30.049	1.00	0.00	3A7
ATOM	3289	C	VAL	450	14.256	-26.828	30.431	1.00	0.00	3A7
ATOM	3290	O	VAL	450	13.633	-26.345	31.364	1.00	0.00	3A7
ATOM	3291	N	ASN	451	15.263	-26.162	29.833	1.00	0.00	3A7
ATOM	3292	CA	ASN	451	15.735	-24.855	30.232	1.00	0.00	3A7
ATOM	3293	CB	ASN	451	16.873	-24.401	29.295	1.00	0.00	3A7
ATOM	3294	CG	ASN	451	18.141	-25.243	29.476	1.00	0.00	3A7
ATOM	3295	OD1	ASN	451	18.233	-26.089	30.369	1.00	0.00	3A7
ATOM	3296	ND2	ASN	451	19.145	-24.981	28.583	1.00	0.00	3A7
ATOM	3297	C	ASN	451	14.659	-23.792	30.150	1.00	0.00	3A7
ATOM	3298	O	ASN	451	14.440	-23.023	31.081	1.00	0.00	3A7
ATOM	3299	N	MET	452	13.918	-23.759	29.019	1.00	0.00	3A7
ATOM	3300	CA	MET	452	12.853	-22.808	28.800	1.00	0.00	3A7
ATOM	3301	CB	MET	452	12.311	-22.880	27.353	1.00	0.00	3A7
ATOM	3302	CG	MET	452	13.202	-22.090	26.370	1.00	0.00	3A7
ATOM	3303	SD	MET	452	13.800	-22.975	24.894	1.00	0.00	3A7
ATOM	3304	CE	MET	452	12.280	-23.810	24.359	1.00	0.00	3A7
ATOM	3305	C	MET	452	11.733	-22.982	29.778	1.00	0.00	3A7
ATOM	3306	O	MET	452	11.255	-22.013	30.355	1.00	0.00	3A7
ATOM	3307	N	LYS	453	11.310	-24.236	30.042	1.00	0.00	3A7
ATOM	3308	CA	LYS	453	10.240	-24.536	30.965	1.00	0.00	3A7
ATOM	3309	CB	LYS	453	9.864	-26.021	30.868	1.00	0.00	3A7
ATOM	3310	CG	LYS	453	8.486	-26.409	31.399	1.00	0.00	3A7
ATOM	3311	CD	LYS	453	8.218	-27.911	31.258	1.00	0.00	3A7
ATOM	3312	CE	LYS	453	8.280	-28.457	29.817	1.00	0.00	3A7
ATOM	3313	NZ	LYS	453	9.661	-28.675	29.322	1.00	0.00	3A7
ATOM	3314	C	LYS	453	10.616	-24.214	32.386	1.00	0.00	3A7
ATOM	3315	O	LYS	453	9.869	-23.577	33.112	1.00	0.00	3A7
ATOM	3316	N	LEU	454	11.836	-24.594	32.812	1.00	0.00	3A7
ATOM	3317	CA	LEU	454	12.304	-24.349	34.154	1.00	0.00	3A7
ATOM	3318	CB	LEU	454	13.614	-25.110	34.423	1.00	0.00	3A7
ATOM	3319	CG	LEU	454	13.420	-26.655	34.462	1.00	0.00	3A7
ATOM	3320	CD1	LEU	454	14.712	-27.380	34.874	1.00	0.00	3A7
ATOM	3321	CD2	LEU	454	12.265	-27.101	35.377	1.00	0.00	3A7
ATOM	3322	C	LEU	454	12.488	-22.881	34.440	1.00	0.00	3A7
ATOM	3323	O	LEU	454	12.033	-22.383	35.465	1.00	0.00	3A7
ATOM	3324	N	ALA	455	13.101	-22.129	33.501	1.00	0.00	3A7
ATOM	3325	CA	ALA	455	13.303	-20.699	33.621	1.00	0.00	3A7
ATOM	3326	CB	ALA	455	14.157	-20.149	32.468	1.00	0.00	3A7
ATOM	3327	C	ALA	455	12.006	-19.916	33.668	1.00	0.00	3A7
ATOM	3328	O	ALA	455	11.803	-19.112	34.569	1.00	0.00	3A7
ATOM	3329	N	LEU	456	11.065	-20.169	32.730	1.00	0.00	3A7
ATOM	3330	CA	LEU	456	9.795	-19.468	32.642	1.00	0.00	3A7
ATOM	3331	CB	LEU	456	9.033	-19.835	31.351	1.00	0.00	3A7
ATOM	3332	CG	LEU	456	9.514	-19.139	30.053	1.00	0.00	3A7
ATOM	3333	CD1	LEU	456	10.961	-18.619	30.084	1.00	0.00	3A7
ATOM	3334	CD2	LEU	456	9.277	-20.054	28.836	1.00	0.00	3A7
ATOM	3335	C	LEU	456	8.902	-19.770	33.817	1.00	0.00	3A7
ATOM	3336	O	LEU	456	8.226	-18.888	34.337	1.00	0.00	3A7
ATOM	3337	N	VAL	457	8.933	-21.025	34.323	1.00	0.00	3A7
ATOM	3338	CA	VAL	457	8.191	-21.445	35.499	1.00	0.00	3A7
ATOM	3339	CB	VAL	457	8.444	-22.911	35.843	1.00	0.00	3A7
ATOM	3340	CG1	VAL	457	8.005	-23.325	37.263	1.00	0.00	3A7

ATOM	3341	CG2	VAL	457	7.670	-23.765	34.841	1.00	0.00	3A7
ATOM	3342	C	VAL	457	8.576	-20.633	36.694	1.00	0.00	3A7
ATOM	3343	O	VAL	457	7.731	-20.161	37.444	1.00	0.00	3A7
ATOM	3344	N	ARG	458	9.892	-20.443	36.892	1.00	0.00	3A7
ATOM	3345	CA	ARG	458	10.419	-19.722	38.015	1.00	0.00	3A7
ATOM	3346	CB	ARG	458	11.926	-19.996	38.164	1.00	0.00	3A7
ATOM	3347	CG	ARG	458	12.246	-21.369	38.758	1.00	0.00	3A7
ATOM	3348	CD	ARG	458	13.750	-21.581	38.977	1.00	0.00	3A7
ATOM	3349	NE	ARG	458	14.409	-21.751	37.641	1.00	0.00	3A7
ATOM	3350	CZ	ARG	458	14.920	-22.941	37.197	1.00	0.00	3A7
ATOM	3351	NH1	ARG	458	15.570	-22.979	35.995	1.00	0.00	3A7
ATOM	3352	NH2	ARG	458	14.813	-24.080	37.937	1.00	0.00	3A7
ATOM	3353	C	ARG	458	10.219	-18.233	37.894	1.00	0.00	3A7
ATOM	3354	O	ARG	458	9.873	-17.578	38.869	1.00	0.00	3A7
ATOM	3355	N	VAL	459	10.398	-17.640	36.691	1.00	0.00	3A7
ATOM	3356	CA	VAL	459	10.219	-16.217	36.448	1.00	0.00	3A7
ATOM	3357	CB	VAL	459	10.629	-15.894	35.017	1.00	0.00	3A7
ATOM	3358	CG1	VAL	459	10.199	-14.508	34.526	1.00	0.00	3A7
ATOM	3359	CG2	VAL	459	12.165	-16.014	34.950	1.00	0.00	3A7
ATOM	3360	C	VAL	459	8.793	-15.789	36.752	1.00	0.00	3A7
ATOM	3361	O	VAL	459	8.553	-14.855	37.511	1.00	0.00	3A7
ATOM	3362	N	LEU	460	7.804	-16.538	36.226	1.00	0.00	3A7
ATOM	3363	CA	LEU	460	6.397	-16.237	36.374	1.00	0.00	3A7
ATOM	3364	CB	LEU	460	5.571	-17.011	35.340	1.00	0.00	3A7
ATOM	3365	CG	LEU	460	5.883	-16.588	33.893	1.00	0.00	3A7
ATOM	3366	CD1	LEU	460	5.285	-17.596	32.898	1.00	0.00	3A7
ATOM	3367	CD2	LEU	460	5.418	-15.150	33.610	1.00	0.00	3A7
ATOM	3368	C	LEU	460	5.857	-16.582	37.736	1.00	0.00	3A7
ATOM	3369	O	LEU	460	4.817	-16.068	38.141	1.00	0.00	3A7
ATOM	3370	N	GLN	461	6.570	-17.449	38.498	1.00	0.00	3A7
ATOM	3371	CA	GLN	461	6.249	-17.756	39.877	1.00	0.00	3A7
ATOM	3372	CB	GLN	461	6.961	-19.025	40.414	1.00	0.00	3A7
ATOM	3373	CG	GLN	461	6.204	-19.729	41.554	1.00	0.00	3A7
ATOM	3374	CD	GLN	461	6.924	-21.033	41.909	1.00	0.00	3A7
ATOM	3375	OE1	GLN	461	7.856	-21.463	41.220	1.00	0.00	3A7
ATOM	3376	NE2	GLN	461	6.464	-21.670	43.029	1.00	0.00	3A7
ATOM	3377	C	GLN	461	6.618	-16.632	40.808	1.00	0.00	3A7
ATOM	3378	O	GLN	461	5.945	-16.385	41.809	1.00	0.00	3A7
ATOM	3379	N	ASN	462	7.741	-15.950	40.487	1.00	0.00	3A7
ATOM	3380	CA	ASN	462	8.378	-15.014	41.373	1.00	0.00	3A7
ATOM	3381	CB	ASN	462	9.917	-15.166	41.353	1.00	0.00	3A7
ATOM	3382	CG	ASN	462	10.321	-16.436	42.117	1.00	0.00	3A7
ATOM	3383	OD1	ASN	462	10.091	-17.563	41.666	1.00	0.00	3A7
ATOM	3384	ND2	ASN	462	10.944	-16.227	43.317	1.00	0.00	3A7
ATOM	3385	C	ASN	462	8.026	-13.582	41.041	1.00	0.00	3A7
ATOM	3386	O	ASN	462	8.214	-12.710	41.888	1.00	0.00	3A7
ATOM	3387	N	PHE	463	7.542	-13.284	39.807	1.00	0.00	3A7
ATOM	3388	CA	PHE	463	7.396	-11.906	39.372	1.00	0.00	3A7
ATOM	3389	CB	PHE	463	8.606	-11.416	38.535	1.00	0.00	3A7
ATOM	3390	CG	PHE	463	9.889	-11.494	39.308	1.00	0.00	3A7
ATOM	3391	CD1	PHE	463	10.834	-12.474	38.996	1.00	0.00	3A7
ATOM	3392	CD2	PHE	463	10.162	-10.594	40.340	1.00	0.00	3A7
ATOM	3393	CE1	PHE	463	12.021	-12.568	39.714	1.00	0.00	3A7
ATOM	3394	CE2	PHE	463	11.352	-10.684	41.057	1.00	0.00	3A7
ATOM	3395	CZ	PHE	463	12.280	-11.673	40.747	1.00	0.00	3A7
ATOM	3396	C	PHE	463	6.160	-11.715	38.530	1.00	0.00	3A7
ATOM	3397	O	PHE	463	5.693	-12.637	37.862	1.00	0.00	3A7
ATOM	3398	N	SER	464	5.640	-10.452	38.530	1.00	0.00	3A7
ATOM	3399	CA	SER	464	4.607	-9.957	37.639	1.00	0.00	3A7
ATOM	3400	CB	SER	464	3.437	-9.228	38.330	1.00	0.00	3A7
ATOM	3401	OG	SER	464	3.854	-8.156	39.167	1.00	0.00	3A7
ATOM	3402	C	SER	464	5.295	-9.043	36.654	1.00	0.00	3A7
ATOM	3403	O	SER	464	5.987	-8.102	37.035	1.00	0.00	3A7
ATOM	3404	N	PHE	465	5.122	-9.324	35.343	1.00	0.00	3A7
ATOM	3405	CA	PHE	465	5.823	-8.646	34.275	1.00	0.00	3A7
ATOM	3406	CB	PHE	465	6.320	-9.627	33.195	1.00	0.00	3A7
ATOM	3407	CG	PHE	465	7.476	-10.312	33.835	1.00	0.00	3A7
ATOM	3408	CD1	PHE	465	7.317	-11.547	34.451	1.00	0.00	3A7
ATOM	3409	CD2	PHE	465	8.689	-9.634	33.959	1.00	0.00	3A7
ATOM	3410	CE1	PHE	465	8.353	-12.080	35.204	1.00	0.00	3A7
ATOM	3411	CE2	PHE	465	9.736	-10.176	34.692	1.00	0.00	3A7
ATOM	3412	CZ	PHE	465	9.564	-11.399	35.322	1.00	0.00	3A7

ATOM	3413	C	PHE	465	4.919	-7.687	33.592	1.00	0.00	3A7
ATOM	3414	O	PHE	465	3.724	-7.936	33.425	1.00	0.00	3A7
ATOM	3415	N	LYS	466	5.493	-6.560	33.115	1.00	0.00	3A7
ATOM	3416	CA	LYS	466	4.734	-5.582	32.382	1.00	0.00	3A7
ATOM	3417	CB	LYS	466	4.290	-4.427	33.296	1.00	0.00	3A7
ATOM	3418	CG	LYS	466	3.397	-4.837	34.480	1.00	0.00	3A7
ATOM	3419	CD	LYS	466	2.972	-3.643	35.348	1.00	0.00	3A7
ATOM	3420	CE	LYS	466	2.140	-4.046	36.574	1.00	0.00	3A7
ATOM	3421	NZ	LYS	466	2.919	-4.922	37.481	1.00	0.00	3A7
ATOM	3422	C	LYS	466	5.602	-5.043	31.290	1.00	0.00	3A7
ATOM	3423	O	LYS	466	6.771	-4.756	31.526	1.00	0.00	3A7
ATOM	3424	N	PRO	467	5.061	-4.811	30.080	1.00	0.00	3A7
ATOM	3425	CA	PRO	467	5.708	-4.063	29.024	1.00	0.00	3A7
ATOM	3426	CD	PRO	467	3.897	-5.529	29.577	1.00	0.00	3A7
ATOM	3427	CB	PRO	467	4.867	-4.318	27.759	1.00	0.00	3A7
ATOM	3428	CG	PRO	467	4.104	-5.604	28.064	1.00	0.00	3A7
ATOM	3429	C	PRO	467	5.709	-2.585	29.358	1.00	0.00	3A7
ATOM	3430	O	PRO	467	4.657	-2.040	29.696	1.00	0.00	3A7
ATOM	3431	N	CYS	468	6.875	-1.912	29.284	1.00	0.00	3A7
ATOM	3432	CA	CYS	468	7.012	-0.524	29.684	1.00	0.00	3A7
ATOM	3433	CB	CYS	468	8.466	-0.147	30.062	1.00	0.00	3A7
ATOM	3434	SG	CYS	468	9.057	-1.091	31.487	1.00	0.00	3A7
ATOM	3435	C	CYS	468	6.616	0.383	28.544	1.00	0.00	3A7
ATOM	3436	O	CYS	468	6.411	1.583	28.713	1.00	0.00	3A7
ATOM	3437	N	LYS	469	6.540	-0.205	27.334	1.00	0.00	3A7
ATOM	3438	CA	LYS	469	6.355	0.499	26.104	1.00	0.00	3A7
ATOM	3439	CB	LYS	469	7.640	0.501	25.281	1.00	0.00	3A7
ATOM	3440	CG	LYS	469	8.757	1.350	25.918	1.00	0.00	3A7
ATOM	3441	CD	LYS	469	10.000	1.530	25.028	1.00	0.00	3A7
ATOM	3442	CE	LYS	469	9.788	2.435	23.807	1.00	0.00	3A7
ATOM	3443	NZ	LYS	469	9.393	3.802	24.218	1.00	0.00	3A7
ATOM	3444	C	LYS	469	5.347	-0.291	25.354	1.00	0.00	3A7
ATOM	3445	O	LYS	469	5.575	-1.459	25.050	1.00	0.00	3A7
ATOM	3446	N	GLU	470	4.138	0.226	25.134	1.00	0.00	3A7
ATOM	3447	CA	GLU	470	3.141	-0.604	24.504	1.00	0.00	3A7
ATOM	3448	CB	GLU	470	1.701	-0.299	24.997	1.00	0.00	3A7
ATOM	3449	CG	GLU	470	1.488	-0.619	26.491	1.00	0.00	3A7
ATOM	3450	CD	GLU	470	1.553	-2.121	26.773	1.00	0.00	3A7
ATOM	3451	OE1	GLU	470	1.559	-2.928	25.806	1.00	0.00	3A7
ATOM	3452	OE2	GLU	470	1.584	-2.480	27.981	1.00	0.00	3A7
ATOM	3453	C	GLU	470	3.348	-0.317	23.071	1.00	0.00	3A7
ATOM	3454	O	GLU	470	4.315	-0.740	22.429	1.00	0.00	3A7
ATOM	3455	N	THR	471	2.368	0.501	22.575	1.00	0.00	3A7
ATOM	3456	CA	THR	471	2.160	1.284	21.360	1.00	0.00	3A7
ATOM	3457	CB	THR	471	2.447	2.764	21.659	1.00	0.00	3A7
ATOM	3458	OG1	THR	471	1.929	3.641	20.661	1.00	0.00	3A7
ATOM	3459	CG2	THR	471	3.946	3.049	21.904	1.00	0.00	3A7
ATOM	3460	C	THR	471	2.841	0.808	20.088	1.00	0.00	3A7
ATOM	3461	O	THR	471	3.308	1.608	19.278	1.00	0.00	3A7
ATOM	3462	N	GLN	472	2.875	-0.535	19.884	1.00	0.00	3A7
ATOM	3463	CA	GLN	472	3.410	-1.235	18.731	1.00	0.00	3A7
ATOM	3464	CB	GLN	472	2.623	-0.915	17.428	1.00	0.00	3A7
ATOM	3465	CG	GLN	472	2.830	-1.913	16.270	1.00	0.00	3A7
ATOM	3466	CD	GLN	472	2.412	-3.322	16.703	1.00	0.00	3A7
ATOM	3467	OE1	GLN	472	3.252	-4.222	16.818	1.00	0.00	3A7
ATOM	3468	NE2	GLN	472	1.077	-3.502	16.944	1.00	0.00	3A7
ATOM	3469	C	GLN	472	4.893	-0.974	18.547	1.00	0.00	3A7
ATOM	3470	O	GLN	472	5.362	-0.673	17.450	1.00	0.00	3A7
ATOM	3471	N	ILE	473	5.672	-1.090	19.658	1.00	0.00	3A7
ATOM	3472	CA	ILE	473	7.130	-0.993	19.613	1.00	0.00	3A7
ATOM	3473	CB	ILE	473	7.790	-0.303	20.808	1.00	0.00	3A7
ATOM	3474	CG2	ILE	473	9.304	-0.020	20.648	1.00	0.00	3A7
ATOM	3475	CG1	ILE	473	7.030	1.009	21.146	1.00	0.00	3A7
ATOM	3476	CD	ILE	473	7.180	2.124	20.104	1.00	0.00	3A7
ATOM	3477	C	ILE	473	7.840	-2.153	19.174	1.00	0.00	3A7
ATOM	3478	O	ILE	473	8.886	-1.850	18.619	1.00	0.00	3A7
ATOM	3479	N	PRO	474	7.388	-3.403	19.312	1.00	0.00	3A7
ATOM	3480	CA	PRO	474	8.307	-4.483	19.289	1.00	0.00	3A7
ATOM	3481	CD	PRO	474	6.293	-3.751	20.216	1.00	0.00	3A7
ATOM	3482	CB	PRO	474	7.554	-5.688	19.660	1.00	0.00	3A7
ATOM	3483	CG	PRO	474	6.580	-5.162	20.707	1.00	0.00	3A7
ATOM	3484	C	PRO	474	9.042	-4.735	18.043	1.00	0.00	3A7

ATOM	3485	O	PRO	474	8.461	-4.845	16.967	1.00	0.00	3A7
ATOM	3486	N	LEU	475	10.363	-4.780	18.250	1.00	0.00	3A7
ATOM	3487	CA	LEU	475	11.281	-4.868	17.212	1.00	0.00	3A7
ATOM	3488	CB	LEU	475	12.494	-3.929	17.438	1.00	0.00	3A7
ATOM	3489	CG	LEU	475	12.127	-2.431	17.558	1.00	0.00	3A7
ATOM	3490	CD1	LEU	475	13.371	-1.592	17.906	1.00	0.00	3A7
ATOM	3491	CD2	LEU	475	11.432	-1.891	16.293	1.00	0.00	3A7
ATOM	3492	C	LEU	475	11.786	-6.229	17.109	1.00	0.00	3A7
ATOM	3493	O	LEU	475	12.315	-6.781	18.064	1.00	0.00	3A7
ATOM	3494	N	LYS	476	11.627	-6.792	15.915	1.00	0.00	3A7
ATOM	3495	CA	LYS	476	12.112	-8.088	15.588	1.00	0.00	3A7
ATOM	3496	CB	LYS	476	11.115	-8.801	14.712	1.00	0.00	3A7
ATOM	3497	CG	LYS	476	9.772	-9.009	15.441	1.00	0.00	3A7
ATOM	3498	CD	LYS	476	8.674	-9.612	14.555	1.00	0.00	3A7
ATOM	3499	CE	LYS	476	8.939	-11.068	14.167	1.00	0.00	3A7
ATOM	3500	NZ	LYS	476	7.894	-11.545	13.235	1.00	0.00	3A7
ATOM	3501	C	LYS	476	13.325	-7.870	14.776	1.00	0.00	3A7
ATOM	3502	O	LYS	476	13.337	-7.042	13.874	1.00	0.00	3A7
ATOM	3503	N	LEU	477	14.395	-8.621	15.042	1.00	0.00	3A7
ATOM	3504	CA	LEU	477	15.554	-8.551	14.210	1.00	0.00	3A7
ATOM	3505	CB	LEU	477	16.856	-8.930	14.889	1.00	0.00	3A7
ATOM	3506	CG	LEU	477	18.083	-8.017	14.617	1.00	0.00	3A7
ATOM	3507	CD1	LEU	477	19.159	-8.239	15.698	1.00	0.00	3A7
ATOM	3508	CD2	LEU	477	18.705	-8.182	13.223	1.00	0.00	3A7
ATOM	3509	C	LEU	477	15.422	-9.412	13.099	1.00	0.00	3A7
ATOM	3510	O	LEU	477	14.926	-10.517	13.208	1.00	0.00	3A7
ATOM	3511	N	ARG	478	15.810	-8.885	11.967	1.00	0.00	3A7
ATOM	3512	CA	ARG	478	15.460	-9.604	10.853	1.00	0.00	3A7
ATOM	3513	CB	ARG	478	14.781	-8.647	9.829	1.00	0.00	3A7
ATOM	3514	CG	ARG	478	13.512	-7.955	10.358	1.00	0.00	3A7
ATOM	3515	CD	ARG	478	12.226	-8.561	9.784	1.00	0.00	3A7
ATOM	3516	NE	ARG	478	12.180	-10.004	10.198	1.00	0.00	3A7
ATOM	3517	CZ	ARG	478	11.186	-10.528	10.977	1.00	0.00	3A7
ATOM	3518	NH1	ARG	478	11.256	-11.836	11.366	1.00	0.00	3A7
ATOM	3519	NH2	ARG	478	10.121	-9.764	11.352	1.00	0.00	3A7
ATOM	3520	C	ARG	478	16.502	-10.335	10.080	1.00	0.00	3A7
ATOM	3521	O	ARG	478	16.245	-10.652	8.927	1.00	0.00	3A7
ATOM	3522	N	PHE	479	17.697	-10.610	10.632	1.00	0.00	3A7
ATOM	3523	CA	PHE	479	18.858	-10.706	9.806	1.00	0.00	3A7
ATOM	3524	CB	PHE	479	20.076	-10.235	10.539	1.00	0.00	3A7
ATOM	3525	CG	PHE	479	21.147	-9.680	9.633	1.00	0.00	3A7
ATOM	3526	CD1	PHE	479	20.917	-8.497	8.929	1.00	0.00	3A7
ATOM	3527	CD2	PHE	479	22.379	-10.322	9.495	1.00	0.00	3A7
ATOM	3528	CE1	PHE	479	21.894	-7.970	8.093	1.00	0.00	3A7
ATOM	3529	CE2	PHE	479	23.356	-9.799	8.652	1.00	0.00	3A7
ATOM	3530	CZ	PHE	479	23.115	-8.622	7.951	1.00	0.00	3A7
ATOM	3531	C	PHE	479	19.185	-12.054	9.251	1.00	0.00	3A7
ATOM	3532	O	PHE	479	20.077	-12.120	8.413	1.00	0.00	3A7
ATOM	3533	N	GLY	480	18.507	-13.153	9.632	1.00	0.00	3A7
ATOM	3534	CA	GLY	480	18.751	-14.416	8.969	1.00	0.00	3A7
ATOM	3535	C	GLY	480	19.990	-15.080	9.499	1.00	0.00	3A7
ATOM	3536	O	GLY	480	21.012	-14.455	9.781	1.00	0.00	3A7
ATOM	3537	N	GLY	481	19.874	-16.400	9.691	1.00	0.00	3A7
ATOM	3538	CA	GLY	481	20.747	-17.199	10.480	1.00	0.00	3A7
ATOM	3539	C	GLY	481	19.999	-17.404	11.756	1.00	0.00	3A7
ATOM	3540	O	GLY	481	19.686	-18.530	12.126	1.00	0.00	3A7
ATOM	3541	N	LEU	482	19.687	-16.297	12.465	1.00	0.00	3A7
ATOM	3542	CA	LEU	482	19.157	-16.393	13.801	1.00	0.00	3A7
ATOM	3543	CB	LEU	482	20.314	-16.416	14.840	1.00	0.00	3A7
ATOM	3544	CG	LEU	482	20.009	-17.132	16.175	1.00	0.00	3A7
ATOM	3545	CD1	LEU	482	18.926	-16.443	17.020	1.00	0.00	3A7
ATOM	3546	CD2	LEU	482	19.738	-18.634	15.963	1.00	0.00	3A7
ATOM	3547	C	LEU	482	18.293	-15.192	13.998	1.00	0.00	3A7
ATOM	3548	O	LEU	482	18.787	-14.069	13.996	1.00	0.00	3A7
ATOM	3549	N	LEU	483	16.972	-15.412	14.210	1.00	0.00	3A7
ATOM	3550	CA	LEU	483	16.003	-14.371	14.462	1.00	0.00	3A7
ATOM	3551	CB	LEU	483	14.571	-14.799	14.069	1.00	0.00	3A7
ATOM	3552	CG	LEU	483	14.356	-14.905	12.543	1.00	0.00	3A7
ATOM	3553	CD1	LEU	483	12.892	-15.253	12.231	1.00	0.00	3A7
ATOM	3554	CD2	LEU	483	14.772	-13.634	11.775	1.00	0.00	3A7
ATOM	3555	C	LEU	483	15.995	-14.055	15.923	1.00	0.00	3A7
ATOM	3556	O	LEU	483	15.799	-14.926	16.767	1.00	0.00	3A7

ATOM	3557	N	LEU	484	16.246	-12.778	16.236	1.00	0.00	3A7
ATOM	3558	CA	LEU	484	16.374	-12.310	17.588	1.00	0.00	3A7
ATOM	3559	CB	LEU	484	17.753	-11.620	17.812	1.00	0.00	3A7
ATOM	3560	CG	LEU	484	18.984	-12.548	17.710	1.00	0.00	3A7
ATOM	3561	CD1	LEU	484	20.271	-11.745	17.445	1.00	0.00	3A7
ATOM	3562	CD2	LEU	484	19.140	-13.413	18.970	1.00	0.00	3A7
ATOM	3563	C	LEU	484	15.345	-11.234	17.861	1.00	0.00	3A7
ATOM	3564	O	LEU	484	14.779	-10.598	16.981	1.00	0.00	3A7
ATOM	3565	N	THR	485	15.149	-10.896	19.142	1.00	0.00	3A7
ATOM	3566	CA	THR	485	14.449	-9.702	19.526	1.00	0.00	3A7
ATOM	3567	CB	THR	485	13.528	-9.902	20.697	1.00	0.00	3A7
ATOM	3568	OG1	THR	485	12.643	-10.981	20.430	1.00	0.00	3A7
ATOM	3569	CG2	THR	485	12.694	-8.634	20.978	1.00	0.00	3A7
ATOM	3570	C	THR	485	15.542	-8.739	19.870	1.00	0.00	3A7
ATOM	3571	O	THR	485	16.525	-9.095	20.514	1.00	0.00	3A7
ATOM	3572	N	GLU	486	15.407	-7.491	19.395	1.00	0.00	3A7
ATOM	3573	CA	GLU	486	16.478	-6.537	19.402	1.00	0.00	3A7
ATOM	3574	CB	GLU	486	16.229	-5.476	18.329	1.00	0.00	3A7
ATOM	3575	CG	GLU	486	16.097	-6.056	16.918	1.00	0.00	3A7
ATOM	3576	CD	GLU	486	16.045	-4.920	15.900	1.00	0.00	3A7
ATOM	3577	OE1	GLU	486	15.044	-4.847	15.140	1.00	0.00	3A7
ATOM	3578	OE2	GLU	486	17.014	-4.115	15.863	1.00	0.00	3A7
ATOM	3579	C	GLU	486	16.763	-5.904	20.729	1.00	0.00	3A7
ATOM	3580	O	GLU	486	17.821	-6.121	21.297	1.00	0.00	3A7
ATOM	3581	N	LYS	487	15.871	-5.074	21.275	1.00	0.00	3A7
ATOM	3582	CA	LYS	487	16.181	-4.394	22.523	1.00	0.00	3A7
ATOM	3583	CB	LYS	487	16.681	-2.935	22.345	1.00	0.00	3A7
ATOM	3584	CG	LYS	487	18.078	-2.831	21.710	1.00	0.00	3A7
ATOM	3585	CD	LYS	487	18.582	-1.386	21.553	1.00	0.00	3A7
ATOM	3586	CE	LYS	487	17.737	-0.521	20.606	1.00	0.00	3A7
ATOM	3587	NZ	LYS	487	17.683	-1.111	19.249	1.00	0.00	3A7
ATOM	3588	C	LYS	487	14.847	-4.380	23.208	1.00	0.00	3A7
ATOM	3589	O	LYS	487	14.110	-3.436	22.965	1.00	0.00	3A7
ATOM	3590	N	PRO	488	14.469	-5.369	24.036	1.00	0.00	3A7
ATOM	3591	CA	PRO	488	13.160	-5.418	24.666	1.00	0.00	3A7
ATOM	3592	CD	PRO	488	15.099	-6.687	23.995	1.00	0.00	3A7
ATOM	3593	CB	PRO	488	12.772	-6.900	24.541	1.00	0.00	3A7
ATOM	3594	CG	PRO	488	14.103	-7.653	24.646	1.00	0.00	3A7
ATOM	3595	C	PRO	488	13.285	-4.931	26.063	1.00	0.00	3A7
ATOM	3596	O	PRO	488	14.207	-5.350	26.760	1.00	0.00	3A7
ATOM	3597	N	ILE	489	12.369	-4.042	26.506	1.00	0.00	3A7
ATOM	3598	CA	ILE	489	12.431	-3.564	27.858	1.00	0.00	3A7
ATOM	3599	CB	ILE	489	12.824	-2.096	28.021	1.00	0.00	3A7
ATOM	3600	CG2	ILE	489	14.258	-1.923	27.475	1.00	0.00	3A7
ATOM	3601	CG1	ILE	489	11.831	-1.092	27.392	1.00	0.00	3A7
ATOM	3602	CD	ILE	489	12.182	0.356	27.747	1.00	0.00	3A7
ATOM	3603	C	ILE	489	11.136	-3.837	28.577	1.00	0.00	3A7
ATOM	3604	O	ILE	489	10.052	-3.733	28.009	1.00	0.00	3A7
ATOM	3605	N	VAL	490	11.230	-4.209	29.878	1.00	0.00	3A7
ATOM	3606	CA	VAL	490	10.101	-4.648	30.674	1.00	0.00	3A7
ATOM	3607	CB	VAL	490	9.925	-6.155	30.572	1.00	0.00	3A7
ATOM	3608	CG1	VAL	490	9.245	-6.911	31.734	1.00	0.00	3A7
ATOM	3609	CG2	VAL	490	9.143	-6.483	29.279	1.00	0.00	3A7
ATOM	3610	C	VAL	490	10.398	-4.303	32.085	1.00	0.00	3A7
ATOM	3611	O	VAL	490	11.537	-4.064	32.455	1.00	0.00	3A7
ATOM	3612	N	LEU	491	9.344	-4.289	32.927	1.00	0.00	3A7
ATOM	3613	CA	LEU	491	9.438	-4.005	34.328	1.00	0.00	3A7
ATOM	3614	CB	LEU	491	8.379	-2.956	34.702	1.00	0.00	3A7
ATOM	3615	CG	LEU	491	8.991	-1.575	35.041	1.00	0.00	3A7
ATOM	3616	CD1	LEU	491	7.898	-0.495	35.142	1.00	0.00	3A7
ATOM	3617	CD2	LEU	491	9.848	-1.615	36.322	1.00	0.00	3A7
ATOM	3618	C	LEU	491	9.183	-5.273	35.064	1.00	0.00	3A7
ATOM	3619	O	LEU	491	8.303	-6.043	34.680	1.00	0.00	3A7
ATOM	3620	N	LYS	492	9.934	-5.530	36.165	1.00	0.00	3A7
ATOM	3621	CA	LYS	492	9.855	-6.761	36.930	1.00	0.00	3A7
ATOM	3622	CB	LYS	492	11.254	-7.391	37.203	1.00	0.00	3A7
ATOM	3623	CG	LYS	492	12.184	-6.661	38.201	1.00	0.00	3A7
ATOM	3624	CD	LYS	492	12.735	-5.301	37.743	1.00	0.00	3A7
ATOM	3625	CE	LYS	492	12.568	-4.191	38.784	1.00	0.00	3A7
ATOM	3626	NZ	LYS	492	11.143	-3.831	38.925	1.00	0.00	3A7
ATOM	3627	C	LYS	492	9.148	-6.537	38.247	1.00	0.00	3A7
ATOM	3628	O	LYS	492	9.344	-7.295	39.196	1.00	0.00	3A7

ATOM	3629	N	ALA	493	8.315	-5.466	38.338	1.00	0.00	3A7
ATOM	3630	CA	ALA	493	7.783	-4.923	39.576	1.00	0.00	3A7
ATOM	3631	CB	ALA	493	7.164	-3.529	39.347	1.00	0.00	3A7
ATOM	3632	C	ALA	493	6.735	-5.798	40.223	1.00	0.00	3A7
ATOM	3633	O	ALA	493	5.607	-5.896	39.745	1.00	0.00	3A7
ATOM	3634	N	GLU	494	7.121	-6.449	41.348	1.00	0.00	3A7
ATOM	3635	CA	GLU	494	6.270	-7.353	42.081	1.00	0.00	3A7
ATOM	3636	CB	GLU	494	6.221	-8.771	41.447	1.00	0.00	3A7
ATOM	3637	CG	GLU	494	5.073	-9.691	41.921	1.00	0.00	3A7
ATOM	3638	CD	GLU	494	5.351	-10.327	43.282	1.00	0.00	3A7
ATOM	3639	OE1	GLU	494	6.416	-10.984	43.425	1.00	0.00	3A7
ATOM	3640	OE2	GLU	494	4.495	-10.171	44.193	1.00	0.00	3A7
ATOM	3641	C	GLU	494	6.833	-7.451	43.468	1.00	0.00	3A7
ATOM	3642	O	GLU	494	6.097	-7.692	44.424	1.00	0.00	3A7
ATOM	3643	N	SER	495	8.180	-7.291	43.592	1.00	0.00	3A7
ATOM	3644	CA	SER	495	9.005	-7.634	44.741	1.00	0.00	3A7
ATOM	3645	CB	SER	495	10.488	-7.267	44.500	1.00	0.00	3A7
ATOM	3646	OG	SER	495	10.963	-7.890	43.315	1.00	0.00	3A7
ATOM	3647	C	SER	495	8.584	-6.990	46.046	1.00	0.00	3A7
ATOM	3648	O	SER	495	8.318	-5.791	46.117	1.00	0.00	3A7
ATOM	3649	N	ARG	496	8.506	-7.831	47.102	1.00	0.00	3A7
ATOM	3650	CA	ARG	496	8.050	-7.468	48.419	1.00	0.00	3A7
ATOM	3651	CB	ARG	496	6.781	-8.270	48.810	1.00	0.00	3A7
ATOM	3652	CG	ARG	496	6.173	-7.918	50.178	1.00	0.00	3A7
ATOM	3653	CD	ARG	496	4.896	-8.715	50.471	1.00	0.00	3A7
ATOM	3654	NE	ARG	496	4.413	-8.345	51.841	1.00	0.00	3A7
ATOM	3655	CZ	ARG	496	3.354	-8.981	52.430	1.00	0.00	3A7
ATOM	3656	NH1	ARG	496	2.955	-8.609	53.681	1.00	0.00	3A7
ATOM	3657	NH2	ARG	496	2.696	-9.982	51.778	1.00	0.00	3A7
ATOM	3658	C	ARG	496	9.179	-7.785	49.356	1.00	0.00	3A7
ATOM	3659	O	ARG	496	9.927	-8.738	49.139	1.00	0.00	3A7
ATOM	3660	N	ASP	497	9.312	-6.984	50.445	1.00	0.00	3A7
ATOM	3661	CA	ASP	497	10.298	-7.171	51.489	1.00	0.00	3A7
ATOM	3662	CB	ASP	497	10.821	-5.830	52.089	1.00	0.00	3A7
ATOM	3663	CG	ASP	497	9.707	-4.881	52.551	1.00	0.00	3A7
ATOM	3664	OD1	ASP	497	8.940	-4.387	51.682	1.00	0.00	3A7
ATOM	3665	OD2	ASP	497	9.625	-4.629	53.783	1.00	0.00	3A7
ATOM	3666	C	ASP	497	9.711	-8.068	52.560	1.00	0.00	3A7
ATOM	3667	O	ASP	497	8.985	-7.622	53.447	1.00	0.00	3A7
ATOM	3668	N	GLU	498	10.021	-9.384	52.458	1.00	0.00	3A7
ATOM	3669	CA	GLU	498	9.495	-10.423	53.314	1.00	0.00	3A7
ATOM	3670	CB	GLU	498	8.919	-11.610	52.501	1.00	0.00	3A7
ATOM	3671	CG	GLU	498	7.782	-11.185	51.557	1.00	0.00	3A7
ATOM	3672	CD	GLU	498	7.253	-12.413	50.822	1.00	0.00	3A7
ATOM	3673	OE1	GLU	498	6.045	-12.728	50.989	1.00	0.00	3A7
ATOM	3674	OE2	GLU	498	8.050	-13.049	50.081	1.00	0.00	3A7
ATOM	3675	C	GLU	498	10.610	-10.918	54.195	1.00	0.00	3A7
ATOM	3676	O	GLU	498	11.726	-10.403	54.157	1.00	0.00	3A7
ATOM	3677	N	THR	499	10.311	-11.961	55.010	1.00	0.00	3A7
ATOM	3678	CA	THR	499	11.248	-12.606	55.905	1.00	0.00	3A7
ATOM	3679	CB	THR	499	10.615	-12.970	57.245	1.00	0.00	3A7
ATOM	3680	OG1	THR	499	9.418	-13.726	57.084	1.00	0.00	3A7
ATOM	3681	CG2	THR	499	10.291	-11.664	57.998	1.00	0.00	3A7
ATOM	3682	C	THR	499	11.798	-13.836	55.217	1.00	0.00	3A7
ATOM	3683	O	THR	499	11.311	-14.244	54.163	1.00	0.00	3A7
ATOM	3684	N	VAL	500	12.842	-14.455	55.826	1.00	0.00	3A7
ATOM	3685	CA	VAL	500	13.521	-15.621	55.300	1.00	0.00	3A7
ATOM	3686	CB	VAL	500	15.021	-15.588	55.594	1.00	0.00	3A7
ATOM	3687	CG1	VAL	500	15.312	-15.508	57.109	1.00	0.00	3A7
ATOM	3688	CG2	VAL	500	15.739	-16.768	54.903	1.00	0.00	3A7
ATOM	3689	C	VAL	500	12.857	-16.864	55.847	1.00	0.00	3A7
ATOM	3690	O	VAL	500	12.610	-16.984	57.047	1.00	0.00	3A7
ATOM	3691	N	SER	501	12.542	-17.816	54.939	1.00	0.00	3A7
ATOM	3692	CA	SER	501	11.904	-19.059	55.286	1.00	0.00	3A7
ATOM	3693	CB	SER	501	10.354	-18.950	55.320	1.00	0.00	3A7
ATOM	3694	OG	SER	501	9.744	-20.142	55.806	1.00	0.00	3A7
ATOM	3695	C	SER	501	12.356	-20.035	54.235	1.00	0.00	3A7
ATOM	3696	O	SER	501	12.898	-21.094	54.550	1.00	0.00	3A7
ATOM	3697	N	GLY	502	12.135	-19.677	52.947	1.00	0.00	3A7
ATOM	3698	CA	GLY	502	12.533	-20.464	51.805	1.00	0.00	3A7
ATOM	3699	C	GLY	502	13.587	-19.693	51.074	1.00	0.00	3A7
ATOM	3700	O	GLY	502	13.335	-18.585	50.602	1.00	0.00	3A7

```
ATOM   3701  N   ALA  503      14.804 -20.283  50.980  1.00  0.00          3A7
ATOM   3702  CA  ALA  503      15.970 -19.715  50.338  1.00  0.00          3A7
ATOM   3703  CB  ALA  503      15.775 -19.401  48.838  1.00  0.00          3A7
ATOM   3704  C   ALA  503      16.423 -18.443  51.073  1.00  0.00          3A7
ATOM   3705  OT1 ALA  503      17.016 -18.589  52.175  1.00  0.00          3A7
ATOM   3706  OT2 ALA  503      16.167 -17.323  50.557  1.00  0.00          3A7
TER    3707      ALA  503
HETATM 3708  FE  HEM  600      19.802 -26.909  18.195  1.00  0.00          HEM
HETATM 3709  NA  HEM  600      19.117 -26.973  16.343  1.00  0.00          HEM
HETATM 3710  NB  HEM  600      18.291 -25.763  18.746  1.00  0.00          HEM
HETATM 3711  NC  HEM  600      20.542 -26.830  20.017  1.00  0.00          HEM
HETATM 3712  ND  HEM  600      21.332 -28.034  17.616  1.00  0.00          HEM
HETATM 3713  C1A HEM  600      19.627 -27.653  15.248  1.00  0.00          HEM
HETATM 3714  C2A HEM  600      18.787 -27.461  14.072  1.00  0.00          HEM
HETATM 3715  C3A HEM  600      17.812 -26.605  14.439  1.00  0.00          HEM
HETATM 3716  C4A HEM  600      17.993 -26.338  15.849  1.00  0.00          HEM
HETATM 3717  C1B HEM  600      17.258 -25.288  17.964  1.00  0.00          HEM
HETATM 3718  C2B HEM  600      16.334 -24.465  18.724  1.00  0.00          HEM
HETATM 3719  C3B HEM  600      16.805 -24.471  20.029  1.00  0.00          HEM
HETATM 3720  C4B HEM  600      18.026 -25.267  20.000  1.00  0.00          HEM
HETATM 3721  C1C HEM  600      20.002 -26.220  21.122  1.00  0.00          HEM
HETATM 3722  C2C HEM  600      20.837 -26.398  22.303  1.00  0.00          HEM
HETATM 3723  C3C HEM  600      21.948 -27.105  21.896  1.00  0.00          HEM
HETATM 3724  C4C HEM  600      21.734 -27.359  20.473  1.00  0.00          HEM
HETATM 3725  C1D HEM  600      22.427 -28.419  18.358  1.00  0.00          HEM
HETATM 3726  C2D HEM  600      23.355 -29.229  17.581  1.00  0.00          HEM
HETATM 3727  C3D HEM  600      22.815 -29.362  16.350  1.00  0.00          HEM
HETATM 3728  C4D HEM  600      21.589 -28.591  16.366  1.00  0.00          HEM
HETATM 3729  CHA HEM  600      20.801 -28.392  15.257  1.00  0.00          HEM
HETATM 3730  CHB HEM  600      17.121 -25.582  16.615  1.00  0.00          HEM
HETATM 3731  CHC HEM  600      18.841 -25.488  21.097  1.00  0.00          HEM
HETATM 3732  CHD HEM  600      22.615 -28.078  19.676  1.00  0.00          HEM
HETATM 3733  CMA HEM  600      16.761 -26.027  13.539  1.00  0.00          HEM
HETATM 3734  CAA HEM  600      18.874 -28.152  12.738  1.00  0.00          HEM
HETATM 3735  CBA HEM  600      19.655 -27.341  11.731  1.00  0.00          HEM
HETATM 3736  CGA HEM  600      19.868 -28.082  10.424  1.00  0.00          HEM
HETATM 3737  O1A HEM  600      18.997 -28.897  10.031  1.00  0.00          HEM
HETATM 3738  O2A HEM  600      20.918 -27.812   9.777  1.00  0.00          HEM
HETATM 3739  CMB HEM  600      15.130 -23.749  18.107  1.00  0.00          HEM
HETATM 3740  CAB HEM  600      16.311 -23.874  21.208  1.00  0.00          HEM
HETATM 3741  CBB HEM  600      15.206 -23.138  21.387  1.00  0.00          HEM
HETATM 3742  CMC HEM  600      20.479 -25.906  23.689  1.00  0.00          HEM
HETATM 3743  CAC HEM  600      23.094 -27.556  22.589  1.00  0.00          HEM
HETATM 3744  CBC HEM  600      23.305 -27.610  23.914  1.00  0.00          HEM
HETATM 3745  CMD HEM  600      24.679 -29.779  18.033  1.00  0.00          HEM
HETATM 3746  CAD HEM  600      23.358 -30.183  15.203  1.00  0.00          HEM
HETATM 3747  CBD HEM  600      22.726 -31.591  15.127  1.00  0.00          HEM
HETATM 3748  CGD HEM  600      23.332 -32.470  14.027  1.00  0.00          HEM
HETATM 3749  O1D HEM  600      23.719 -33.625  14.347  1.00  0.00          HEM
HETATM 3750  O2D HEM  600      23.390 -32.020  12.856  1.00  0.00          HEM
END
```

Sequences :

SEQ ID N°1: P450 Nor, crystal structure 1rom

SEQ ID N°2: P450 Ery F, crystal structure 1oxa

SEQ ID N°3: P450 Terp, crystal structure 1cpt

SEQ ID N°4: P450 Cam, crystal structure 3cpp

SEQ ID N°5: P450 BM3, crystal structure 2hpd

The sequence corresponding to the PDB structure includes 471 residues. For more clarity in Figure 1, the last 12 residues have been omitted, the C-terminal part having no equivalent counterpart in the other structures aligned.

SEQ ID N°6: P450 2C5, crystal structure 1dt6

Cyp2C5 from Oryctolagus cuniculus (Rabbit), with membrane spanning residues 3-21 deleted and a 4 residue histidine tag at the C-Terminus containing additional internal mutations.

SEQ ID N°7: P450 2C5 rabbit

Sequence corresponding to the non-mutated CYP 2C5 gene from Oryctolagus cuniculus (Rabbit), consistently with SwissProt CPC5_RABIT P00179.

SEQ ID N° 8: CYP51, crystal structure 1e9x

Cyp51 from Mycobacterium tuberculosis, with a 4 residue histidine tag at the C-Terminus.

SEQ ID N°9: CYP3A1 rat

SEQ ID N°10: CYP3A3 human

Cytochrome P-450, a possible variant of CYP3A4, inducible by glucocorticoids in human liver.

SEQ ID N°11: CYP3A4 human

Numbering starts at Ala 1 (first residue Met is not included, consistently with SwissProt CP34_HUMAN P08684)

SEQ ID N°12: CYP3A5 human

SEQ ID N°13: CYP3A43 human

SEQ ID N°14: CYP3A6 rabbit

SEQ ID N°15: CYP3A7 human

SEQ ID N°16: CYP3A12 dog

SEQ ID N°17: CYP3A29 pig

SEQ ID N°18: CYP3A13 mouse

Figure 1: Structure-based alignment of human cytochromes P450 3A3, 3A4, 3A5, 3A7 and 3A43 and of selected mammalian P450 3A isozymes, with bacterial P450 crystal template structures and rabbit P450 2C5 crystal template structure.

Sequence numbering is indicated for each enzyme of the structural template and for the human 3A4 and 3A7 isozymes, as examples given in the present invention. This alignment is first based on the structural alignment of bacterial P450s and rabbit P450 2C5 derived from GOK analysis. Human P450 3A sequences were then aligned with in-house tools that locates the CSBs on the target sequence. The alignment shown outside the CSBs is not relevant, as there is no structural information available in these regions. The CSB sequences are indicated by bold uppercase characters and are highlighted in grey. Amino acids strictly conserved between CYP3A and 2C5, or between CYP3A and all the sequences of crystal structures, are highlighted in black.

Figure 2: Ramachandran plot of a lowest energy model of CYP3A4 produced by DYANA-XPLOR calculations from the six-template structural alignement.

Figure 3: view of one optimized CYP3A4 model. This figure can be replaced by the whole set of coordinates file of table 3 in the PDB format.

Figure 4: final position of testosterone into the CYP3A4 and CYP3A7 active sites after soft-restrained dynamics docking. The active sites are characterized by six Substrates Recognition Sites (SRS, after Gotoh 1989, in bold) associated to fragments of secondary element structures (in italic).

Panel 4A In CYP3A4 active site, the docked testosterone molecule is oriented so that the A steroid cycle (carrying in position 3 a carbonyl function with an oxygen atom symbolized by a large ball) is close to the heminic iron. This supports the propensity of CYP3A4 to metabolize testosterone in 6 β position as indicated by the black solid arrow.

Panel 4B In CYP3A7 active site, the docked testosterone molecule is oriented so that the D steroid cycle (carrying in position 17 a hydroxylic function with an oxygen atom symbolized by a large ball) is close to the heminic iron. This supports the propensity of CYP3A7 to metabolize testosterone in 16 α position as indicated by the black solid arrow

Figure 5: Energy profile of the soft-restrained dynamics docking of testosterone into CYP3A4 model.

Example 1: Determination of the 3D-structure of P450 3A4.

Material

The coordinates of the six P450 crystal structures: P450cam (3cpp), P450terp (1cpt), P450BM-3 (2hpd), P450eryF (1oxa), P450 nor (1rom) and P450 2C5 (1dt6) were retrieved from the Brookhaven Protein data bank. The structural alignment and the conserved regions determination were realized using the GOK software (Jean et al. 1997) running on an Octane Silicon-Graphics workstation. Structures were built using the DYANA (Güntert et al. 1997), and X-PLOR softwares (Brünger 1992). Docking studies were performed with SYBYL 6.6 (Tripos Inc.) and TRIPOS force field. The structures were analyzed using Procheck-NMR (Laskowski et al. 1993) and visualized under SYBYL 6.6 (Tripos Inc.).

Common Structural Blocks (CSB) determination.

The first key point of this homology modeling study is the identification of the structural elements (hereafter designed as CSBs for Common Structural Blocks) conserved among the family of cytochromes P450 of known 3D structures, and the localization of these elements in the target sequence. These two tasks are performed using the GOK software (Jean et al. 1997), and are well described in a forthcoming article (Minoletti et al., *Proteins, Structure, Function and Genetics*, 2002). In brief, the basic idea of CSB identification by GOK is to use an internal coordinate representation – (α,τ) in our case (another representation of ϕ, ψ and ω angles) – and to search for fragments in the six-template proteins having similar local trajectories in the internal coordinate space. GOK provides two adjustable parameters (the α-mesh and the α-margin) that define the tolerance on the comparison of the trajectories. These parameters were adjusted recursively to values ranging from 15 to 30° (α-mesh) and 1 to 3 (α-margin in mesh units). The evaluation of the quality of the match was measured using two multiple-way rmsd calculated in the cartesian coordinates space: mp-rms (the mean of all pairwise rms deviations) and s-rms (the mean of the deviations calculated with respect to a mean structure obtained from the average internal coordinates). For the different CSBs,

mp-rms value ranged between 0.3 and 4.9 Å in average, and s-rms between 0.04 and 2.4 Å.

CYP3A4 sequence alignment and evaluation of the profile

The multiple sequence alignment derived from the CSB identification was then used to build a similarity profile. The profile is defined as a position-specific scoring table created from aligned gap-free segments such as CSBs (Jean et al. 1997). The alignment then consists in a search of the best match (as per the best score) between a CSB of sequences defined structurally (*i.e.* independently of the nature of the aligned residues) and several other sequences that are well-aligned and exhibit a high sequence identity. In the P450 3A subfamily, many proteins exhibit high sequence identity. We extended our profile search program to take this information into account, i.e. to align the profile with a pre-defined multiple alignment of the cytochromes P450 3A subfamily members sequences (Gotoh 1992; Nelson et al. 1996). The similarity score was calculated using BLOSUM62 matrix (Henikoff and Henikoff 1992). The in-house tool SmartConsAlign (Atelier de Bio-informatique, Université Paris VI) described in Jean et al. 1997, allows to move the consensus matrix along the multiple sequence alignment of P450 3A family, and computes for each position a score of similarity. The best alignment found of CYP3A4 on CSBs is shown in **Figure 1**.

Once the alignment is completed, the 3D model rebuilding process can incorporate the atom Cartesian coordinates of the template structures only for amino acids located in structurally conserved regions (*i.e.* the CSBs). The coordinates of any of the template structures can be used for determining the final template. In each CSB, amino acid positions have been renumbered according to the sequence of human P450 3A4. At a given position, when residues are identical between all the template structures and the target sequence, the 3D coordinates of the reference residues are purely assigned to the modeled (target) residue. When residues differ, only the coordinates of the backbone atoms are assigned (Cα), and sometimes Cβ when they exist. Side chains are rebuilt from libraries giving the most probable rotamers for each amino acid (see below). In some cases, it was possible to superimpose the positions of carbon atoms of lateral chains up to ranks γ and δ along the sidechain, thus explicitly defining a unique rotamer.

For amino acids located outside the CSBs (structurally variable zones that include generally loops), the rebuilding is more complex, and can be done only after rebuilding of structurally conserved zones. In the multiple structural alignment (**Figure 1**), the regions separating the CSBs bring no structural information at all. Short loops are rebuilt entirely, since solutions of acceptable geometry for atoms are in limited number, *i.e.* the lowest energy drives the selection of the good geometry. For longer segments, various structures are provided by the constrained minimization runs, and a manual selection is operated.

Constraints derivation and rebuilding

A strategy inspired of the techniques commonly used to built structures from NMR data (Patard et al. 1996) is applied. The main idea is to express all available information issued from the comparison of the templates in term of geometrical constraints (distances and angles). Each constraint will be defined as an interval (for a given pair of atoms, this is the average of the six atom-atom distances found in the template structures +/- the standard deviation), similarly to the strategy developed by Havel and Snow (Havel and Snow 1991). However, the number of constraints corresponding to all atom-atom distances, for example, would be prohibitive for a protein of the size of the P450 (around 1,000,000 inter-residual distances if we consider 250 conserved residues and an average of four atoms per residues). Previous NMR studies (Patard et al. 1996) have shown that local constraints are sufficient to allow a correct reconstruction of a structure. This reduces drastically the number of constraints needed, and increases the flexibility of the model. In addition, similarly to what is done in protein structure determination by NMR, we can build a family of structures instead of a single model. This allows an easier analysis of the well or less well-predicted regions. This is also an advantage for the analysis of the side-chain positions, particularly in prevision of a substrate docking study. Finally, the loops are passively reconstructed with the rest of the structure. The only specific information we have introduced in variable regions was to guide all their residues to an allowed region of the Ramachandran diagram. Indeed, analysis of well-defined structures shows that nearly all residues, including those of the loops, should belong to an allowed region. The lower the proportion of residues

found outside the allowed Ramachandran regions, the better the structure is. This criterion of quality has been applied to derive the model described herein.

Accordingly, we retained for model rebuilding all the distance and angle intervals corresponding to the following principles:

- all distances for which the lower boundary was less than 8 Å. This cutoff is totally sufficient to ensure, at least, the formation of the local structure elements. Such a cutoff is relatively high and thus costly in terms of size of constraints file, but proved necessary to ensure good results for the P450s. This may be due to the fact that P450 enzymes are mostly formed of α-helices, the average distance between two helices being larger than between two adjacent β-strands. In addition, the percentage of residues located outside CSBs is rather high in the structural alignment of P450s, and a better convergence can be obtained only at the expense of a high number of rebuilding distance constraints.
- all the distances involving at least one side-chain atom, to preserve the spatial arrangement between CSBs
- finally, all the distances involving atoms of the heme group, to fix as much as possible the neighborhood of the iron atom.

The total number of distance constraints was, in these conditions, equal to 58506.

Similarly, angular constraints were calculated in each building block. A CSB is indeed defined as a conserved trajectory in the φ,ψ coordinates space (or α,τ). Thus, dihedral angles φ and ψ of all residues located in CSBs can be defined as constraints, given by the average values of corresponding φ,ψ angles in the six templates +/- the standard deviation. To these backbone dihedral angles, can be added the side chains torsion angles χ_1, χ_2 whenever possible, as determined by the rotamer selection. The total number of dihedral angle constraints was, in these conditions, equal to 761.

Rotamer selection

In proteins, the preferential orientation of the side chain (60°, -60°, 180°) depends on the local conformation of the residue, and thus on the nature of the secondary structure in which the residue is involved. According to the rotamer library built by Karplus and coll. (Dunbrack and Karplus 1993), to a given (φ, ψ) couple in the

Ramachandran diagram can be associated a specific rotamer for each type of residue. These tables have been used to determine the most probable rotamer for each residue located in CSB, except when there are conserved atoms in the side chain that assign unambiguously a rotamer (χ_1, χ_2). The selected (χ_1, χ_2) couples were included in the above-mentioned set of angle 761 dihedral constraints.

Structure calculation and optimization

We used a procedure similar to structure calculation starting from NMR constraints. A first set of structures was calculated using the DYANA software (Güntert et al. 1997) and the 58506 distance and 761 angular constraints. Families of structures are generated. The energy of each structure is minimized with the procedure vtfmin in DYANA.

Due to the size and the amount of loops in the molecule, some structures presented topological defects and were discarded. The others were further optimized by using the X-PLOR software. A set of constraints was added at this stage in order to guide the loop residues to the nearest allowed region in the Ramachandran diagram. The topology and parameter files of CHARMM22 were used. The electrostatic term was turned off.

The DYANA software is unable to deal with disconnected objects. A new residue type was, thus, added to the standard amino acid library to take into account the the presence of the heme. This residue was obtained by combining the heme to a cysteine and was inserted at position 441 in the sequence of the protein (**Figure 1**).

Description of the CYP3A4 Model

We rebuilt a model of the protein depleted of its first 50 residues (N-terminal domain). This segment is highly hydrophobic, and supposed to form the anchor of the protein in the membrane. There is no structural information about this putative transmembrane domain, and this segment was thus not incorporated into the modeling process, and in the final model. Such a "free" segment (with no constraints) would perturbate the convergence of computation or the stability of the whole rebuilt structure.

The quality of the various structures optimized under XPLOR was checked for the stereochemical quality (backbone and side chain conformation) by PROCHECK

(Laskowski et al. 1993). The Ramachadran plot shows that our six-template approach generated converging models, possessing the same fold. The lowest energy models had 73% of their non-glycine and non-proline residues with φ, ψ conformation in the most favoured regions of the Ramachandran plot (core region), 20% in additional allowed regions, and 5% in the generously allowed regions. Only 2.3% (9 residues) had their φ, ψ conformation in disallowed regions (**Figure 2**). The total number of residues in the model is 452; which 399 are non-glycine and non-proline residues, and number of residues in the native sequence is 502.

When compared to the CYP2C5 crystal structure, it can be noticed that the CYP3A4 model exhibits a good 3D similarity in the global fold than expected, since this structure counts only for one in the six-template approach. This proves that in this approach, there is no "averaging" effect, *i.e.* the mammalian structure had a decisive influence over the five bacterial (and fungus) templates. Our final fold of CYP3A4 is very consistent with a mammalian one, despite the fact that it has been rebuilt by using the structural information contained in non-mammalian cytochromes P450.

The active site is delimited by the six substrate recognition sites (SRS) that have been first identified and described by Gotoh (Gotoh 1992) from the unique structure available in the early 1990s ($P450_{cam}$), and that are today commonly accepted for depicting substrate recognition by various cytochromes P450 (especially from the family 2, but extended to other P450 families). These sites are associated with the active site and are located in the less conserved regions of the CYPs, thus possibly accounting for the various substrate specificity among P450s. When comparing our various optimized structures, it is found that SRS1 (100-125, includes helix B), SRS 2 (205-218, includes C-terminus of helix F), and SRS3 (237-249, includes N-terminus part of helix G) are located in less-defined regions, with significant variability in spatial position (flexibility). These regions correspond also to parts of the sequence that are less well-aligned. At the opposite, the SRS4 (295-320, central part of helix I), SRS5 (363-380, C-term of helix K and β-sheet β1-4) and SRS6 (470-490, β-sheets β4-1 and β4-2) are well-defined fragments of the structures. SRS4 and SRS5 segments in particular are correlated to regions in the sequence that are unequivocally aligned.

The only model structure of CYP3A4 that has been described in the literature and that we can handle for structural comparison, is that of Szklarz and Halpert, derived from a multiple-template approach (four-bacterial template) (Szklarz and Halpert 1997). Roughly, the same secondary structures are identified, but we found divergences in SRS location between their model and those derived from the present approach. SRS4 and SRS5 match well, but SRS2 is shifted (divergence in the position of helix F along the sequence), while SRS1 (helix B'), SRS3 (helix G) and SRS6 (sheet β4) are more notably displaced. The loops connecting the secondary structures of these SRS significantly disagree. These differences are likely to issue from a wrong alignment with the crystal P450 structures in the model of Szklarz and Halpert.

Example 2: Determination of the 3D-structure of P450 3A7.

The model rebuilding of CYP3A7 was performed according to the techniques described above in example 1 for CYP3A4, except that we used a restrained set of four-template structures, still including the mammalian CYP2C5, in order to test the robustness of the modeling approach. Below are pointed out only the differences in input data and the results relevant to CYP3A7.

Material

The coordinates of the four P450 crystal structures: P450BM-3 (2hpd), P450eryF (1oxa), P450 51-like from *Mycobacterium tuberculosis* (1e9x) and P450 2C5 (1dt6) were retrieved from the Brookhaven Protein data bank and used as initial template for GOK analysis.

Common Structural Blocks (CSB) determination.

The GOK parameters were adjusted recursively to values ranging from 10 to 30° (α-mesh) and 1 to 3 (α-margin in mesh units). Occasionally, the α-mesh value was pushed up to 60° to refine some local structured loops (DE loop, HI loop) or short helices (such as J'). 27 CSBs have been identified. New CSBs were detected: the block 7* (between blocks 6 and 7A), the block 7B* (between 7B and 8) and the block 7C (between 7B* and 8). For the different CSBs, mp-rms value ranged between 0.12 and 4.57 Å in average.

The best alignment found of CYP3A7 on CSBs is shown in **Figure 1**. On the 459 residues comprised in the model structure (the protein was rebuilt depleted of its first 44 residues from the N-terminal domain), 337 residues were found located in CSBs, i.e. 73% of residues belong to structurally conserved regions of the four-template set.

Constraints derivation and rebuilding

With a larger cutoff (12 Å), we obtained around 73000 distance constraints, and 900 dihedral constraints.

The residue covalently linked to the heme group is at position 442 in the sequence of the protein (**Figure 1**).

Description of the CYP3A7 model

The four-template approach generated converging models, possessing the same fold. The PROCHECK analysis for structure quality assessment for the lowest energy models showed 74.4% of their non-glycine and non-proline residues with φ, ψ conformation in the most favoured regions of the Ramachandran plot (core region), 18.2% in additional allowed regions, and 4.7% in the generously allowed regions. 2.7% (11 residues) had their φ, ψ conformation in disallowed regions. The total number of residues in the model is 459; which 407 are non-glycine and non-proline residues, and number of residues in the native sequence is 503.

A closer inspection of the structure, and after the results of dynamics docking experiments (see below), revealed that several hydrogen bonds can hinder the main access to the active site. Thus, key residues that are likely to be involved in the recognition and admission of the substrate are **Q79; F102; R105; R106; F108; F248; F304 and E374, and additionally C98 and C377 (Figure 4B)**. More specifically, R105, R106, Q79 and E374 can establish mutual hydrogen bonds in one of the access channels, and are thus involved in the access of the substrate towards the active site.

Example 3: Docking Strategy

Our aim in this example was to obtain the different positions of the known substrates of CYP3A in the active site, consistent with the oxidation sites and

biochemical differences among the CYP3A isoforms. Considering the fact that the heme-binding site is deeply buried in the protein structure, and thus the selection and the pathway of the substrates within the enzyme structure are strongly dependent on the various possibilities of structure opening, we implemented a special approach more appropriate to flexible structures, hereafter referred as "restrained dynamics docking" or "soft-restrained dynamics docking". This technique employs constrained molecular dynamics simulations, where the only constraints are heme-substrate distances. The successive steps are:

Conversion of the PDB XPLOR file in PDB for SYBYL file

The optimized structures with XPLOR (PDB format) are visualized with the SYBYL 6.6 software (Tripos Inc.), which implies a conversion of the file (atoms types correction) so as to make it compatible and exploitable in the constrained dynamics which will be performed with SYBYL.

Stabilization of the P450 3A4 model generated under XPLOR

Then, we do agregate N°1 (in the meaning of SYBYL) with all the $NC_{\alpha}CO$ atoms of the peptide backbone of the protein. The structure is relaxed with a dynamic of 10ns at 100K followed by a minimization of 100 steps. Agregate N°1 is then deleted.

We do agregate N°2 constituted of the protein C_{α} only. The protein relaxation is reiterated with a dynamic of 10 ns at 100K and a minimization of 100 steps. Agregate N°2 is then deleted.

The all protein is then relaxed with a first dynamic of 1ns at 100K, followed by a dynamic of 1ns at 200K and a dynamic of 10ns at 300K. We terminate with a minimization of 100 steps.

Restrained dynamics docking of the substrate (example: testosterone)

We do agregate N°3 constituted of all atoms outside a sphere of 20Å around the C_{α} of residues constituting the heart of the B' loop. We also add heminic iron to this aggregate.

The substrate is placed inside the protein, at around 30Å from the heminic iron and next to SRS1 and SRS5 sites. The substrate is placed so that the contraints between

the heminic iron and the substrate backbone go between SRS1, SRS5 and SRS3. Thus, for testosterone docking, we establish 4 distance contraints (limit below 3Å, above 10Å) between heminic iron and C3, C8, C10 and C13 carbons with a constraint of 2 kcal/Å on the entire structure so as to avoid to favour the approach of one part of the substrate more than the other.

We begin to perform a dynamic without contraints of the entire system at 20 K during 2ns to stabilize the system, then we perform a dynamic under contraints at 20 K during 5ns. We observe that the substrate worms between SRS1, SRS3 et SRS5 to reach a position at the vicinity of heminic iron. We terminate with a dynamic without contraints at 300 K to relax the system and we realize a minimization of 1000 steps.

Results

We found that the testosterone molecule is positioned at the vicinity of heminic iron in such way that the C6 of testosterone be at 4.9Å of the iron, which is compatible with the hydroxylation of this compound to give 6β-hydroxy-testosterone (**Figure 4A**).

Minimizations and dynamics with the SYBYL software are performed with the Tripos force field following the parameters: dielectric constant equal to 1 and distance-dependent, minimization method of POWELL, a minimum gradient of $0.05 kcal.mol^{-1}.Å^{-1}$, electrostatics charges calculated according to the Gasteiger-Hückel method, and a NB cutoff of 8.0Å (non-bond energies). The energetic diagram of dynamic docking of testosterone is shown in **Figure 5**.

Interest of this docking strategy:

Most P450 isozymes recognize only one substrate (for specific catalysis in a metabolic pathway), or a very limited number of substrates, all chemically closely related. At the contrary, CYP 3A isozymes are known to recognize a large palette of substrates, and are also capable of multiple binding in the active site, up to three molecules in the vicinity of the heme, according to the model developed by Hosea et al. 2000. Multiple pharmacophoric behavior (Ekins et al. 2003), as well as allosteric or synergistic effects, characterize the members of this P450 subfamily.

The docking strategy described above can be easily extended to different binding and metabolism scenario.

For example, the docking of two or three testosterone molecules, or of two testosterone molecules and one alpha-naphtoflavone molecule (αNF) can be simulated in the following manner:

- In a first step, a testosterone molecule is dynamically docked under constraints, and then released of its constraints to freely evolve in the active site and find a first bound equilibrium position.
- In a next step, an external testosterone is presented, at the same entrance of the protein structure or in the vicinity of another access channel, and then dynamically docked under constraints. The system first evolves under constraints applied to the second molecule, and can be released for a subsequent free MD simulation of the two molecules bound in the active site. One can see the first bound molecule (testosterone or another substrate) to be re-oriented under the effect of the second docking, simulating a situation of cooperativity.
- Similarly, the second molecule docked can be different from the first bound, *e.g.* . a first testosterone bound to the active site followed by the docking of an αNF molecule, or the reverse situation.
- One can combine of course the possibilities: for example, two molecules (identical or of different chemical nature) are docked following the two steps above, and then, after stabilization around an equilibrium position, a third molecule is introduced under constraints, and then released from its constraints to let the system evolving towards a favorable energetic conformational state. In this way, two αNF and one testosterone or one αNF and two testosterone can be docked.

Of course, not only substrates can be docked, but also inhibitors. The docking procedure above can help to measure the potential inhibitory power of a molecule, for example a compound comprising an imidazole group. A first step would include a standard constrained dynamic docking of the potential inhibitor, followed by a free MD simulation (constraints are released when the inhibitor is in the active site), or by a specifically-constrained MD simulation where the imidazole group is confined in the vicinity of the heminic iron by using an additional distance constraint Fe-imidazole. In a following step, a second substrate is dynamically docked under constraints from the exterior, and one can determine in what

conditions the second molecule can chase the first one from its binding position. The strength of the additional constraint can be a measurement of the inhibitory potential.

Correspondingly, the exit pathway of the metabolites can be explored by simulating the exit of the molecule bound to the active site, using either free MD simulation (if the chemical nature of the transformed molecule allows an energetical instability), or using inverted constraints, *i.e.* soft distance constraints (between an external point and the bound molecule) that help to expel out the metabolite. Additionally, the best exit pathway can be deduced from the most favored energy profiles.

References

Aninat, C., Hayashi, Y., André, F., and Delaforge, M. 2001. Molecular requirements for inhibition of cytochrome p450 activities by roquefortine. *Chem Res Toxicol.* **14**: 1259-1265.

Brünger, A.T. 1992. X-PLOR Version 3.1. A system for X-ray crystallography and NMR. version 3.1. Yale University Press, New Haven, CT, USA.

Chothia, C., and Lesk, A.M. 1986. The relation between the divergence of sequence and structure in proteins. *Embo J* **5**: 823-826.

Cupp-Vickery, J.R., and Poulos, T.L. 1995. Structure of cytochrome P450eryF involved in erythromycin biosynthesis. *Nature Struct. Biology* **2**: 144-153.

Delaforge, M., André, F., Jaouen, M., Dolgos, H., Benech, H., Gomis, J.M., Noël, J.P., Cavelier, F., Verducci, J., Aubagnac, J.L., and Liebermann, B. 1997. Metabolism of tentoxin by hepatic cytochrome P-450 3A isozymes. *Eur J Biochem.* **250**: 150-157.

Delaforge, M., Bouillé, G., Jaouen, M., Jankowski, C.K., Lamouroux, C., Bensoussan, C. 2001. Recognition and oxidative metabolism of cyclodipeptides by hepatic cytochrome P450. *Peptides* **22**: 557-565.

Domanski, T.L., Liu, J., Harlow, G.R., and Halpert, J.R. 1998. Analysis of four residues within substrate recognition site 4 of human cytochrome P450 3A4: role in steroid hydroxylase activity and alpha-naphthoflavone stimulation. *Arch. Biochem. Biophys.* **350**: 223-232.)

Dunbrack, R.L.J., and Karplus, M. 1993. Backbone-dependent rotamer library for proteins- Application to side chain prediction. *J. Mol. Biol.* **230**: 543-574.

Ekins, S., Stresser, D.M., and Williams, J.A. 2003. In vitro and pharmacophore insights into CYP3A enzymes. *Trends Pharmacol Sci.* **24**: 161-166.

Ferenczy, G., and Morris, G. 1989. The active site of cytochrome P450 nifedipine oxidation model building study. *J. Mol. Graph.* **7**: 206-211.

Gellner, K., Eiselt, R., Hustert, E., Arnold, H., Koch, I., Haberl, M., Deglmann, C.J., Burk, O., Buntefuss, D., Escher, S., Bishop, C., Koebe, H.G., Brinkmann, U., Klenk, H.P., Kleine, K., Meyer, U.A., and Wojnowski, L.

2001. Genomic organization of the human CYP3A locus: identification of a new inducible CYP3A gene. *Pharmacogenetics.* **11:** 111-121.

Gotoh, O. 1992. Substrate Recognition Sites in Cytochrome-P450 Family-2 (CYP2) Proteins Inferred from Comparative Analyses of Amino Acid and Coding Nucleotide Sequences. *Journal of Biological Chemistry* **267:** 83-90.

Guenguerich, F. P. 1995. Human cytochrome P450 enzymes. In "Cytochrome P450: structure, mechanism and biochemistry", P. R. Ortiz de Montellano Ed., Plenum Press, pp. 537-574, New York.

Güntert, P., Mumenthaler, C., and Wüthrich, K. 1997. Torsion angle dynamics for NMR structure calculation with the new program DYANA. *J. Mol. Biol.* **273:** 283-298.

Hasemann, C.A., Ravichandran, K.G., Peterson, J.A., and Deisenhofer, J. 1994. Crystal Structure and Refinement of Cytochrome P450(Terp) at 2.3 Å Resolution. *J. Mol. Biol.* **236:** 1169-1185.

Havel, T.F., and Snow, M.E. 1991. A new method for building protein conformations from sequence alignments with homologues of known structure. *J Mol Biol* **217:** 1-7.

Henikoff, S., and Henikoff, J.G. 1992. Amino acid substitution matrices from protein blocks. *Proc Natl Acad Sci U S A* **89:** 10915-10919.

Hilbert, M., Bohm, G., and Jaenicke, R. 1993. Structural relationships of homologous proteins as a fundamental principle in homology modeling. *Proteins* **17:** 138-151.

Hosea, N.A., Miller, G.P., and Guengerich, F.P. 2000. Elucidation of distinct ligand binding sites for cytochrome P450 3A4. Biochemistry **39**: 5929-5939.

Inoue, E., Takahashi, Y., Imai, Y., Kamataki, T. Development of bacterial expression system with high yield of CYP3A7, a human fetus-specific form of cytochrome P450. Biochem Biophys Res Commun. 2000 Mar 16;269(2):623-7.

Jean, P., Pothier, J., Dansette, P.M., Mansuy, D., and Viari, A. 1997. Automated multiple analysis of protein structures: application to homology modeling of cytochromes P450. *Proteins* **28:** 388-404.

Karplus, M. and McCammon, J.A. 2002. Molecular dynamics simulations of biomolecules. *Nat. Struct. Biol.* **9:** 646-652.

Koch, I., Weil, R., Wolbold, R., Brockmoller, J., Hustert, E., Burk, O., Nuessler, A., Neuhaus, P., Eichelbaum, M., Zanger, U., Wojnowski, L. 2002. Interindividual variability and tissue-specificity in the expression of cytochrome P450 3A mRNA. *Drug Metab Dispos.* **30:** 1108-1114.

Laskowski, R.A., MacArthur, M., Moss, D.S., and Thorntorn, J. 1993. PROCHECK: a program to check the stereochemical quality of protein structures. *J. Appl. Crystallog.* **26:** 283-291.

Lewis, D.F.V. 2001. *Guide to cytochrome P450 structure and function.* Taylor & Francis, New York, pp. cm.

Lewis, D.F.V., Eddershaw, P.J., Goldfarb, P.S., and Tarbit, M.H. 1996. Molecular modelling of CYP3A4 from an alignment with CYP102: Identification of key interactions between putative active site residues and CYP3A-specific chemicals. *Xenobiotica* **26:** 1067-1086.

Loiseau, N. 2002. Conception d'analogues structuraux d'un cyclopeptide modèle: étude du mode de reconnaissance moléculaire par trois systèmes enzymatiques membranaires. Université Paris XI, Orsay.

Nelson, D.R. 1999. Cytochrome P450 and the individuality of species. *Arch Biochem Biophys* **369:** 1-10.

Nelson, D.R., Koymans, L., Kamataki, T., Stegeman, J.J., Feyereisen, R., Waxman, D.J., Waterman, M.R., Gotoh, O., Coon, M.J., Estabrook, R.W., et al. 1996. P450 superfamily: Update on new sequences, gene mapping, accession numbers and nomenclature. *Pharmacogenetics* **6:** 1-42.

Park, S.Y., Shimizu, H., Adachi, S., Nakagawa, A., Tanaka, I., Nakahara, K., Shoun, H., Obayashi, E., Nakamura, H., Iizuka, T., et al. 1997. Crystal structure of nitric oxide reductase from denitrifying fungus Fusarium oxysporum. *Nature Struct. Biology* **4:** 827-832.

Patard, L., Stoven, V., Gharib, B., Bontems, F., Lallemand, J.Y., and De Reggi, M. 1996. What function for human lithostathine? Structural investigations by three-dimensional structure modeling and high-resolution NMR spectroscopy. *Protein Eng* **9:** 949-957.

Podust, L.M., Poulos, T.L., and Waterman, M.R. 2001. Crystal structure of cytochrome P450 14alpha -sterol demethylase (CYP51) from

Mycobacterium tuberculosis in complex with azole inhibitors. *Proc Natl Acad Sci U S A* **98:** 3068-3073.

Poulos, T.L., Finzel, B.C., Gunsalus, I.C., Wagner, G.C., and Kraut, J. 1985. The 2.6 Å crystal structure of Pseudomonas putida cytochrome P450cam. *J. Biol. Chem* **260:** 16122-16130.

Raag, R., and Poulos, T.L. 1989. Crystal structure of the carbon monoxide-substrat-cytochrome P-450cam ternary complex. *Biochemistry* **28:** 7586-7592.

Ravichandran, K.G., Boddupalli, S.S., Hasemann, C.A., Peterson, J.A., and Deisenhofer, J. 1993. Crystal Structure of Hemoprotein Domain of P450BM-3, a Prototype for Microsomal P450's. *Science* **261:** 731-736.

Sanchez, R., Pieper, U., Melo, F., Eswar, N., Marti-Renom, M.A., Madhusudhan, M.S., Mirkovic, N., and Sali, A. 2000. Protein structure modeling for structural genomics. *Nat Struct Biol* **7 Suppl:** 986-990.

Schmiedlin-Ren, P., Edwards, D.J., Fitzsimmons, M.E., He, K., Lown, K.S., Woster, P.M., Rahman, A., Thummel, K.E., Fisher, J.M., Hollenberg, P.F., and Watkins, P.B. 1997. Mechanisms of enhanced oral availability of CYP3A4 substrates by grapefruit constituents. Decreased enterocyte CYP3A4 concentration and mechanism-based inactivation by furanocoumarins. *Drug Metab Dispos.* **25:** 1228-1233.

Szklarz, G.D., and Halpert, J.R. 1997. Molecular modeling of cytochrome P450 3A4. *J Comput Aid Molec Design* **11:** 265-272.

Westlind-Johnsson, A., Malmebo, S., Johansson, A., Otter, C., Andersson, T.B., Johansson, I., Edwards, R.J., Boobis, A.R., and Ingelman-Sundberg, M. 2003. Comparative analysis of CYP3A expression in human liver suggests only a minor role for CYP3A5 in drug metabolism. *Drug Metab Dispos.* **31:** 755-761.

Williams, P.A., Cosme, J., Sridhar, V., Johnson, E.F., and McRee, D.E. 2000. Mammalian microsomal cytochrome P450 monooxygenase: structural adaptations for membrane binding and functional diversity. *Molecular Cell* **5:** 121-131.

Williams, J.A., Ring, B.J., Cantrell, V.E., Jones, D.R., Eckstein, J., Ruterbories, K., Hamman, M.A., Hall, S.D., and Wrighton, S.A. 2002. Comparative

metabolic capabilities of CYP3A4, CYP3A5, and CYP3A7. *Drug Metab Dispos.* **30**: 883-891.

Wrighton, S.A., Schuetz, E.G., Thummel, K.E., Shen, D.D., Korzekwa, K.R., Watkins, P.B. 2000. The human CYP3A subfamily: practical considerations. *Drug Metab Rev.* **32**: 339-361.

Yano, J.K., Koo, L.S., Schuller, D.J., Li, H., Ortiz de Montellano, P.R., and Poulos, T.L. 2000. Crystal structure of a thermophilic cytochrome P450 from the archaeon Sulfolobus solfataricus. *J Biol Chem* **275**: 31086-31092.

Claims

1. A method for designing a 3-dimentional (3-D) model of a protein, the 3-D representation of at least three family members has already been experimentally obtained, [said 3-D representation presenting similarities], comprising the steps of:

a. identification of common structural blocks (CSBs) among said members of said family,

b. alignment of the amino-acids primary sequence of said family members according to said structural similarities, represented by said CSBs, in order to obtain a first alignment,

c. alignment of said protein as compared on said first alignment, in order to obtain a second alignment, wherein:

i. alignment of said protein is performed in order to optimize the amino-acids alignment between said protein and said first alignment,
when one or more consensus amino-acid exists in said aligned CSBs in said first alignment, and in the amino-acid sequence of said protein, said consensus amino-acids are anchors of said second alignment,

ii. no insertion or deletion of amino-acids can be performed in the aligned CSBs, wherein insertion or deletions are possible in out-of-block regions, if better to align the primary amino-acids sequences,

d. definition of the 3-D structure of CSBs of said protein, according to the 3-D structure of the CSBs of said family members,

e. definition of the global constraints (distance and angular constraints) derived from the comparisons of the structural templates in CSBs, and definition of the local constraints (distance and angular constraints) for the atoms of residues that are not structurally determined after step d. (that are not in the CSBs),

f. selection of rotamers,

g. determination of a family of 3-D model structures of said protein, taking into account said 3-D structure of CSBs obtained in step **d.**, said global and local constraints defined in step **e.**, and said rotamers defined in step **f.**,

h. optimization of said family of 3-D models obtained in step **g.**, by

i discarding structures that present topological defects, and

ii recalculating 3-D structures by taking electrostatic forces into account,

and performing the method again from step **c.** downward, with modifications in the alignment between the primary sequence of said protein and said first alignment, when the obtained model structures do not satisfactorily account for known mutations having biological effects.

2. The method of claim 1, wherein said 3-D representation of family members has been obtained by crystallography or NMR.

3. The method of claim 1, wherein said alignment of said CSBs in step **b.** is performed by use of the GOK software.

4. The method of claim 1, wherein said alignment of said CSBs in step **c.** is performed by use of the GOK software.

5. The method of claim 1, wherein step **d.** is performed according to the following rules:

i. at a given position, when residues are identical between all the template structures and the target sequence, the 3D coordinates of the reference residues are purely assigned to the target residue,

ii. When residues differ, only the coordinates of the backbone atoms are assigned (Cα), and sometimes Cβ or Cγ when they exist.

6. The method of claim 1, wherein said definition of local constraints in step **e.** is performed by analysis of the allowed regions in Ramachandran diagram.

7. The method of claim 1, wherein global and local constraints are selected in step **e.** by the following rules:

i. all distances for which the lower boundary was less than 8 Å.

ii. all the distances involving at least one side-chain atom, to preserve the spatial arrangement between CSBs

iii. all the distances involving atoms of any active group such as an heme group, to fix as much as possible the neighborhood of said active group, such as an iron atom.

8. The method of claim 1, wherein angular constraints are selected in step **e.** by the following rule:

i. dihedral angles ϕ and ψ of all residues located in CSBs are defined as constraints, given by the average values of corresponding ϕ, ψ angles in said family members +/- the calculated standard deviation.

9. The method of claim 1, wherein said rotamers in step **f.** are selected from the couples according to the tables of Dunbrack and Karplus, where the choice of rotamers of a given amino acid is guided by the most favored zones in Ramachandran χ_1, χ_2 maps.

10. The method of claim 1, wherein said step **g.** is performed with the DYANA software.

11. The method of claim 1, wherein said optimization in step **h.** comprises the use of the X-Plor software, as described in A. T. Brunger, X-PLOR, version 3.1.

12. The method of claim 1, wherein said protein is a cytochrome P450 subfamily 3A comprising mammal and human cytochromes P450 3A.

13. The method of claim 12, wherein said mammal cytochrome P450 3A is selected from the group comprising CYP3A6 (SEQ ID N°14), CYP3A12 (SEQ ID N°16), CYP3A29 (SEQ ID N°17) and CYP3A13 (SEQ ID N°18).

14. The method of claim 12, wherein said human cytochrome P450 subfamily 3A is selected from the group comprising CYP3A4 (SEQ ID N°11), CYP3A7 (SEQ ID N°15), CYP3A5 (SEQ ID N°12) and CYP3A43 (SEQ ID N°13).

15. The method of claims 1 and 14, wherein said family members that are used for performing said first alignment for designing a 3-D model of CYP3A4 are chosen from Nor (SEQ ID N° 1), Ery F (SEQ ID N° 2), terp (SEQ ID N° 3), Cam (SEQ ID N° 4), BM3 (SEQ ID N° 5) and 2C5 (SEQ ID N° 6).

16. The method of claims 1 and 14, wherein said family members that are used for performing said first alignment for designing a 3-D model of CYP3A7 are chosen from Ery F (SEQ ID N° 2), BM3 (SEQ ID N° 5), CYP51 (SEQ ID N° 8) and 2C5 (SEQ ID N° 6).

17. A 3-D structure model of a protein, obtained by the method according to claim 1.

18. The model of claim 17, wherein said protein is a cytochrome P450 subfamily 3A comprising mammal and human cytochromes P450 3A.

19. The model of claim 18, wherein said mammal cytochrome P450 3A is selected from the group comprising CYP3A6 (SEQ ID N°14), CYP3A12 (SEQ ID N°16), CYP3A29 (SEQ ID N°17) and CYP3A13 (SEQ ID N°18).

20. The model of claim 18, wherein said human cytochrome P450 subfamily 3A is selected from the group comprising CYP3A4 (SEQ ID N°11), CYP3A7 (SEQ ID N°15), CYP3A5 (SEQ ID N°12) and CYP3A43 (SEQ ID N°13).

21. The model of claim 20, wherein said protein is a cytochrome P450 3A4 or 3A7.

22. The model of claim 21, wherein the residues C97; R104; F101; F107; F247; F303 and C376 are involved in the CYP 3A4 for the recognition and uptake of the substrate at the entry site, and its binding into the active site.

23. The model of claim 20, wherein the residues Q79; F102; R105; R106; F108; F248; F304 and E374 are involved in the CYP 3A7 for the recognition and uptake of the substrate at the entry site, and its binding into the active site.

24. The model of claim 22, having the 3-D atomic coordinates of Table 3.

25 The model of claim 23, having the 3-D atomic coordinates of Table 4.

26. A method for designing a protein, biological functions of which are altered, comprising:

a) obtaining a 3-D model of said protein by the method of claim 1,

b) analyzing said model of step **a.**, and determining the amino-acids that are putatively involved in the biological functions of said protein,

c) changing said amino-acids by mutating the corresponding nucleotides on the nucleic acid sequence coding for said protein, in order to obtain a mutated protein having altered properties.

27. A computer-assisted method for performing restrained dynamics docking of a substrate on an enzyme, a 3-D structure of which is available, comprising the steps of

j. determining a force field, and independently simulating the presence of said enzyme in said force field,

k. minimizing the potential energy (Ep) linked to said force field of said 3-D structure, wherein the spatial position of some atoms of said enzyme is fixed, and wherein the other atoms are mobile, by allowing mobility of the mobile atoms, by

i. simulating an increase in temperature (in order to give kinetic energy),

ii. and minimizing the potential energy by re-specifying the temperature as 0 Kelvin (K)

l. optionally repeating step k in order to obtain other Ep minima, wherein said Ep minima are such that the structure of the protein remains folded,

m. minimizing Ep in said force field of said 3-D structure, wherein all the atoms of the protein are mobile, by

i. simulating an increase in temperature (in order to give kinetic energy), and

ii. minimizing the potential energy by re-specifying the temperature as 0 Kelvin (K)

n. simulating, at 0 K the presence of said substrate next to said enzyme,

o. optionally generating a molecular dynamics simulation on said substrate and enzyme (simulating an increase in temperature, in order to allow mobility of the atoms)

p. generating some constraints to said substrate, in order to impose that it has interaction with said enzyme,

q. generating a molecular dynamics simulation on said substrate and enzyme, with said constraints imposed in step **p.**,

r. optionally, generating a molecular dynamics simulation on said substrate and enzyme without said constraints of step **p.**

28. The method of claim 27, wherein said fixed atoms in step **k.** are the backbone atoms N-Cα-CO in the first minimization step and only Cα in subsequent minimization steps.

29. The method of claim 27, wherein said kinetic energy is simulated by temperature increase to about 100 K for about 5-20 ns.

30. The method of claim 27, wherein said force field in step **j.** comprises forces linked to

a. the distance between atoms,

b. the angles of valence,

c. the dihedral angles,

d. the deformation with regard to planar geometry,

e. the electrostatic field,

f. the Van der Waals forces,

g. hydrogen bonds.

31. The method of claim 27, wherein said constraints in step **p.** are attraction constraints to force said substrate in the active site, and wherein said constraints are not prejudiced to the exact spatial conformation of the substrate in the active site.

32. The method of claim 31, wherein said constraints are final distance constraints between some atoms of said substrate and some atoms of amino-acids present in said active site.

33. The method of claim 27, wherein step **o.** is performed with a simulated temperature of between about 15 and 50 K.

34. The method of claim 27, wherein step **q.** is performed with a simulated temperature of between about 15 and 50 K.

35. The method of claim 27, wherein step **r.** is performed with a simulated temperature of between about 200 and 350 K.

36. The method of claim 27, wherein said enzyme is a cytochrome P450 subfamily 3A comprising mammal and human cytochromes.

37. The method of claim 36, wherein said cytochrome is a cytochrome P450 3A4, and said structure is the structure obtained by the method of claim 15, in particular the model structure of claim 22.

38. The method of claim 36, wherein said substrate is a small organic compound which size can range for example from MW 288 (testosterone) to MW 1203 (cyclosporine A).

39. The method of claim 38, wherein said substrate is testosterone.

40. A computer-assisted method for performing restrained dynamics docking of at least two substrates on an enzyme, a 3-D structure of which is available, comprising the steps consisting of performing the steps depicted in claim 27 with a first substrate and repeating said steps with a second substrate when the first substrate reaches an unconstrained state after molecular dynamics simulation..

41. The method of claim 40, wherein the first and second substrates are the same molecule.

42. The method of claim 40, wherein the first and second substrates are different molecules.

43. The method of claim 41, wherein the first and second substrates display an allosteric effect.

44. The method of claim 41, wherein the first and second substrates display a synergistic effect.

45. The method of claims 41 and 42, wherein at least one of the substrates is an inhibitor or display an inhibitor-based mechanism.

46. The method of claims 41 and 42, wherein at least one of the substrates is an agonist.

47. The method of claim 40 comprising successively repeating the steps of claim 20 with a 3rd, 4th or 5th substrate, some of them being the same or different molecules.

48. The method of claim 40, wherein said fixed atoms in step **k.** are the backbone atoms N-Cα-CO in the first minimization step and only Cα in subsequent minimization steps.

49. The method of claim 40, wherein said kinetic energy is simulated by temperature increase to about 100 K for about 5-20 ns.

50. The method of claim 40, wherein said force field in step **j.** comprises forces linked to:

a. the distance between atoms,

b. the angles of valence

c. the dihedral angles,

d. the deformation with regard to planar geometry,

e. the electrostatic field,

f. the Van der Waals forces

g. hydrogen bonds

51. The method of claim 40, wherein said constraints in step **p.** are attraction constraints to force said substrate in the active site, and wherein said constraints are not prejudiced to the exact spatial conformation of the substrate in the active site.

52. The method of claim 51, wherein said constraints are final distance constraints between some atoms of said substrate and some atoms of amino-acids present in said active site.

53. The method of claim 40, wherein step **o.** is performed with a simulated temperature of between about 15 and 50 K.

54. The method of claim 40, wherein step **q.** is performed with a simulated temperature of between about 15 and 50 K.

55. The method of claim 40, wherein step **r.** is performed with a simulated temperature of between about 200 and 350 K.

56 The method of claim 40, wherein said enzyme is a cytochrome P450 subfamily 3A comprising mammal and human cytochromes P450 3A.

57. The method of claim 56, wherein said cytochrome is cytochrome P450 3A4, and said structure is the structure obtained by the method of claim 15, in particular the model structure of claim 22.

58. The method of claim 40, wherein said first and second substrates are small organic compounds which size can range from MW 288 (testosterone) to MW 1203 (cyclosporine A).

59. The method of claim 58, wherein said substrate is testosterone.

60. The use of the method according to claim 27 or 40 for screening, designing or identifying natural, unnatural substrates or substrate analogs, as well as inhibitors, activators or modulators of said enzyme.

61. The use of the method according to claim 40 or 47 for determining the effect of a first substrate on a second substrate.

62. The use according to claim 61 applied to pharmaceutical products.

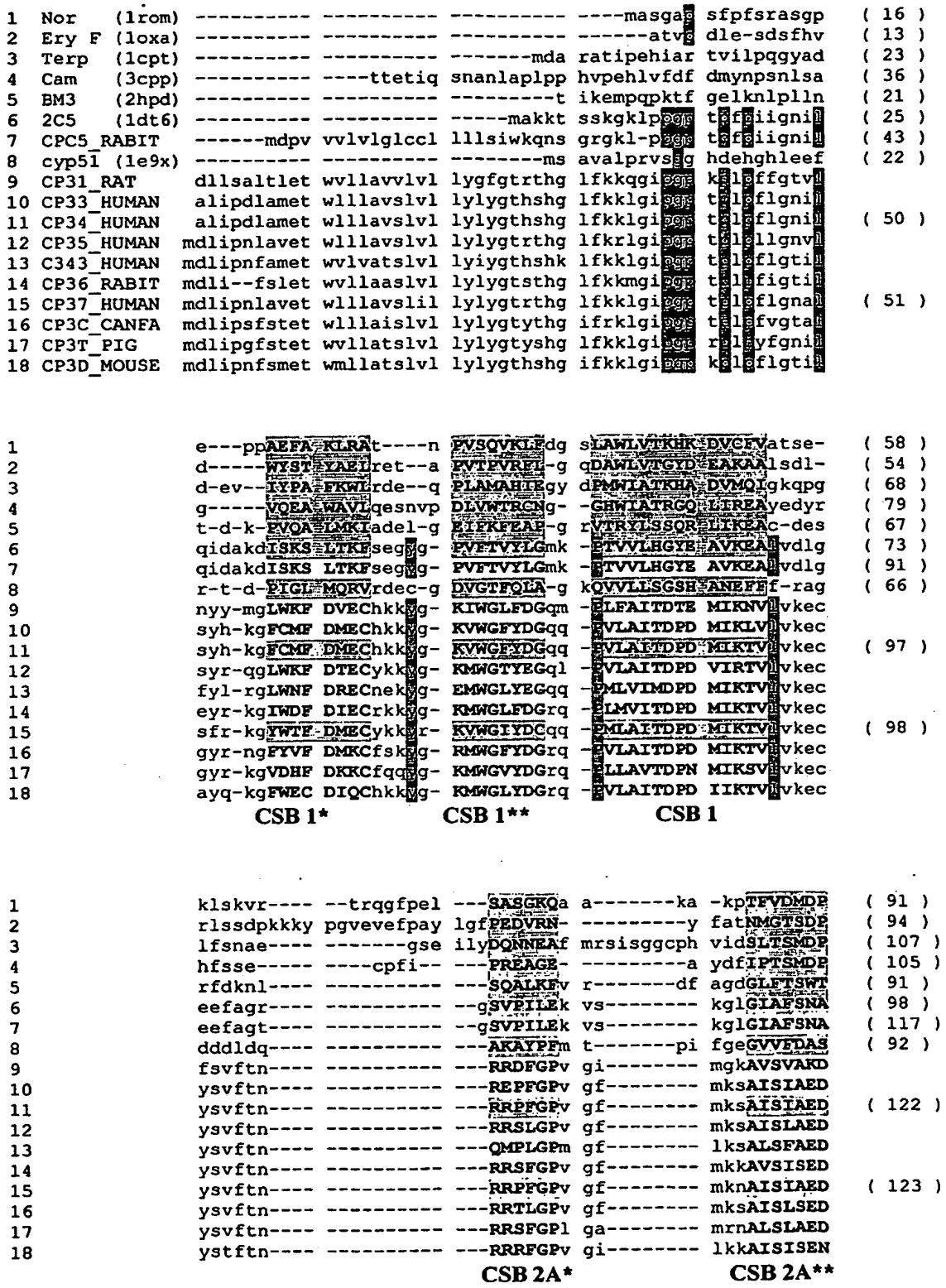
63. The use of the method according to claim 40 or 47 for determining the effect of a first testosterone molecule on a second testosterone molecule.

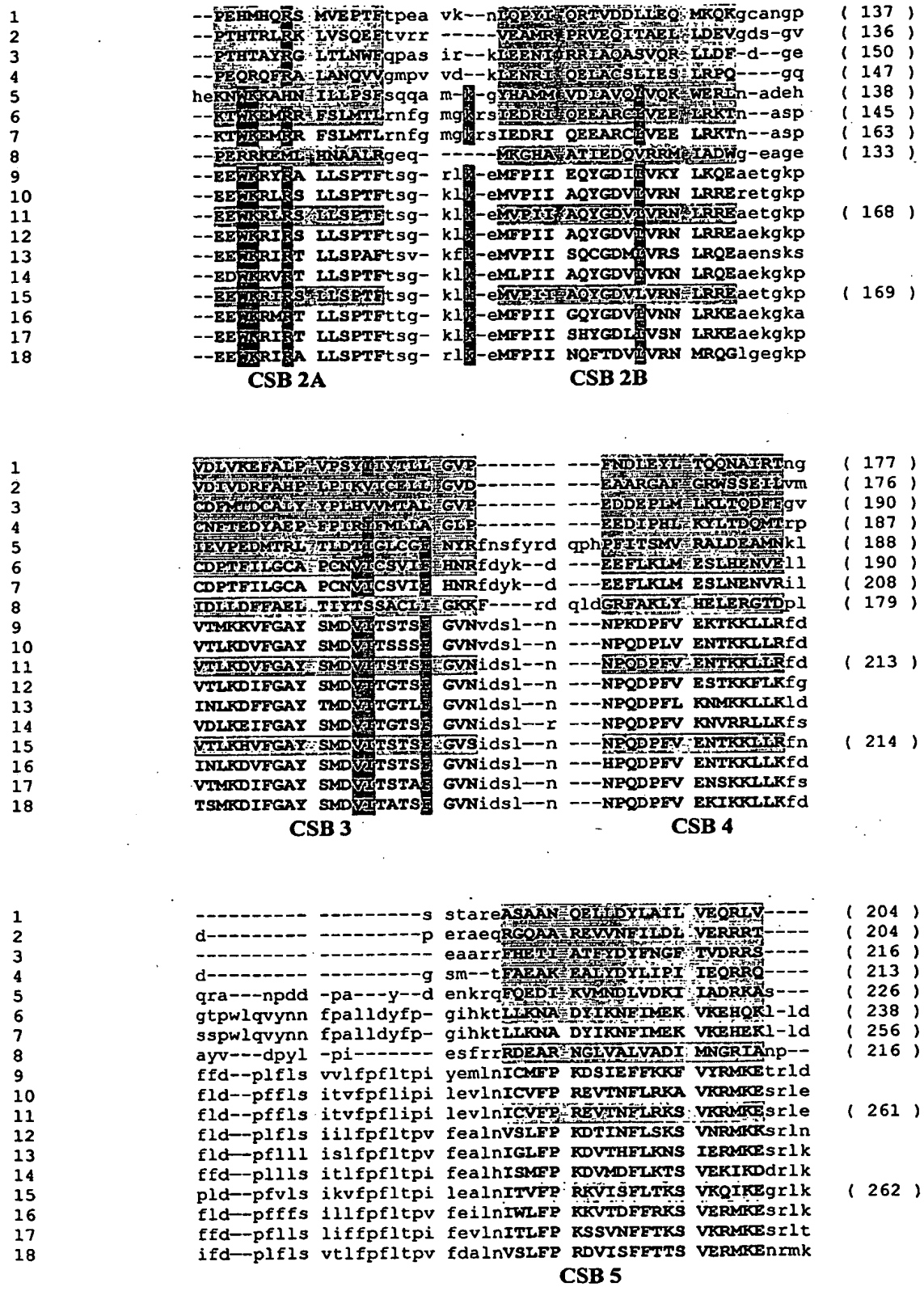
64. The use of the method according to claim 40 or 47 for determining the effect of a first testosterone molecule on a second alpha-naphtoflavone molecule.

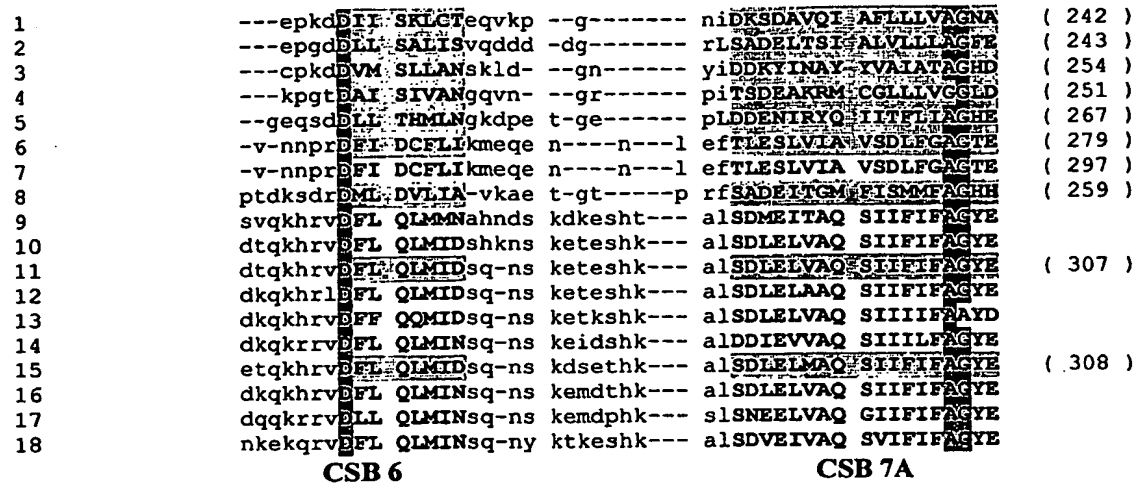
65. The use of the method according to claim 27 to 47 for determining the oxidative modification of the substrate according to the proximity to the heme of a part of the substrate.

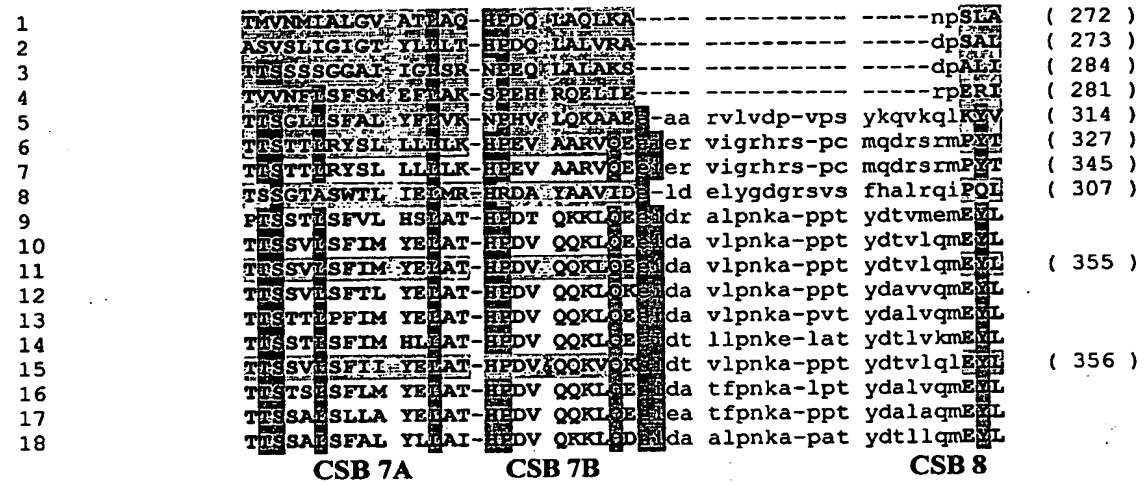
66. The use of the method according to claim 27 to 39, or 40 to 47, for performing dynamic docking of the said metabolite, either in the absence or in the presence of the second substrate in the computed simulation.

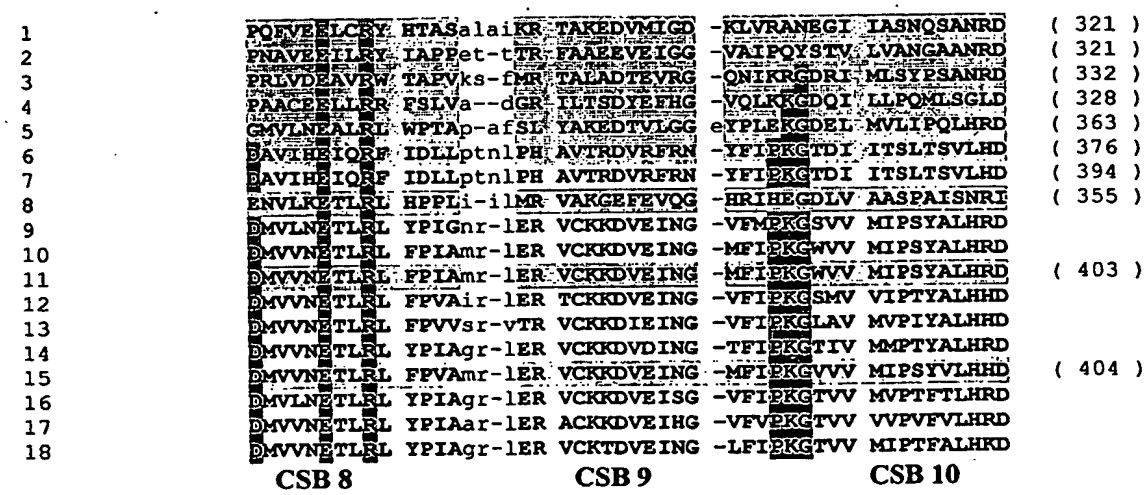
67. The use of the method according to claims 27 to 39, or 40 to 47, to compare the energy of the bound metabolite relatively to the energy of its parent substrate bound, in order to determine if the exit of the given metabolite from the enzyme is favored or not.

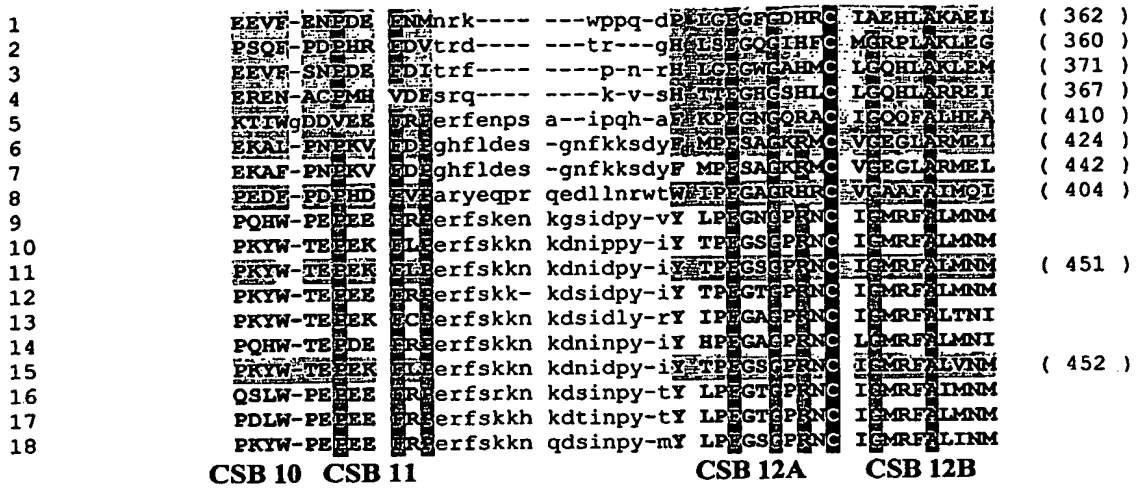

CSB 1*
CSB 1**
CSB 1
CSB 2A*
CSB 2A**


CSB 2A
CSB 2B
CSB 3
CSB 4
CSB 5


CSB 6
CSB 7A


CSB 7A
CSB 7B
CSB 8


CSB 8
CSB 9
CSB 10



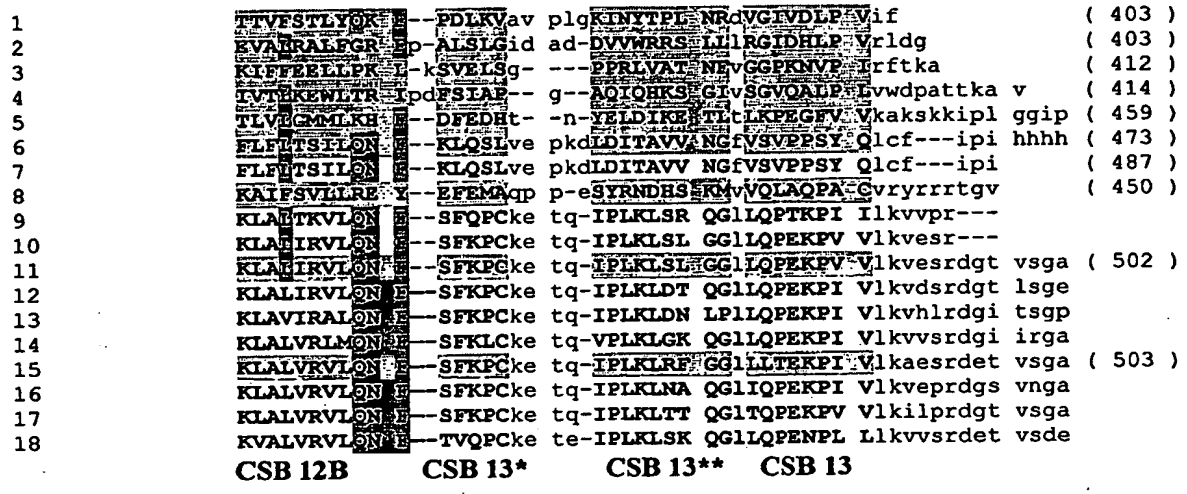
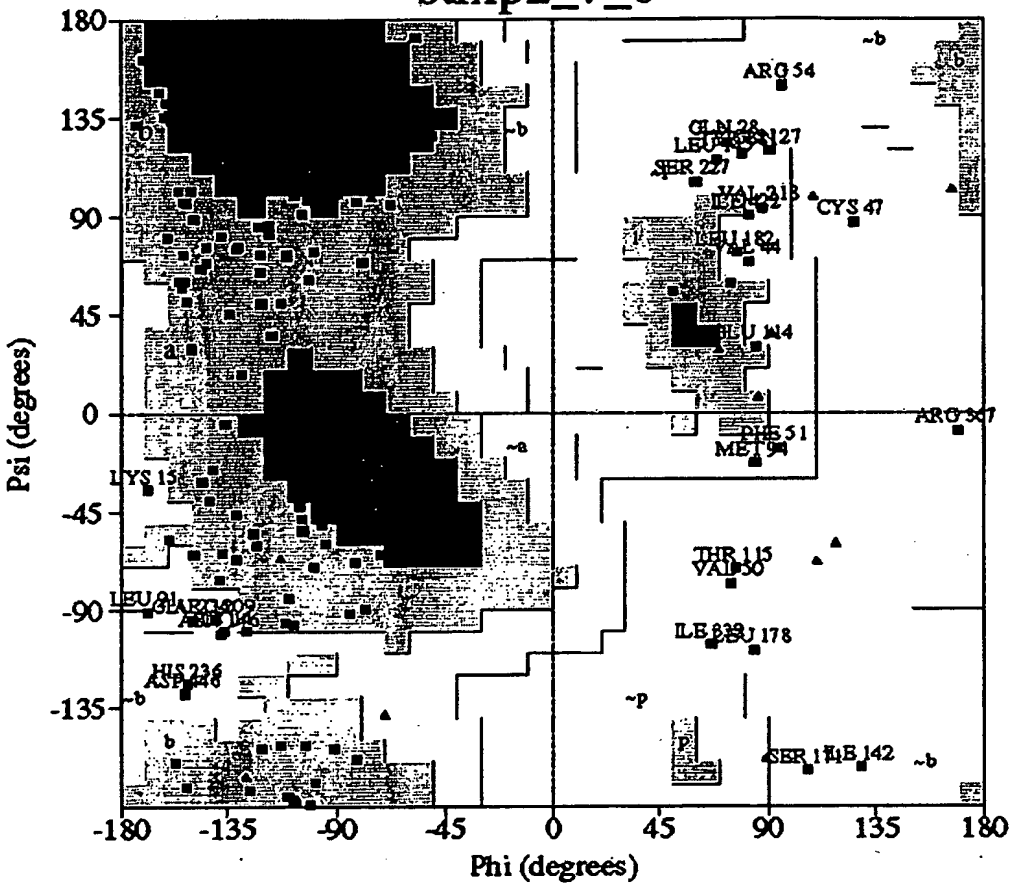


FIGURE 1

PROCHECK

Ramachandran Plot

strxp2_7_0



Plot statistics

Residues in most favoured regions [A,B,L]	291	72.9%
Residues in additional allowed regions [a,b,l,p]	79	19.8%
Residues in generously allowed regions [~a,~b,~l,~p]	20	5.0%
Residues in disallowed regions	9	2.3%
Number of non-glycine and non-proline residues	399	100.0%
Number of end-residues (excl. Gly and Pro)	2	
Number of glycine residues (shown as triangles)	21	
Number of proline residues	30	
Total number of residues	452	

FIGURE 2

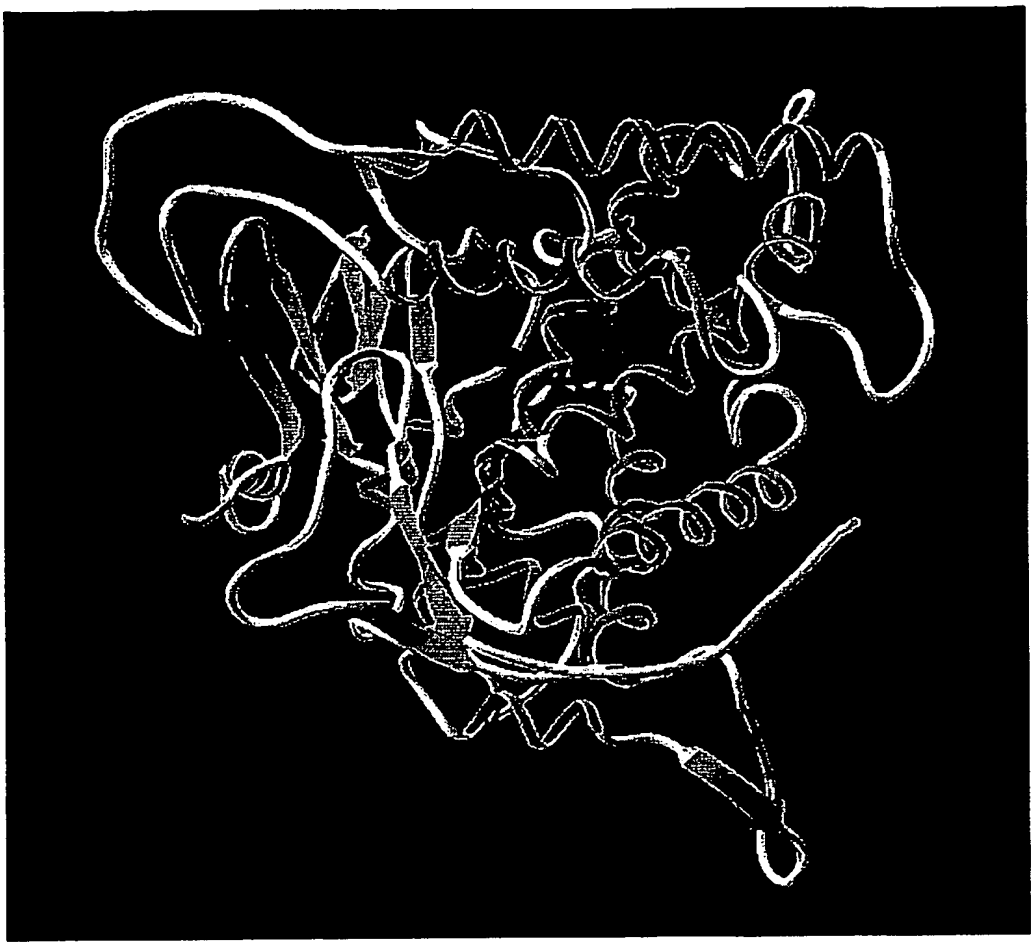
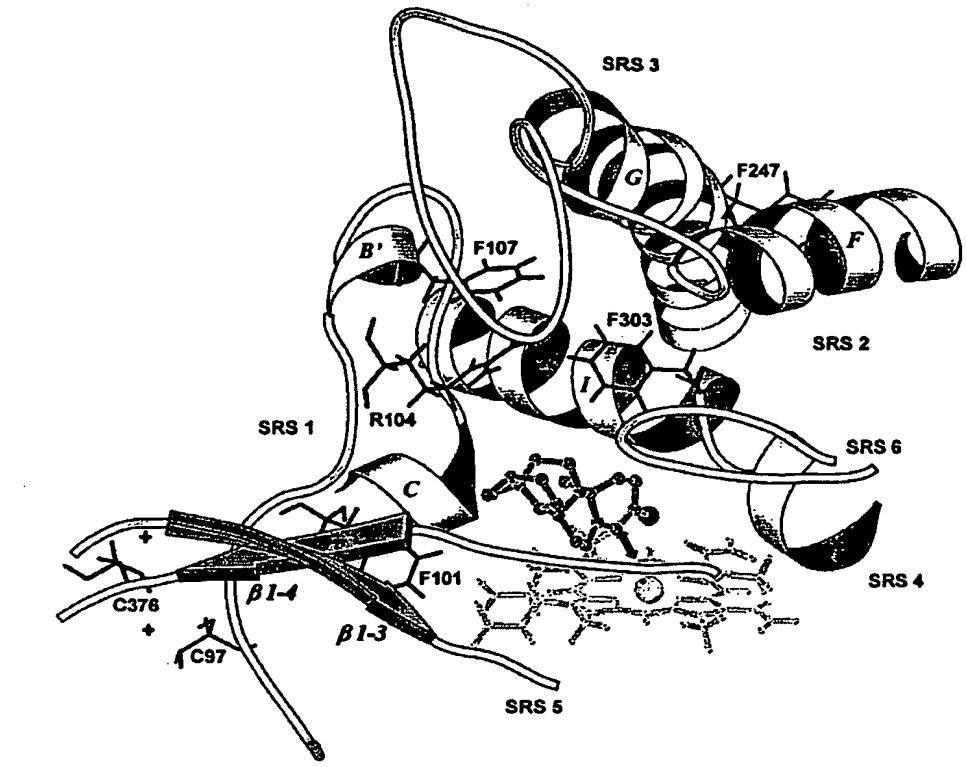


FIGURE 3


SRS 3
G
F247
F
B'
F107
F303
SRS 2
I
SRS 1
R104
SRS 6
C
N
F101
SRS 4
C376
β1-4
β1-3
C97
SRS 5

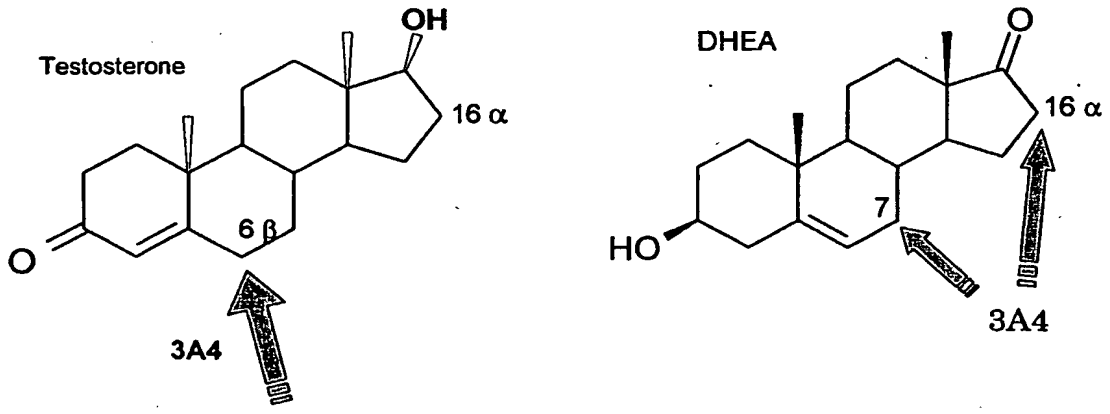
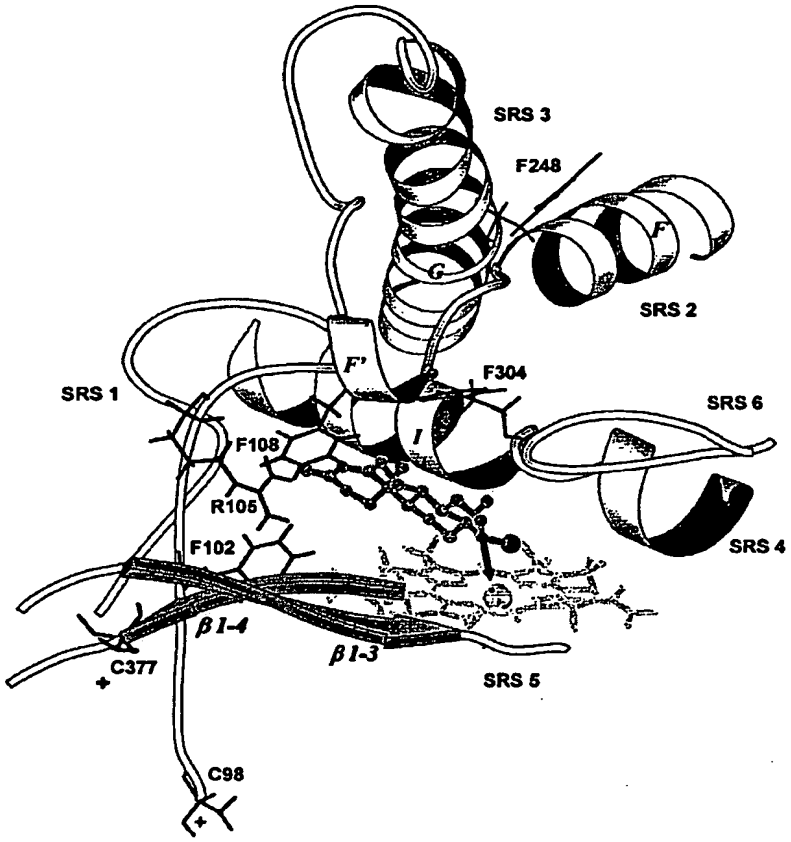

Testosterone
OH
16 α
6 β
O
3A4
DHEA
O
16 α
7
HO
3A4

FIGURE 4A


SRS 3
F248
F
G
SRS 2
F'
F304
SRS 1
SRS 6
I
F108
R105
F102
SRS 4
β1-4
β1-3
C377
SRS 5
C98

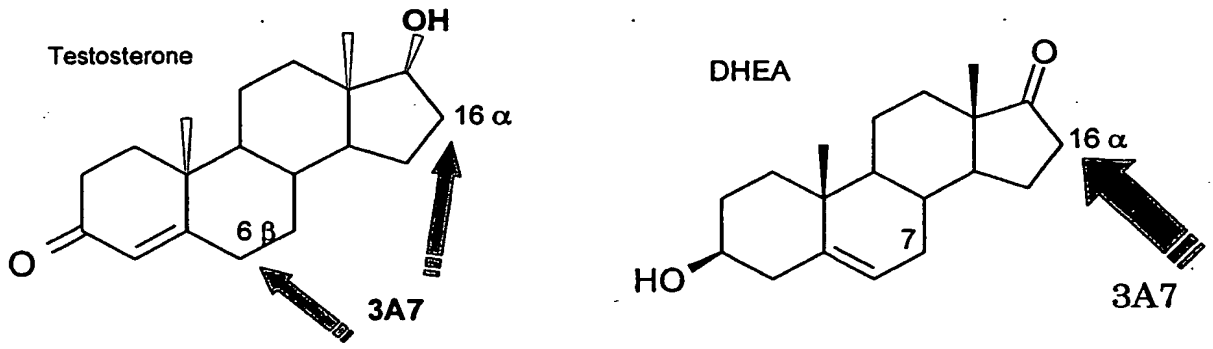

Testosterone
OH
16 α
6 β
O
3A7
DHEA
O
16 α
7
HO
3A7

FIGURE 4B

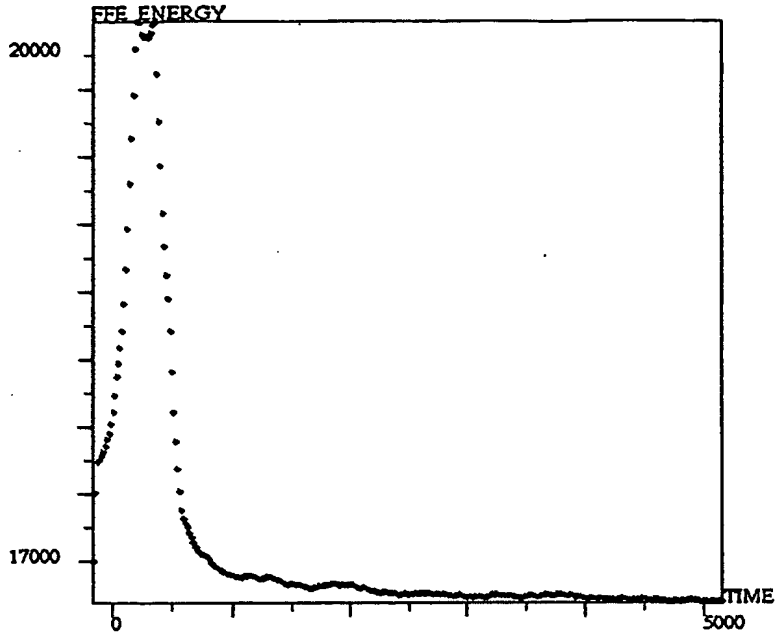


FIGURE 5